

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization  
International Bureau



(43) International Publication Date  
10 April 2003 (10.04.2003)

PCT

(10) International Publication Number  
WO 03/029432 A2

- (51) International Patent Classification<sup>7</sup>: C12N
- (21) International Application Number: PCT/US02/31662
- (22) International Filing Date: 3 October 2002 (03.10.2002)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data:
- |            |                                |    |
|------------|--------------------------------|----|
| 60/327,140 | 3 October 2001 (03.10.2001)    | US |
| 60/334,277 | 28 November 2001 (28.11.2001)  | US |
| 60/352,636 | 28 January 2002 (28.01.2002)   | US |
| 60/412,450 | 20 September 2002 (20.09.2002) | US |

(71) Applicant (for all designated States except US): UNIVERSITY OF SOUTH FLORIDA [US/US]; 4202 East Fowler Avenue, L'AO 126, Tampa, FL 33620-7900 (US).

(72) Inventor; and

(75) Inventor/Applicant (for US only): SESHI, Beerelli [US/US]; 9128 Highland Ridge Way, Tampa, FL 33647 (US).

(74) Agent: RINALDO, Amy, E.; Kohn & Associates, P.L.C., 30500 Northwestern Highway, Suite 410, Farmington Hills, MI 48334 (US).

(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.

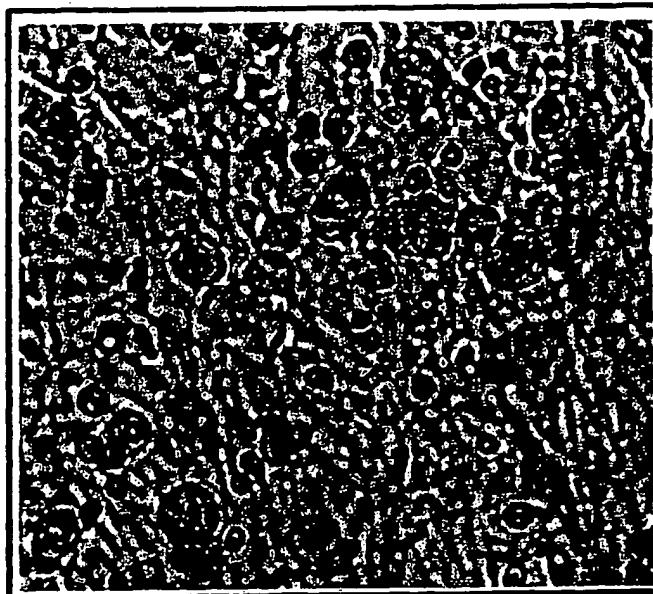
(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: HUMAN MESENCHYMAL PROGENITOR CELL



(57) Abstract: Pluri-differentiated human mesenchymal progenitor cells (MPCs) are isolated. A method isolates and purifies human mesenchymal progenitor cells from Dexter-type cultures for characterization of and uses, particularly therapeutic uses for such cells. Specifically, isolated MPCs can be used for diagnostic purposes, to enhance the engraftment of hematopoietic progenitor cells, enhance bone marrow transplantation, or aid in the treatment or prevention of graft versus host disease.



WO 03/029432 A2

## **HUMAN MESENCHYMAL PROGENITOR CELL**

### **FIELD OF THE INVENTION**

The present invention generally relates to pluri-differentiated mesenchymal progenitor cells and therapeutic uses for the same. More specifically, the isolated mesenchymal progenitor cells are isolated from hematopoietic cells and macrophages in Dexter-type cultures cells.

### **BACKGROUND OF THE INVENTION**

Bone marrow, the site of blood cell production and home to various leukemia and lymphoma cells, comprises a complex cellular population including hematopoietic progenitor or stem cells and the stromal cells that support them. Hematopoietic stem cells have the capacity for self-regeneration and for generating all blood cell lineages while stromal stem cells have the capacity for self-renewal and for producing the hematopoietic microenvironment.

Two bone-marrow culture systems introduced in the mid-1970's have evolved as favored media for the *in vitro* analysis of mesengensis and hematopoiesis. The Friedenstein culture system was introduced in 1976 as a media for the analysis and study of mesengensis. (Friedenstein, et al, in *Exp Hematol* 4,267-74 (1976). In order to obtain mesenchymal stem cells (MSCs) for expansion in the culture medium, it is necessary to first isolate rare pluripotent mesenchymal stem cells from other cells in the bone marrow. In the Friedenstein culture system, isolating the nonhematopoietic cells is achieved by utilizing their tendency to adhere to plastic. Once isolated, a monolayer of homogeneous, undifferentiated stromal cells is then grown in the culture medium, in the absence of hematopoietic cells. The stromal cells from this system have the potential to differentiate into discrete mesenchymal tissues, namely bone, cartilage, adipose tissue and muscle depending on specific growth supplements. These MSCs have been the target of extensive investigation including exploration of their potential clinical utility in repair or replacement of genetically damaged mesenchymal tissues.

In 1977, Dexter, *et al.* developed another bone marrow culture system for the study of hematopoiesis. (Dexter et al. *J Cell Physiol* 91, 335-44 (1977). The Dexter culture does not require isolation of the mesenchymal cells before culturing. Thus, the monolayer of stromal cells is grown in the presence of hematopoietic cells. Greenberger later modified the Dexter system by the addition of hydrocortisone to

the culture medium, making it more reproducible (Greenberger, *Nature* 275, 752-4 (1978)).

Based on the Dexter system's ability to support sustained growth and preservation of hematopoietic progenitor cells, it has become the standard *in vitro* model for the study of hematopoiesis. Although the Dexter-type stromal cells and the MSCs in Friedenstein-type cultures express similar cytokine/growth factor profiles, the Dexter cultures have been found to be more efficient at maintaining preservation of hematopoietic progenitor cells. Over the last 23 years, questions have remained as to whether the cells from the Dexter cultures retained the potential to differentiate, like the MSCs in the Friedenstein culture, or whether they have differentiated into another and discrete phenotype due to their interaction with the hematopoietic cells (Prockop, *Science* v276 n5309, p71(4)(April 1997)). It has been widely believed that the stromal cells of the Dexter cultures are a heterogeneous mixture of adipocytes, osteoblasts, fibroblasts, muscle cells, and vascular endothelial cells.

The *in vitro* analysis and study of hematopoiesis in Friedenstein and Dexter culture systems has been of great importance in both veterinary and human medicine. A number of diseases and immune disorders, as well as malignancies, appear to be related to disruptions within the hematopoietic system.

Allogeneic bone marrow transplantation is the preferred treatment for a variety of malignant and genetic diseases of the blood and blood-forming cells. The success rate of allogeneic bone marrow transplantation is, in large part, dependent on the ability to closely match the major histocompatibility complex of the donor cells with that of the recipient cells to minimize the antigenic differences between the donor and the recipient, thereby reducing the frequency of host-versus-graft responses and graft-versus-host disease (GvHD). Unfortunately, only about 20% of all potential candidates for bone marrow transplantation have a suitable family member match.

Bone marrow transplantation can be offered to those patients who lack an appropriate sibling donor by using bone marrow from antigenically matched, genetically unrelated donors (identified through a national registry), or by using bone marrow from a genetically related sibling or parent whose transplantation antigens differ by one to three of six human leukocyte antigens from those of the patient. Unfortunately, the likelihood of fatal GvHD and/or graft rejection increases from 20%

for matched sibling donors to 50% in the cases of matched, unrelated donors and un-matched donors from the patient's family.

The potential benefits of bone marrow transplantation have stimulated research on the cause and prevention of GvHD. The removal of T cells from the bone marrow obtained from matched unrelated or unmatched sibling donors results in a decreased incidence of graft versus host reactions, but an increased incidence of rejection of the allogeneic bone marrow graft by the patient.

Current therapy for GvHD is imperfect, and the disease can be disfiguring and/or lethal. Thus, risk of GvHD restricts the use of bone marrow transplantation to patients with otherwise fatal diseases, such as severe immunodeficiency disorders, severe aplastic anemia, and malignancies.

The potential to enhance engraftment of bone marrow or stem cells from antigenically mis-matched donors to patients without graft rejection or GvHD would greatly extend the availability of bone marrow transplantation to those patients without an antigenically matched sibling donor.

Thus, it would be useful to develop methods of improving and/or enhance bone marrow transplantation by enhancing the engraftment of bone marrow or hematopoietic progenitor cells and/or decreasing the occurrence of graft rejection or GvHD in allogenic transplants.

Studies of hematopoiesis and mesengensis and the urgent need for improved methods of treatment in the field of bone marrow transplants have led to the isolation of MSCs from bone marrow stroma. These MSCs are the same pluri-potential cells that result from expansion in Friedenstein type cultures. Several patents describe the isolation and therapeutic uses of these MSCs.

U.S. Patent No. 5,486,359, to Caplan, *et al.*, discloses isolated human MSCs, and a method for their isolation, purification, and culturing. Caplan, *et al.* also describes methods for characterizing and using the purified mesenchymal stem cells for research, diagnostic, and therapeutic purposes. The invention in '359, to Caplan, *et al.*, describes pluri-potential cells that remain pluri-potential, even after cultural expansion. Caplan, *et al.* also teaches that it is necessary to first isolate the pluri-potent MSCs from other cells in the bone marrow and then, in some applications, uses culture medium to expand the population of the isolated MSCs. The Caplan *et al.* patent fails to disclose the use of Dexter-type cultures, pluri-



differentiated mesenchymal progenitor cells, or the isolation of cells from Dexter-type cultures.

U.S. Patent No. 5,733,542, to Haynesworth, *et al.*, discloses methods and preparations for enhancing bone marrow engraftment in an individual by administering culturally expanded MSC preparations and a bone marrow graft. U.S. Patent 6,010,696, to Caplan, *et al.*, discloses methods and preparations for enhancing hematopoietic progenitor cell engraftment in an individual by administering culturally expanded MSC preparations and hematopoietic progenitor cells. The cells utilized in the Haynesworth, *et al.* patent and the '696 patent to Caplan, *et al.* are the pluri-potential cells described in U.S. Patent 5,486,359. Neither patent discloses the use of Dexter-type cultures, pluri-differentiated mesenchymal progenitor cells, or the isolation of cells from Dexter-type cultures.

Mesenchymal stem cells that are isolated from bone marrow are further described by Prockop, in *Science* v276 n5309, p71 (4)(1997) and Pittenger, *et al.* in *Science* v284 i5411, p143 (1). These articles also describe pluri-potential but undifferentiated MSCs and fail to teach or disclose a pluri-differentiated mesenchymal cell or the isolation of mesenchymal cells from Dexter-type cultures.

While the cells disclosed in the prior art may provide some benefit, the isolated MSCs in the prior art have not solved the problems associated with engraftment of hematopoietic progenitor cells or bone marrow. Consequently, there exists a need in the art for methods of improving engraftment of hematopoietic progenitor cells and bone marrow in mammals in need of such treatment. There also exists a need in the art for treating and preventing the occurrence of GvHD in mammals that receive allogeneic bone marrow transplants.

#### **SUMMARY OF THE INVENTION**

According to the present invention there is provided isolated pluri-differentiated mesenchymal progenitor cells, a method of isolation, diagnostic uses, and therapeutic uses relating to enhancing the engraftment of human bone marrow or hematopoietic progenitor cells and treating GvHD.

The present invention provides an isolated mesenchymal progenitor cell that is pluri-differentiated.

Accordingly, the present invention also provides a method for purifying pluri-differentiated mesenchymal progenitor cells including the steps of: providing a

cell culture preparation by the Dexter method, treating the cells to obtain a cell suspension, removing macrophages, fractionating the cells, and collecting the fraction of pluri-differentiated mesenchymal progenitor cells.

The present invention also provides a method for enhancing bone marrow engraftment in a mammal in need thereof which includes administering to  
5 the mammal (i) isolated pluri-differentiated mesenchymal progenitor cells and (ii) a bone marrow graft, wherein the pluri-differentiated mesenchymal progenitor cells are administered in an amount effective to promote engraftment of the bone marrow in the mammal.

10 The present invention provides a method for enhancing engraftment of hematopoietic progenitor cells in a mammal in need thereof which includes the step of administering to the mammal (i) isolated pluri-differentiated mesenchymal progenitor cells and (ii) hematopoietic progenitor cells, wherein the pluri-differentiated mesenchymal progenitor cells are administered in an amount effective  
15 to promote engraftment of the hematopoietic progenitor cells in the mammal.

Another embodiment of the present invention provides a method for treating graft-versus-host disease (GvHD) in a mammal about to undergo bone marrow or organ transplantation or suffering from GvHD caused by bone marrow or organ transplantation, by administering to the mammal an effective amount of  
20 isolated pluri-differentiated mesenchymal progenitor cells.

Yet another embodiment of the present invention provides a method for diagnosing a disease state by: a) establishing gene expression patterns of normal state bone marrow derived isolated pluri-differentiated mesenchymal progenitor cells; b) establishing gene expression patterns of various leukemic state  
25 bone marrow derived isolated pluri-differentiated mesenchymal progenitor cells; c) identifying gene sets that are unique to a given state; and d) comparing a profile of bone marrow derived isolated mesenchymal progenitor cell of unknown state to the gene sets.

Additionally, the present invention provides a method for identifying  
30 therapeutic targets for treatment of hematopoietic function by: a) determining the median gene expression profile of bone marrow isolated pluri-differentiated mesenchymal progenitor cells associated with each disease state of interest; b)

identifying gene groups that are up-regulated, down regulated, and common to each disease state; and c) identifying gene sets that are unique to a given state.

The present invention also includes therapeutic compositions including isolated pluri-differentiated mesenchymal progenitor cells and a pharmaceutically acceptable carrier, wherein the pluri-differentiated mesenchymal progenitor cells are present in an amount effective to enhance bone marrow engraftment in a mammal in need thereof; enhance hematopoietic progenitor cell engraftment in a mammal in need thereof; or treat GvHD in a mammal about to undergo bone marrow or organ transplantation or suffering from GvHD caused by bone marrow or organ transplantation.

### **BRIEF DESCRIPTION OF THE FIGURES**

Other advantages of the present invention can be readily appreciated as the same becomes better understood by reference to the following detailed description when considered in connection with the accompanying drawings. The following is a brief description of the drawings which are presented only for the purposes of further illustrating the invention and not for the purposes of limiting same. Referring to the drawing figures, like reference numerals designate identical or corresponding elements throughout the several figures.

Figure 1 is a photograph showing the phase contrast photomicrograph view of a Dexter-type stromal cell monolayer reflecting on cellular complexity.

Figure 2 is a photograph showing the percoll gradient centrifugation technique of the present invention that purifies the MPCs (2) in large quantities to greater than 95% purity.

Figure 3 is a photograph showing the Wright-Giemsa staining of Dexter-type stromal cell cultures depicting three morphologically identifiable cell populations, macrophages (5), hematopoietic cells (3), and the mesenchymal progenitor cells (4) of the present invention.

Figures 4A-H show a series of photomicrographs showing the morphologic and phenotypic characteristics of the MPCs of the present invention, as uncovered by staining for representative mesenchymal cell lineage markers. The methods applied are shown in parentheses. (Figure 4A) Wright-Giemsa (Harleco stain using HMS Series Programmable Slide Stainer, Carl Zeiss, Inc.). (Figure 4B) Immunostain using anti-CD68 antibody (Immunotech, Clone PG-M1; Vector,

Vectastain Elite ABC Kit). (Figure 4C) Immunostain using anti-CD45 antibody (Dako, Clone PD7/26 & 2B11; ABC Kit). (Figure 4D) Periodic acid-Schiff (Sigma). (Figure 4E) Nile Red (Sigma), counterstained with DAPI (Vector). (Figure 4F) Alkaline phosphatase (Sigma Kit No. 85), counterstained with Nuclear Fast Red (Baker).  
 5 (Figure 4G) Immunostain using antibody to fibronectin (Immunotech, Clone 120.5; ABC Kit). (Figure 4H) Immunostain using anti-muscle actin antibody (Ventana, clone HUC 1-1; Ventana system using a section of formalin-fixed, paraffin-embedded cell block, instead of a cytospin). Appropriate positive controls and isotype-matched negative controls were employed to ascertain antibody staining-specificity. All parts  
 10 of figure as shown, except 4E and 4H, have clearly identifiable built-in cell controls. The morphological features of the cells are listed in row 1 of Table 1.

Figure 5 is a photograph which shows a transmission electron micrograph of an MPC of the present invention bearing microvilli, irregular nucleus, and pools of glycogen (6) in the ectoplasm (x 4,600).

15 Figure 6A-M are photographs which show Northern blot analysis of bone marrow stromal cell RNAs for expression of genes specific for multiple mesenchymal cell lineages. Figures 6A-M represent different gene probes used for hybridization. The following outlines the sources of the gene probes employed and the approximate sizes of the major transcripts observed (shown in parentheses):  
 20 Figure 6A) CD68 (Clone ID 3176179, Genome Systems, Inc (GSI); 2-3 kb); Figure 6B) Cathepsin B (Clone ID 2806166, GSI; 2-3 kb); Figure 6C) GAPDH probe (generated using PCR primers from R&D Systems, Inc; ~2 kb) hybridized to same blot as A and B; Figure 6 D) Adipsin (probe generated using PCR primers as described, Ref 20; 0.5-1 kb); Figure 6E) Osteoblast-specific cadherin-11 (Clone ID  
 25 434771, GSI; ~3 kb); Figure 6F) Chondroitin sulfate proteoglycan 2 (Clone ID 1623237, GSI; >10 kb); Figure 6G) Collagen type I alpha 1 (Clone ID 782235, GSI; >10 kb); Figure 6H) Decorin (Clone ID 3820761, GSI; 2-3 kb); Figure 6I) GAPDH probe hybridized to same blot as D-H; Figure 6J) Fibronectin (Clone ID 3553729, GSI; >10 kb); Figure 6K) Caldesmon (Clone ID 1319608, GSI; ~4 kb); Figure 6L)  
 30 Transgelin (Clone ID 4049957, GSI; ~1.5 kb); and Figure 6M) GAPDH probe hybridized to same blot as J-L.

Figure 7 is a photograph which shows RT-PCR analysis for expression of representative hematopoietic growth factors (G-CSF and SCF) and extracellular

matrix receptors (ICAM-1, VCAM-1, and ALCAM) by the MPCs of the present invention.

Figure 8 is a graph comparing of the ability to support *in vitro* hematopoiesis by the purified MPCs (heavy fraction represented by gray) of the present invention vs. unfractionated bone marrow stromal cells (represented by black).

Figures 9A and Figure 9B are graphs showing flow cytometric evidence of human hematopoietic cell engraftment in a SCID mouse cotransplanted with the MPCs of the present invention. Figure 9A shows CD45+/CD34+ progenitors in the marrow. Figure 9B shows CD45/CD34- mature hematopoietic cells circulating in the blood.

Figures 10A-H are photographs which show engraftment of human hematopoietic cells in a SCID mouse cotransplanted with the purified marrow MPCs of the present invention. Figure 10A shows a serial section of a mouse spleen stained with H & E. Figure 10B shows a serial section of a mouse spleen stained with immunoperoxidase stain for CD45. Figure 10C shows bone marrow stained for CD45. Figure 10D shows a serial section of the mouse liver stained with H&E depicting involvement of periportal areas. Figure 10E shows a serial section of the mouse stomach stained with H&E showing transmural infiltration. Figure 10F shows a serial section of the mouse lung stained with H&E showing involvement of peribronchial area. Figure 10G shows a serial section of the mouse pancreas stained with H&E. Figure 10H shows a serial section of the mouse paravertebral ganglia stained with H&E.

Figure 11A is a photomicrograph of a serial section of the spleen of a normal BALB/C mouse showing white pulp populated by darkly staining lymphocytes (H&E). Figure 11B is a photomicrograph of the spleen of a SCID mouse showing white pulp largely consisting of lightly staining stromal framework (H&E). Figure 11C is a photomicrograph of the spleen of a SCID mouse cotransplanted with human bone marrow MNC and the purified bone marrow MPCs of the present invention showing homing (engraftment) of human B cells to white pulp.

Figures 12A-C are photographs which show Southern blotting data. Figure 12A shows that hybridization of sample DNA using a DNA probe specific for human chromosome 17 alpha satellite DNA (p17H8) results in a 2.7 Kb band (7)

(arrow; autoradiogram exposed for only 45 minutes). Figure 12B shows EcoR1 digest of thymic genomic DNA from SCID mice. Figure 12C shows EcoR1 digest of lymph node genomic DNA from SCID mice. Figure 13A and Figure 13B show graphs comparing the survival rate and engraftment of human hematopoietic cells in SCID mice cotransplanted with the purified bone marrow MPCs of the present invention vs. unpurified bone marrow stromal cells. In the line graphs provided the line with diamonds represents MPCs and bone marrow mononuclear cells, squares represents bone marrow mononuclear cells only, triangles represents unfractionated bone marrow stromal cells, the Xs represent MPCs only, and the circles represent the control. In the bar graphs, the gray bars represent mice that survived and the black bars represent mice with engraftment. Figures 14A-C are photographs which demonstrate apoptosis by TUNEL assay in organs of SCID mice that died after transplantation. Figure 14A shows a serial section of the liver of the mouse that survived. Figure 14B shows a serial section of the liver of the mouse that died. Figure 14C shows a serial section of the spleen of the mouse that survived. Figure 14D shows a serial section of the spleen of the mouse that died.

Figure 15 shows photomicrographs of single-cell MPCs that were isolated by laser capture microdissection (LCM) and subsequently targeted for microarray analysis.

Figure 16 shows a Venn diagram displaying the stromal-cell gene-list. Stromal cell genes are operationally defined as being active in at least 9 out of 10 single cell MPCs AND 4 out of 5 collective MPC samples AND 7 out of 8 collective USC samples, i.e., 20 of 23 samples tested. This criterion was very stringent and automatically excluded the outliers, independently of filtering for genes with weak expressions on the basis of control strength (referred to as C or CS). The stromal cell gene list of 2755 includes 13 AFFX microarray-assay positive controls.

Figure 17 shows a two-dimensional hierarchical clustering of 2755 stromal cell genes based on the expression profiles of 23 samples. The gene tree is displayed on top and the experiment or sample tree is shown on left. Accordingly, each column represents a particular gene on the chip and each row represents a separate stromal cell sample.

Figure 18 shows composite gene-expression plots of 2755 stromal cell genes comparing collective purified stromal cell samples (cMPC), collective

unpurified stromal cell samples (cUSC) and single-cell stromal cell samples (sMPC). Individual samples are represented on X-axis. Normalized intensity of gene expression is shown on Y-axis in log scale.

Figures 19 A & B show gene-expression plots of diverse mesenchymal lineage-associated genes and housekeeping genes by collective MPCs and single-cell MPCs. Individual samples are represented on X-axis. Signal intensity of a transcript in log scale normalized across samples is shown on Y-axis. Note the differing log scales, particularly the wide range of log scale for ACTB. Representative lineage markers are shown as follows. Osteoblast markers: osteoblast-specific factor 2 (probe ID 1451\_s-at), osteoblast cadherin 11 (ID 2087\_s\_at) and collagen 1 alpha 2 (ID 32306\_g\_at). Muscle markers: caldesmon (ID 41738\_at), transgelin-2 (ID 36678\_at) and smooth muscle myosin heavy chain (ID 32838\_at). Fibroblast markers: fibronectin (ID 31719\_at) and prolyl 4-hydroxylase (ID 37037\_at). Adipocyte markers: adipsin (ID 40282\_at) and adipocyte-specific ECM protein (ID 39673\_i\_at). Housekeeping genes: GAPD (ID 35905\_s\_at) and ACTB (ID 32318\_s\_at). Samples 1-5, respectively, represent MPC A, MPC B R2, MPC C R2, MPC D R1, MPC D R2. Samples 6-15, respectively, represent SCA1, SCA2, SCA3, SCB1, SCB3, SCC1, SCC3, SCD1, SCD2, SCD3.

Figure 20 shows gene-expression plots of representative precursor B-lymphocyte-associated genes by collective MPCs and single-cell MPCs. Individual samples are represented on X-axis. Signal intensity of a transcript in log scale normalized across samples is shown on Y-axis. Note that the CD markers that are traditionally associated with hematopoietic cells, CD45 (probe ID 40518\_at), CD19 (ID 1116\_at) and CD34 (ID 538\_at), are expressed by sMPCs. CD45, when present, is more abundantly detected in single MPCs than in collective MPCs, and is particularly noticeable by wide range of log scale for CD45. The other pre-B cell associated markers that are expressed by sMPCs are CD10 (ID 1389\_at), HLA-Dr (ID 33261\_at) and CD79A (ID 34391\_at). Samples 1-5, respectively, represent MPC A, MPC B R2, MPC C R2, MPC D R1, MPC D R2. Samples 6-15, respectively, represent SCA1, SCA2, SCA3, SCB1, SCB3, SCC1, SCC3, SCD1, SCD2, SCD3.

Figure 21 shows the master stromal cell table.

### **DETAILED DESCRIPTION OF THE INVENTION**

Generally, the present invention provides isolated and purified mesenchymal progenitor cells that are pluri-differentiated. Also provided by the present invention is a therapeutic composition including an effective amount of isolated and purified pluri-differentiated mesenchymal progenitor cells and a pharmaceutically acceptable carrier.

The terms "enhance" or "improve" as used herein are intended to indicate that there is a more beneficial end result. In other words, the product provides a more effective result.

The term "pluri-differentiated" as used herein refers to cells that are a single cell type co-expressing genes specific for multiple lineages. The term "pluri-potential" as used herein refers to cells that are undifferentiated and have the potential to be differentiated into discrete mesenchymal tissues.

Dexter-type cultures contain stromal cells that co-express multiple message lineage markers. These pluri-differentiated cells are referred to by the inventor as mesenchymal progenitor cells (MPCs). Disclosed herein is a process for isolating and purifying MPCs from Dexter-type cultures. Purified MPCs provide a sufficiently defined system to permit detailed elucidation of the role of bone marrow in normal and leukemic hematopoiesis.

The present invention also provides various methods for using MPCs to enhance bone marrow transplantation, enhance hematopoietic progenitor cell engraftment, for diagnostic purposes, or for the treatment of GvHD.

The exact cell types in Dexter cultures have been identified. No evidence was found for the existence of discrete cellular populations, such as adipocytes, osteoblasts, fibroblasts, smooth muscle cells and endothelial cells, notwithstanding the abundance of literature and wide spread belief (See, J.L. Liesveld *et al.*, *Blood* 73, 1794 (1989); A.K. Sullivan, D. Claxton, G. Shematek *et al.*, *Lab Invest* 60, 667 (1989); K. Dorshkind, *Ann Rev Immunol* 8, 126 (1990); S. Perkins, R.A. Fleischman, *Blood* 75, 620 (1990); I.A. Denkers, R.H. Beelen, G.J. Ossenkoppele *et al.*, *Ann Hematol* 64, 210 (1992); P.E. Penn, D.Z. Jiang, R.G. Fei *et al.*, *Blood* 81, 1205 (1993); E. de Wynter *et al.*, *J Cell Sci* 106, 761 (1993); A. Ferrajoli *et al.*, *Stem Cells (Dayt)* 12, 638 (1994); B.R. Clark, A. Keating, *Ann NY Acad Sci* 770, 70 (1995); B.S. Wilkins, D.B. Jones, *Br J Haematol* 90, 757 (1995); S. Gronthos, P.J. Simmons, *J Hematother* 5, 15 (1996); D. Soligo *et al.*, Abstract



#3926, *Blood* 94, Supplement 1 (Part 2 of 2), p. 168b, Forty 1<sup>st</sup> Annual Meeting of the American Society of Hematology, New Orleans, LA, December 3-7, 1999, M-A. Dorheim *et al.*, *J Cell Physiol* 154, 317 (1993), M.K. Majumdar, M.A. Thiede, J.D. Mosca *et al.*, *J Cell Physiol* 176, 57 (1998), D.J. Prockop, *Science* 276, 71 (1997),  
 5 R.S. Taichman, S.G. Emerson, *J Exp Med* 179, 1677 (1994); R.S. Taichman, M.J. Reilly, S.G. Emerson, *Blood* 87, 518 (1996); C.M. Verfaillie, in *HEMATOLOGY: Basic Principles and Practice*, R. Hoffman, *et al.*, Eds. (Churchill Livingstone, New York, 2000), pp. 140-142.), A.J. Henderson, A. Johnson, K. Dorshkind, *J Immunol* 145, 423 (1990); M.W. Long, J.L. Williams, K.G. Mann, *J Clin Invest* 86, 1387  
 10 (1990); P.J. Simmons, S. Gronthos, A. Zannettino *et al.*, *Prog Clin Biol Res* 389, 271 (1994); B.A. Roecklein, B. Torok-Storb, *Blood* 85, 997 (1995); J. Wineman, K. Moore, I. Lemischka *et al.*, *Blood* 87, 4082 (1996); K.A. Kelly, J.M. Gimble, *Endocrinology* 139, 2622 (1998); K.C. Hicok *et al.*, *J Bone Miner Res* 13, 205 (1998); S.R. Park, R.O. Oreffo, J.T. Triffitt, *Bone* 24, 549 (1999); J.E. Dennis *et al.*, *J Bone Miner Res*  
 15 14, 700 (1999); and B. Torok-Storb *et al.*, *Ann NY Acad Sci* 872, 164 (1999)). Instead, the inventor determined that there are only three types of cells in Dexter-type cultures, namely, macrophages (~35%), hematopoietic cells (~5%), and a type applicant calls "nonhematopoietic cells" (~60%)(Figure 3, Figure 4A, and Table 1).

Bone marrow mesenchymal cells, the nonhematopoietic cells in Dexter  
 20 type cultures, possess distinctive features that have previously gone unrecognized. There is both direct visual (Figures 4A-E and Figure 5) and molecular biological (Figure 6) evidence to support the existence of this unique cell type. These findings challenge the prevailing belief that stromal cells derived from Dexter cultures comprise multiple singly-differentiated mesenchymal cell types. Because Dexter  
 25 cultures represent a primary cell culture system, and not a cell line, these studies indicate that cells in these primary cultures themselves are pluri-differentiated, which has been previously unsuspected. The nonhematopoietic cells of the present invention (MPCs) simultaneously express marker genes specific for multiple mesenchymal cell lineages, including adipocytes, osteoblasts, fibroblasts and  
 30 smooth muscle cells. As shown in the present disclosure, MPCs can also differentiate into B cells and therefore be useful in affecting the functionality of the immune system.

The MPCs in Dexter type cultures were characterized using a variety of techniques. Cytospins were prepared using aliquots of unfractionated cells for performance of various cytological, cytochemical and immunocytochemical stains. Reactivity patterns of the bone marrow culture cells are outlined in Table 1. Figures 4A-E illustrate morphologic and phenotypic characteristics, as uncovered by staining for representative cell lineage markers.

Only rarely have investigators in this field taken the approach of preparing a cell suspension and staining cells on cytospins as was done to characterize the cells of the present invention (Simmons, *et al.*, *Nature* 328, p429-32 (1987)) and no other group has used this method to address the issue of pluridifferentiation by bone marrow stromal cells. Almost all of the published studies in the field, with a rare exception (Simmons, *et al.*, *Nature*, 328, p429-32 (1987)), conducted cytochemical and immunocytochemical staining on layers of stromal cells grown to confluence on coverslips. In this situation, the stromal cultures appear very complex especially in the areas of hematopoietic activity, so-called "cobblestones" with macrophages and hematopoietic cells enmeshed in them. Macrophages and nonhematopoietic cells spread themselves and assume varied shapes when they adhere to and grow on plastic or glass. This spreading further contributes to the perceived heterogeneity and complexity. The complexity precludes a clear morphological visualization of the nonhematopoietic cells and consequently interferes with the determination of what percent of what cell type is positive for any given marker.

In terms of lineage markers, up to 100% of the nonhematopoietic cells or MPCs of the present invention expressed two fat cell markers (Nile Red (Figure 4E) and Oil Red O); an osteoblast marker (alkaline phosphatase (Figure 4F)); and two fibroblast markers (fibronectin (Figure 4G) and prolyl-4-hydroxylase). Greater than 85% of the MPCs were also positive for a muscle marker, actin (Figure 4H). There was no evidence of expression of endothelial cell differentiation, as judged by immunohistochemical staining for CD34 and CD31.

In addition, the Dexter type stromal cells had not previously been subjected to Periodic Acid-Schiff (PAS) staining, which revealed a strong and uniform positivity by almost 100% of the MPCs studied. This indicates the presence of large stores of glycogen (Figure 4D). The presence of glycogen (6) was confirmed

by electron microscopy (see Figure 5). In this respect, MPCs are reminiscent of the glycogen-laden reticular cells in the developing bone marrow of human fetuses (observed by L-T. Chen, L.Weiss, *Blood* 46, 389 (1975)). Glycogen deposition is viewed to be a developmentally regulated process during morphogenesis (H. Ohshima, J. Wartiovaara, I. Thesleff, *Cell Tissue Res.* **297**, 271 (1999)).

The MPCs also exhibited cytoplasm compartmentalization into endoplasm and ectoplasm. This morphologic finding sheds light on their internal architecture because of correlation of restricted localization of glycogen and smooth muscle actin to ectoplasm; and the restricted localization of acid phosphatase, alkaline phosphatase, Nile Red, Oil Red O, fibronectin, and prolyl-4-hydrolase to endoplasm.

Additional sets of multiple mesenchymal lineage markers were assessed by Northern blotting of unfractionated cells and purified MPCs to eliminate any observer bias that might be inherent in morphological assessment. Figures 6A-M represent different gene probes used for hybridization.

Compared to unfractionated cells, the purified nonhematopoietic cells expressed significantly higher levels of markers representing fat cells (adipsin, Figure 6D); osteoblasts (osteoblast-specific cadherin-11, chondroitin sulfate, collagen type 1 and decorin, Figures 6E-H); fibroblasts (fibronectin, Figure 6J); and smooth muscle cells (caldesmon and transgelin, Figures 6K-L).

Taken together, the morphologic, cytochemical, and immunocytochemical results (Figure 4A-H and Table 1), and the Northern blotting data (Figure 6A-M) indicate that the nonhematopoietic stromal cells of the Dexter cultures co-express markers specific for at least four different mesenchymal cell lineages. Using a variety of techniques, applicant has demonstrated that the MPCs co-express multilineage mesenchymal cell phenotypes, and in this respect the multi- or pluri-differentiated MPCs are distinct from the pluri-potential, but undifferentiated, MSCs of Friedenstein cultures (Prockop, *Science* 276, 71-74 (1997)).

The nonhematopoietic cells of the present invention were purified from the macrophages, the dominant "contaminating" cell type, using a Percoll gradient method developed by applicant. MPCs were purified by the following process: cells from a Dexter-type culture were treated to obtain a cell suspension, the macrophages were removed, and the cells were fractionated using discontinuous

Percoll gradient centrifugation (Figure 2). The isolated MPCs were then collected and washed.

The purity of the nonhematopoietic cells was demonstrated by a near complete absence of two macrophage markers, CD68 and cathepsin B (as shown by Northern blotting data, Figure 6A and 6B). As a positive control, bone marrow mononuclear cells rich in myelomonocytic cells abundantly expressed CD68 (lanes 5 & 6, Figure 6A). The Northern blot results are consistent with a purity estimate of ~95% (vs. 60% in unfractionated samples) based on morphology and immunocytochemical staining for CD68.

A purified source of MPCs is desirable for a number of reasons. The relative ease with which large numbers of the MPCs can be purified and their distinctive phenotypic characteristics make them valuable targets for future investigations. Purified MPCs provide a sufficiently defined system to permit detailed elucidation of the role of bone marrow in normal and leukemic hematopoiesis in addition to aiding in bone marrow transplantation.

Another major reason that purified cells are desirable is that Dexter cultures also contain a significant percentage of highly immunogenic macrophages that can cause onset of GvHD after transplantation. The MPCs of the present invention are purified to ~95% free of macrophages and hematopoietic cells. Note the increased survival rate in Severe Combined Immunodeficiency Disease (SCID) mice that received purified MPCs versus those that received unfractionated bone marrow stromal cells in Figure 13B. This data establishes that stromal cells in combination with engraftment or other similar procedures enhances the effectiveness of the treatment.

The present invention also provides methods of enhancing the engraftment of hematopoietic cells and of enhancing the engraftment of bone marrow. The hematopoietic support capacity of the Dexter-type cultures has been repeatedly demonstrated by a number of investigators. RT-PCR analysis showed that Dexter cultures and Friedenstein cultures expressed a similar pattern of cytokine and growth factor mRNAs; yet, Dexter cultures were found to be more efficient than Friedenstein cultures in achieving preservation of hematopoietic progenitors (Majumdar, *et al.*, *J.Cell.Physiol.*, 176, 57-66.). The pluri-differentiated MPC is capable of supporting hematopoiesis, as shown by its ability to express

representative hematopoietic growth factors/cytokines, i.e., G-CSF and SCF as well as matrix receptors/hematopoietic cell adhesion molecules, i.e., ICAM-1, VCAM-1 and ALCAM (Figure 7).

Clarification of the nature of the stromal cells and the ability to purify these cells makes it possible to use them as an adjuvant in bone marrow transplantation following high-dose chemotherapy and radiation therapy. These treatment modalities not only cause damage to the hematopoietic stem cells but also to the supportive stromal cells. However, because the bone marrow microenvironment is destroyed, hematopoietic progenitor cell engraftment is delayed until the stromal environment is restored. As a result, a critical aspect of the current invention is directed to the advantages of transplanting isolated mesenchymal progenitor cells to accelerate the process of stromal reconstruction and ultimately bone marrow engraftment. The stromal cells present in the standard bone marrow transplant are not sufficient in number and can be supplemented with the cultured MPCs of the present invention.

Yet another embodiment of the current invention provides the use of MPC transplantation to major leukemic conditions, such as acute myeloid leukemia (AML), myelodysplastic syndromes (MDS), chronic myeloid leukemia (CML) and multiple myeloma (MM). This is based on applicant's determination that bone marrow stromal cells in a leukemia patient are functionally and structurally defective, regardless of the damage caused by chemotherapy and radiation therapy. Such defects in bone marrow stromal cells are likely to aid and abet leukemia development. Alternatively, stromal cell defects could be secondarily induced by surrounding leukemia cells, thus contributing to the loss of hematopoietic support function of stromal cells and hematopoietic failure, which is an invariable feature in leukemia. Regardless whether the observed stromal cell defects are primary or secondary to the leukemic process, by reason of their indisputable impact on normal hematopoiesis, these defects remain to be corrected to improve the hematopoietic function.

Stromal cells have never been carefully investigated in terms of genomics in view of the widespread belief that they represent a heterogeneous mixture of cell types. Tissue or cellular heterogeneity presents a major challenge for the application of microarray technology. The purified stromal cells of the present

invention represent a single pluridifferentiated MPC which allows for genomic study of the stromal cells and the development of new, more objective diagnostic tools for patients suffering from leukemia conditions.

The present invention provides a comprehensive phenotype of cultured  
5 bone marrow stromal cells at single cell level for the first time. These findings pave the road for ultimate identification and investigation of these cells in fresh samples of marrow, normal as well as diseased, in which they occur at a low frequency and are extremely difficult to study at the present time. The development of this phenotype forms the basis for various diagnostic tests including a comprehensive test that can  
10 be used to screen for different abnormalities of bone marrow stromal cells in various hematologic diseases and other diseases effecting stromal cells.

Results show that isolated single stromal cells simultaneously express transcripts for osteoblasts, fibroblasts, muscle cells and adipocytes. Furthermore, there is shown that isolated single stromal cells simultaneously express transcripts  
15 for epithelial cells and neural/glial cells as well as transcripts for CD45, CD19, CD10, CD79a, and representative proto-oncogenes and transcription factors, typically known to be affiliated with normal and neoplastic hematopoietic cells. These findings are evidence of existence of a progenitor cell that is common to nonhematopoietic mesenchymal cells and hematopoietic cells, particularly B-lymphocytes. "Lineage  
20 burst" characterized by simultaneous activation of diverse differentiation pathways within the same cell appears to be the signature profile of a stromal cell, indicating that a "pluripotent" cell is "pluridifferentiated" at the molecular level. That is, prior to a selective and full-fledged lineage differentiation, progenitors express genes associated with multiple lineages to which they might possibly commit, thus  
25 providing insight into the molecular basis of cellular plasticity.

Transcriptomic analysis has been undeniably contributing to the molecular definition of new disease categories with demonstrable therapeutic benefit. The present invention contributes to the further definition of the stromal cell by refining its molecular signature. The *in vivo* identification of the stromal cell and its  
30 possible ontogenic variants as they might occur in different hematological diseases and subsequent targeting of these cells holds the key to ultimately treating some, if not all, of these diseases.

By comprehensively defining the gene expression profile of these cells, the present invention demonstrates the technical applicability of single-cell genomics toward understanding the physiology and pathology of both hematopoietic and nonhematopoietic microenvironments. Classically, the adventitial reticular cells located on the abluminal side of the vascular endothelium within the bone marrow microenvironment were thought to represent the stromal cells or their precursors. As with hematopoietic stem or progenitor cells, the stromal progenitor cells are rare in bone marrow occurring at an estimated frequency of 1 in  $10^5$  nucleated cells. Cultured stromal cells represent the progeny of the stromal cell, and not necessarily the stromal cell itself, for which no *in vivo* assay exists as yet. The technology of single-cell genomics and the blueprint as described in the present invention allows screening for the abnormalities of bone marrow stromal cells in fresh marrow samples that reflect on the ultimate *in vivo* context.

The ability to purify culture-expanded MPCs from both normal individuals and patients afflicted with various leukemias also allows testing of the hematopoietic supportive role of MPCs in mice models. These systems provide an *in vivo* model in which to examine the role of human bone marrow microenvironment in normal and leukemic hematopoiesis.

The SCID mouse model is an ideal system in which to investigate MPC function. Engraftment of human hematopoietic progenitors in SCID mice has required either coadministration of exogenous human cytokines, or cotransplantation of human bone marrow plugs or bone fragments. As disclosed herein MPCs are a convenient, new source for human bone marrow stromal cells for enhancing transplantation that does not require cytokines, bone fragment, or marrow.

Unlike prior methods, the isolated MPCs of the present invention support human hematopoiesis in the SCID mouse model as effectively as whole marrow stroma. The transplantation of human marrow mononuclear cells combined with purified MPCs results in dramatically vigorous engraftment of human cells in spleen, bone marrow, liver, pancreas, lungs, stomach, and paravertebral neuronal ganglia of SCID mice (Figures 10A-H and Figures 11A-C). By contrast, mice receiving human bone marrow mononuclear cells alone or MPCs alone expectedly showed no detectable evidence of human hematopoietic cell engraftment (Figure 13A and Figure 13B).

The present invention also provides for a method of preventing or treating GvHD. The highest mortality rate, Figure 13B, was observed in mice receiving the unpurified whole marrow stroma and the bone marrow mononuclear cells. The increased mortality observed is related to the presence of highly immunogenic macrophages and consequent GvHD. The mice with the highest survival rate, shown in Figure 13A, were the mice receiving purified MPCs and bone marrow mononuclear cells.

Notably, there is discrete TUNEL-positive nuclei in the liver of the expired mouse in Figure 14B and complete absence of staining in the liver of the surviving mouse ( see Figure 14A). While some ill-defined globules of staining are observed in the spleen of the mouse that survived, the nuclear integrity of most of the cells is well preserved suggesting minimal or no apoptosis (Figure 14C). In contrast, the dead mouse spleen (Figure 14D) showed extensive TUNEL positivity precluding accurate interpretation. Control mouse liver and spleen showed results similar to those of the mouse that survived.

The above results indicate that purified MPCs can support human hematopoiesis in SCID mice as effectively as whole marrow stroma. Equally important is that the purified MPCs increased the survival rate. The evidence shows that the increased survival is due to a reduction in GvHD.

Allogeneic bone marrow transplantation is the preferred method of treatment for a variety of malignant and genetic diseases of the blood and blood forming cells. However, failure of hematopoietic cell engraftment can occur for a number of reasons. These include, microenvironmental defects as part of the underlying disease itself (e.g., aplastic anemia), and/ or stromal cell damage caused by chemoradiotherapy and/ or microenvironmental damage as part of GvHD which is a dreaded complication following bone marrow transplantation. In GvHD, donor T cells present in the hematopoietic cell graft destroy host tissues. GvHD can involve multiple organs such as skin, liver, GI system etc. The current treatment modalities for preventing or treating graft failure or GvHD are cumbersome, costly and involve some form of immunosuppression. Stromal cell lesions, either primary to the disease process or secondarily induced by allogeneic bone marrow transplantation, play a prominent role in the success or failure of the hematopoietic cell graft. Cotransplantation of MPC not only enhances hematopoietic cell engraftment but



also prolongs the life of graft recipients by minimizing GvHD. Co-transplantation of healthy, culture-expanded MPC is a viable option in these situations.

The human bone marrow used in the Dexter-type cultures of the present invention can be obtained from a number of different sources in accordance with the procedures known in the art, including from plugs of femoral head cancerous bone pieces or from aspirated marrow. The cells used in the Dexter culture can be autologous, from the tissue donor, or from other individuals.

Modes of administration of MPCs include, but are not limited to, systemic intravenous injection and injection directly to the intended site of activity. The MPCs can be administered by any convenient route, for example by infusion or bolus injection, and can be administered together with other biologically active agents. Administration is preferably systemic.

The methods of the present invention can be altered, particularly by (1) increasing or decreasing the time interval between administering MPCs and implanting the tissue, cells, or implanting the organs; (2) increasing or decreasing the amount of MPCs administered; (3) varying the number of MPC administrations; (4) varying the method of delivery of the MPCs; and/or (5) varying the source of MPCs.

The MPC preparations are used in an amount effective to promote engraftment of hematopoietic progenitor cells or bone marrow cells; or for the treatment or prevention of GvHD in the recipient. The pharmaceutically effective amount for the purposes herein is thus determined by such considerations as are known in the art. In general, such amounts are typically at least  $1 \times 10^4$  MPCs per kg of body weight and most generally need not be more than  $7 \times 10^5$  MPCs/kg.

The present invention also provides pharmaceutical compositions. Such compositions comprise a therapeutically effective amount of MPCs and a pharmaceutically acceptable carrier or excipient. Such a carrier includes but is not limited to McCoy's medium, saline, buffered saline, dextrose, water, and combinations thereof. The formulation should suit the method of administration as is known by those of skill in the art.

In one embodiment, the MPC preparation or composition is formulated in accordance with routine procedures as a pharmaceutical composition adapted for intravenous administration to human beings. Typically, compositions for intravenous

administration are solutions in sterile isotonic aqueous buffer. Where necessary, the composition can also include a local anesthetic to ameliorate any pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a cryopreserved concentrate in a hermetically sealed container such as an ampoule indicating the quantity of active agent. Where the composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water or saline. Where the composition is administered by injection, an ampoule of sterile water for injection or saline can be provided so that the ingredients can be mixed prior to administration.

The present invention paves the way for applications of mesenchymal progenitor cells in the field of transplantation with respect to hematopoietic support, immunoregulation, and graft facilitation. MPCs can be used as a supporting cell type in bone marrow transplantation, particularly in diseases where defects in the hematopoietic stromal microenvironment are believed to prevail, such as aplastic anemia, myelofibrosis, and bone marrow failure following high dose chemotherapy and radiation therapy.

Another aspect of the invention provides a method for diagnosing various disease states in mammals by identifying new diagnostic markers, specifically the classification and diagnosis of leukemia. Prior to the present invention, stromal cells were not carefully investigated in terms of genomics because of the widespread belief that they represent a heterogeneous mixture of cell types and cellular heterogeneity presents significant challenges for the application of genetic analysis such as microarray technology. The isolated MPCs of the present invention represent a single cell type and allow for genomic study of the stromal cells.

Using the methods of the present invention, it has been determined that bone marrow stromal cells in leukemia patients are functionally and structurally defective regardless of the damage caused by chemotherapy and radiation therapy. Given the almost 25 year history and intense interest in bone marrow stromal cell cultures, previous documentation of stromal cell abnormalities has been disappointingly low (Martinez & Martinez, *Exp. Hematol* 11:522-26 (1983); Budak-Alpdogan, *et al.*, *Am.J.Hematol*, 62:212-20 (1999); Nagao, *et al.*, *Blood*, 61:589-92

(1983); Peled, et al., Exp.Hematol 24:728-37 (1996); Bhatia, et al., Blood 85:3636-45 (1995); Agarwal, et al., Blood 85:1306-12 (1995); Diana, et al., Blood 96:357a(2000)). By identifying gene sets that are unique to a given state, these differences in the stromal cells can be utilized for diagnostic purposes.

5 In one embodiment of the invention, isolated MPCs from a patient are assayed for expression of a large number of genes. The gene expression profile is projected into a profile of gene set expression values according to the definition of gene sets. A reference database containing a number of reference projected profiles is also created from the isolated MPCs of patients with known states, such as normal and various leukemic disease states. The projected profile is then compared with the reference database containing the reference projected profiles. If the projected profile of the patient matches best with the profile of a particular disease state in the database, the patient is diagnosed as having such disease state. Various computer systems and software (see Example 5) can be utilized for  
10 implementing the analytical methods of this invention and are apparent to one of skill in the art. Some of these software programs include Cluster & TreeView (Stanford, URLs: rana.lbl.gov or www.microarray.org), GeneCluster (MIT/Whitehead Institute, URL: MPR/GeneCluster/GeneCluster.html), Array Explorer (SpotFire Inc, URL: http://www.spotfire.com/products/scicomp.asp#SAE) and GeneSpring (Silicon  
15 Genetics Inc, URL: http://www.sigenetics.com/Products/GeneSpring/index.html) (for computer systems and software, see also U.S. Patent No. 6,203,987).

The methods of the present invention can also be useful for monitoring the progression of diseases and the effectiveness of treatments. For example, by comparing the projected profile prior to treatment with the profile after treatment.

25 One aspect of the present invention provides methods for therapeutic and drug discovery utilizing bone marrow derived isolated mesenchymal progenitor cells. The present invention can be utilized to identify stromal cell genes that can be therapeutic targets for improvement of normal hematopoietic function, which is constantly compromised, in leukemic patients. In one embodiment, gene sets are defined using cluster analysis. The genes within a gene set are indicated as  
30 potentially co-regulated under the conditions of interest. Co-regulated genes are further explored as potentially being involved in a regulatory pathway. Identification

of genes involved in a regulatory pathway provides useful information for designing and screening new drugs.

Some embodiments of the present invention employ gene set definition and projection to identify drug action pathways. In one embodiment, the expression changes of a large number of genes in response to the application of a drug are measured. The expression change profile is projected into a gene set expression change profile. In some cases, each of the gene sets represents one particular pathway with a defined biological purpose. By examining the change of gene sets, the action pathway can be deciphered. In some other cases, the expression change profile is compared with a database of projected profiles obtained by perturbing many different pathways. If the projected profile is similar to a projected profile derived from a known perturbation, the action pathway of the drug is indicated as similar to the known perturbation. Identification of drug action pathways is useful for drug discovery. See, Stoughton and Friend, Methods for Identifying pathways of Drug Action, U.S. patent application Ser. No. 09/074,983.

The present invention provides a genomics strategy method for identifying genes differentially expressed in MPCs. The method begins with the preparation of total RNA from MPC samples, which leads to the generation of cDNA. From the cDNA, ds DNA can be prepared for *in vitro* transcription into cRNA. The cRNA is then fragmented for the hybridization of target RNA to a microarray of known genes (Affymetrix genechip containing DNA from ~12,000 known human genes, e.g., U95A oligonucleotide microarray). Finally, analysis of differentially expressed genes is accomplished using appropriate software (GeneSpring) to discern the patterns of gene expression or genomic signatures by a given MPC type (e.g., up-regulation or down-regulation).

Up-regulated and down-regulated gene sets for a given disease-associated or cytokine-stimulated MPC are combined. The combination enables those of skill in the art to identify gene sets with minimal number of elements that are unique to a given MPC type with a capability to discriminate one MPC type from another (this can be accomplished by means of a series of Venn diagrams and lists of required genes obtained via GeneSpring). Such gene sets are of immense diagnostic value as they can be routinely used in assays that are simpler than microarray analysis (for example "real-time" quantitative PCR). Such gene sets also

provide insights into pathogenesis and targets for design of new drugs. For example, the method allows one to establish transcriptional profiles of MPC genes that are pathologically altered.

Those of skill in the art can use the data and methods contained herein for the following: a) study select gene or sets of genes that are relevant to hematopoietic disease conditions by using relatively inexpensive but low-throughput technologies such as Northern blotting, RNase protection assays and/or PCR intended for gene expression analysis; b) identify newer drug targets and diagnostic markers relevant to specific diseases, such as MM or CML etc depending on the research interests of the individual investigators.

The present invention also provides a large-format 2-D gel electrophoretic system for the reproducible separation of MPC proteins and for preparing 2-D PAGE protein maps for normal bone marrow-derived MPCs (untreated and treated with representative cytokines, e.g., TNF- $\alpha$  and/or IL-4) and for MPCs derived from patients with representative pre-leukemic/ premalignant and leukemic/ malignant conditions. The pre-leukemic conditions include myelodysplastic syndromes (MDS) and the leukemic conditions include chronic myeloid leukemia (CML), acute myeloid leukemia (AML), chronic lymphocytic leukemia (CLL), acute lymphocytic leukemia (ALL), and multiple myeloma (MM). The protein samples consist of culture supernatants/secreted proteins, extracellular matrix (ECM) proteins, plasma membrane proteins solubilized using a three-step differential extraction protocol, employing conditions of progressively increasing solubility; and whole cell lysate proteins similarly solubilized using the three-step differential extraction protocol. This subproteome approach not only simplifies the 2-D PAGE electrophoretic protein patterns but also reveals additional proteins, which would otherwise have gone undetected.

The 2-D system described herein utilizes an immobilized pH gradient gel (pH 4-7) in the first dimension and a mini non-denaturing but high-resolution lithium dodecyl sulfate-polyacrylamide gel electrophoresis (LDS-PAGE) in the second dimension. As identified by silver staining, this system has resolved greater than 800 protein spots in a pH interval of 2.5 units (4.25-6.75, the isoelectric pH range for most of plasma membrane proteins to migrate) and a molecular mass range of 10-150 kDa. Equally important, the system is compatible with high sample

loads (up to 1.5 to 2.0 mg of total protein in up to 350  $\mu$ l sample volume). All the protein species identifiable by a silver stain that is compatible with subsequent mass spectrometric analysis have been analyzed by a 2-D gel software with respect to isoelectric point, molecular weight and mass abundance. The lectin-binding status of these proteins has also been determined by lectin blotting. Lectin blots and Western blots have subsequently been stained by a gold stain for detection of total proteins on the same PVDF membrane. Although gold-staining of the Western blot is not as sensitive as silver-staining of the gel, gold-staining of the Western blot generates the necessary landmarks for alignment with the silver stained gel, facilitating excision of spots of interest from the gel for identification by MALDI-MS. Representative protein spots were excised from gel and subjected to mass spectrometric profiling (MALDI-MS) and/or sequencing (Nano ESI MS/MS) with subsequent database searching, resulting in a productive identification of ten proteins.

The invention is further described in detail by reference to the following experimental examples. These examples are provided for the purpose of illustration only, and are not intended to be limiting unless otherwise specified. Thus, the invention should in no way be construed as being limited to the following examples, but rather, should be construed to encompass any and all variations which become evident as a result of the teaching provided herein.

## EXAMPLES

The examples presented herein can be summarized as follows. The data disclosed herein demonstrate that Dexter cultures consist of only three cell types macrophages (~35%), hematopoietic cells (~5%), and nonhematopoietic cells (~60%). Using a percoll gradient centrifugation technique, the nonhematopoietic mesenchymal progenitor cells were isolated, free of macrophages and hematopoietic cells. A variety of techniques were used to identify the isolated cells as a multi-differentiated mesenchymal cell lineage co-expressing genes specific for multiple mesenchymal cell lineages including adipocytes, osteoblasts, fibroblasts and muscle cells.

Evidence that this multi- or pluri-differentiated mesenchymal progenitor cell is capable of supporting hematopoiesis is shown by the expression of a number of hematopoietic growth factors and extracellular matrix receptors. The SCID mouse experimental data provides evidence that since the MPCs can be purified to near

homogeneity (95%) with relative ease, MPCs can be of value for enhancing engraftment of hematopoietic stem cells and bone marrow transplants. Additionally, increased survival rate in the SCID mouse model indicates that isolated MPCs can also be useful for the treatment of GvHD. An example of the administration of bone marrow cells and MPCs to breast cancer patients treated with chemotherapy is also provided.

A stepwise genomics strategy and an example of the genomic changes observed in leukemia associated MPCs is also provided. Cluster analysis was performed to show gene expression patterns in isolated MPCs of a normal individual and individuals with different leukemic conditions. The approach presented provides the basis for a new more objective means to diagnose patients suffering from leukemic conditions.

### EXAMPLE 1

#### *Isolation and Characterization of MPCs from Dexter-Type Bone Marrow Stromal Cell Culture Systems*

##### *Bone marrow culture:*

Bone marrow samples were obtained from posterior superior iliac crest under general anesthesia for standard marrow transplantation. Marrow stromal cell cultures were set up using the residual cells recovered from the filters of Fenwal Bone Marrow Collection System after complete filtration of the marrow samples. The filters were rinsed with phosphate-buffered saline without  $\text{Ca}^{2+}$  and  $\text{Mg}^{2+}$  (PBS-CMF). The cell suspension was subjected to Ficoll gradient isolation of the mononuclear cells (bone marrow MNCs). The bone marrow MNCs were washed (x2) in PBS-CMF and suspended in McCoy's 5A with HEPES medium containing 12.5% fetal bovine serum (FBS), 12.5% horse serum, 1  $\mu\text{M/L}$  hydrocortisone and 1% penicillin/streptomycin (for this study McCoy's complete medium) and cultured under standard stromal-cell culture conditions (Figure 1) (Seshi, *et al. Blood* 83, 2399 (1994) and Gartner, *et al. Proc Natl Acad Sci USA* 77, 4756 (1980). After two weeks, confluent stromal cell cultures were trypsinized (first passage), followed by splitting each T75 flask into two T150 flasks.

*Morphologic and phenotypic characteristics of MPCs as uncovered by staining for representative mesenchymal cell lineage markers:*

Two weeks after the first passage (above), confluent stromal cells were again trypsinized. Cytospins were prepared using aliquots of unfractionated cells for performance of various cytological, cytochemical and immunocytochemical stains.

Reactivity patterns of the bone marrow culture cells are outlined in Table 1. Figures 4A-E illustrate morphologic and phenotypic characteristics, as uncovered by staining for representative cell lineage markers. As illustrated in Table 1 and Figures 3 and 4A, Wright-Giemsa staining revealed three morphologically identifiable cell populations in Dexter type stromal cell cultures, macrophages, hematopoietic cells, and nonhematopoietic cells (labeled 4, 3, and 5, respectively).

The identity of macrophages was confirmed by immunostain using anti-CD68 antibody (Figure 4B) and cytochemical stains for acid phosphatase and Sudan black. The identity of hematopoietic cells (including macrophages) was confirmed by immunostain using anti-CD45 antibody (Figure 4C).

The remaining nonhematopoietic cells stained intensely positive for Periodic acid-Schiff, which was diastase sensitive, signifying the presence of large stores of glycogen (Figure 4D). The presence of glycogen (6) was confirmed by electron microscopy (see Figure 5). In this respect, MPCs are reminiscent of the glycogen-laden reticular cells in the developing bone marrow of human fetuses (observed by L-T. Chen, L.Weiss, *Blood* 46, 389 (1975)). Glycogen deposition is viewed to be a developmentally regulated process during morphogenesis (H. Ohshima, J. Wartiovaara, I. Thesleff, *Cell Tissue Res.* 297, 271 (1999)).

In terms of lineage markers, up to 100% of the nonhematopoietic cells expressed two fat cell markers (Nile Red (Figure 4E) and Oil Red O); an osteoblast marker (alkaline phosphatase (Figure 4F)); and two fibroblast markers (fibronectin (Figure 4G) and prolyl-4-hydroxylase). Greater than 85% of the nonhematopoietic cells were also positive for a muscle marker, actin (Figure 4H). There was no evidence of expression of endothelial cell differentiation, as judged by immunohistochemical staining for CD34 and CD31 (data not shown).

The results indicate that the nonhematopoietic cells of the Dexter cultures are in fact a single, pluri-differentiated cell type co-expressing multiple mesenchymal cell lineage markers. The pluri-differentiated mesenchymal progenitor cells reported here are to be distinguished from the pluri-potential, but



undifferentiated, MSCs that are generated in the absence of hematopoietic cells, such as in Friedenstein-type cultures.

**Table 1. Reactivity patterns of bone marrow stromal cells based on cytological, cytochemical and immunocytochemical stains\*,\*\***

5

	Figure	Test Utilized	Macrophages	Hematopoietic cells	Mesenchymal progenitor cells
1	3 and 4A	Wright-Giemsa (Harleco)	Large cells with a small round nucleus & foamy cytoplasm: 35% of total cells	Small cells with minimal amount of cytoplasm: 5% of total cells	Large cells with a relatively irregular nucleus & cytoplasm compartmentalized into ectoplasm and endoplasm: 60% of total cells
2	4D	Periodic acid-Schiff (PAS) (Sigma)	0	0	~100% MPCs: staining restricted to ectoplasm in a ring-like fashion; and completely abolished by diastase digestion
3	4C	CD45 (Dako, PD7/26 & 2B11)	100% macrophages (MΦ)	100% HCs	0
4	4B	CD68 (Immunotec h, clone PG-M1)	100% MΦ	0	0
5		Sudan Black (Sigma)	~100% MΦ	0	0
6		Acid phosphatase (Sigma Kit No. 387)	100% MΦ; positive granules packed throughout cytoplasm	0	100% MPCs; positive granules in moderate amounts; staining restricted to endoplasm
7	4E	Nile Red (Sigma)	0	0	~100% MPCs: staining restricted to endoplasm
8		Oil Red O (Sigma)	0	0	~ 95% MPCs: variable number of positive granules; staining preferentially in the endoplasm
9	4F	Alkaline phosphatase (Sigma Kit No. 85)	0	0	~100% MPCs: variable number of positive granules; staining restricted to endoplasm & plasma membrane**
10	4G	Fibronectin (Immunotec h, clone 120.5)	0	0	~100% MPCs: staining restricted to endoplasm
11		Prolyl-4-hydroxylase (Dako,	0	0	~100% MPCs: staining preferentially in the endoplasm

		clone 5B5)			
1 2	4H	Muscle actin (Ventana, clone HUC 1-1)	0	0	> 85% MPCs: variable staining restricted to ectoplasm

\*The lineages of the markers tested above are: 3, hematopoietic cell marker; 4, 5 and 6, monocyte/macrophage markers; 7 and 8, adipocyte markers; 9, osteoblast marker; 10 and 11, fibroblast markers; 12 muscle marker.

- 5 \*\*One earlier study (Simmons, *et al.*, Nature 328, 429-432) interpreted the localization of alkaline phosphatase staining as confined to the plasma membrane when in fact it is predominately present within the endoplasm (compare Figure 1C of this reference with Figure 4F).

- 10 \*\*\* While well-accepted mesenchymal lineage markers were used, these markers do not necessarily lend themselves to simultaneous assessment of the same cell. For example, muscle-specific actin antibody worked only on formalin-fixed, paraffin embedded material, whereas stains like alkaline phosphatase, Oil Red and Nile Red are not anti-body based and involve varying fixing and staining conditions. Thus, the evidence shows that close to 100% of members of a morphologically distinct population express multiple lineage markers of interest.

*Bone marrow mesenchymal progenitor cell (MPC) purification:*

- 20 To further investigate the characteristics of the MPCs, the nonhematopoietic stromal cells were then purified from the macrophages (~95% pure), the dominant "contaminating" cell type using the following method. Confluent monolayers of stromal cells resulting from first passage, above, were washed for three minutes in  $\text{Ca}^{2+}/\text{Mg}^{2+}$  free Hanks' balanced salt solution. Cells were incubated at room temperature for 45 minutes with intermittent mixing in serum-free McCoy's medium containing 10 mM L-leucine methyl ester (LME, Sigma). LME is a lysosomotropic agent that selectively kills and detaches macrophages. The detached macrophages were removed by washing the monolayers twice in McCoy's complete medium, followed by trypsinization of the monolayers. The resulting single cell suspensions were fractionated by discontinuous Percoll gradient (70%, 50%, 30%, 20%, 10%) centrifugation at 800xG for 15 minutes at 4°C in a fixed angle rotor (Avanti-J25 Beckman centrifuge) (Figure 2). Low-density cells representing the

macrophages resistant to detachment by LME separate as a band at the interface of serum and 10% Percoll and were discarded (1). High-density nonhematopoietic cells representing MPCs form a layer in the region of 30-50% Percoll (2). These were collected and washed twice by centrifugation through PBS-CMF. This protocol is conservatively expected to yield,  $>2.5 \times 10^6$  MPCs per T-150 flask (i.e.,  $>50 \times 10^6$  MPCs per batch of 20 flasks). The purity of these preparations, typically about 95%, was routinely monitored by Wright-Giemsa staining.

*Northern Blotting:*

Additional sets of multiple mesenchymal lineage markers were assessed by Northern blotting to eliminate any observer bias that might be inherent in morphological assessment. Figures 6A-M represent different gene probes used for hybridization. The sources of the gene probes employed and the major transcripts observed are outlined in the brief description of the figures.

Total RNA was prepared by dissolving the high-density cell pellets in Trizol (Life-Technologies). Total RNA samples from unfractionated stromal cells and BM-MNCs were similarly prepared. The RNA samples were electrophoresed in a standard 1% agarose gel containing 2% formaldehyde in MOPS/EDTA buffer and blotted onto Immobilon-Ny+ membrane. Probes were labeled using Prime-A-Gene Kit (Promega) and a  $^{32}\text{P}$  dCTP (NEN). Hybridization was performed at 65°C in modified Church's hybridization solution using  $3 \times 10^6$  counts/ml in 10 ml (Millipore, 1998).

In Figures 6A-M, Northern blot analysis was performed side-by-side on fractionated stromal cells, non-hematopoietic cells freed of macrophages, and initial bone marrow mononuclear cell samples. Lanes 1 and 2 represent total RNA samples (10µg each) from unfractionated stromal cells (subjects S1 and S2, respectively). Lanes 3 and 4 represent total RNA samples (10µg each) from purified stromal MPCs (subjects S1 and S2, respectively). Lanes 5 and 6 represent total RNA samples (10µg each) from bone marrow mononuclear cells, the starting cells for bone marrow cell cultures (subjects S3 and S4, respectively).

The large transcripts, especially of collagen (lane 1, Figure 6G) and fibronectin (lane 1, Figure 6J), in RNA extracted from unfractionated stromal cells of subject 1 showed difficulty migrating into the gel. This observation correlates with the presence of an artifact of unresolved positive material in lane 1, Figure 6A. Since

the RNA extracted from unfractionated stromal cells of the subject 2 did not present this problem (lane 2, Figure 6G, Figure 6J and Figure 6A), the observation does not impact on the overall interpretation of the results (see text). The lineages of markers tested were: monocyte/macrophage markers, CD68 and cathepsin B; adipocyte marker, adipsin; osteoblast markers, osteoblast-specific cadherin-11, chondroitin sulfate proteoglycan 2, collagen type I alpha 1 and decorin; fibroblast marker, fibronectin; muscle markers, caldesmon and transgelin. Marker signals were normalized to the amount of RNA loaded, which was based on densitometry of the GAPDH signals on the corresponding blot (Bio-Rad Model GS-700 Imaging Densitometer). Attenuation or enhancement of the marker signals in the purified stromal MPCs (i.e., lanes 3 and 4) relative to unfractionated stromal cells (i.e., lanes 1 and 2, respectively) is shown as fold  $\Delta$  (decrease/increase) underneath the lanes 3 and 4; ND, means not determined.

The purity of the nonhematopoietic cells was demonstrated by a near complete absence of two macrophage markers, CD68 and cathepsin B (as shown by Northern blotting data, Figure 6A and 6B). As a positive control, bone marrow mononuclear cells rich in myelomonocytic cells abundantly expressed CD68 (lanes 5 & 6, Figure 6A). The Northern blot results are consistent with a purity estimate of ~95% (vs. 60% in unfractionated samples) based on morphology and immunocytochemical staining for CD68.

Compared to unfractionated cells, the purified nonhematopoietic cells expressed significantly higher levels of markers representing fat cells (adipsin, Figure 6D); osteoblasts (osteoblast-specific cadherin-11, chondroitin sulfate, collagen type 1 and decorin, Figures 6E-H); fibroblasts (fibronectin, Figure 6J); and smooth muscle cells (caldesmon and transgelin, Figures 6K-L).

No trace of osteoblast, fibroblast, or smooth muscle cell markers were detected in the bone marrow mononuclear cells, suggesting a less than detectable level of stromal cells or their precursors in bone marrow mononuclear cells. However, the fat cell marker, adipsin, was detected in all samples including the bone marrow mononuclear cells.

Taken together, the morphologic, cytochemical and immunocytochemical results (Figure 4A-H and Table 1), and the Northern blotting data (Figure 6A-M) indicate that the nonhematopoietic stromal cells of the Dexter

cultures co-express markers specific for at least four different mesenchymal cell lineages.

This finding is especially intriguing because pluri-differentiation is often a feature of neoplastic cells (Brambilla and Brambilla, *Rev. Mal. Respir.* 3,235 (1986); Pfeifer et al., *Cancer Res.* 51, 3793-3801 (1991); Tolmay et al., *Virchow's Arch* 430, 209-12 (1997). However, a cytogenetic analysis of the Percoll-gradient purified MPCs showed a normal GTW banding pattern.

*RT-PCR Analysis for expression of representative hematopoietic growth factors and extracellular matrix receptors by MPCs*

RT-PCR was conducted in a total reaction volume of 100 µl using 2 µg each of total RNA; corresponding primers; and a master mix of the PCR reagents. The RT conditions included sequential incubations at 42°C for 15 minutes, 99°C for five minutes, and 5°C for five minutes. The PCR conditions included: initial melting at 94°C for four minutes; and cyclical melting at 94°C for 45 seconds, annealing at 55°C for 45 seconds and extension at 72°C for 45 seconds with 34 cycles. PCR was terminated after final extension at 72°C for ten minutes. Reaction products (G-CSF, SCF, each 25 µl; VCAM-1, ALCAM, each 50 µl; ICAM-1, 75 µl) were concentrated as necessary; electrophoresed along with a 100-bp DNA ladder (GIBCO-BRL) in a standard agarose (1%) gel in TAE buffer; and stained with ethidium bromide.

PCR products, shown in Figure 7 lanes labeled 1-2, were generated using aliquots of the same RNA samples from purified stromal MPCs, as used for Northern blotting shown under Figure 6 lanes 3 and 4 respectively. The gene transcripts amplified were as follows: G-CSF (granulocyte-colony stimulating factor); (Tachibana et al., *Br. J. Cancer*, 76, 163-74 (1997); SCF (stem cell factor, i.e., c-Kit ligand); (Saito et al., *Biochem, Biophys. Res. Commun.*, 13, 1762-69 (1994); ICAM-1 (intercellular adhesion molecule-1, CD54) and VCAM-1 (vascular cell adhesion molecule-1, CD106) (primers from R&D); and ALCAM (activated leukocyte cell adhesion molecule, CD166) (Bruder et al., *J. Bone Miner. Res.*, 13, 655-63 (1998)).

The observed PCR products for G-CSF (600 bp, i.e., the top bright band) and ALCAM (175 bp) were significantly different from the expected sizes (278 bp; 372 bp, respectively). However, sequencing of the gel-purified PCR bands and subsequent BLAST search showed a 99-100% identity with respective members. Attempts to detect c-Kit (i.e., SCF receptor) using primers as described (Saito et al.,

*Biochem, Biophys. Res. Commun.*, 13, 1762-69 (1994)) amplified a PCR product of ~300 bp with no homology to c-Kit (data not shown). The observed product sizes for SCF (~730 bp); ICAM-1 (~750 bp); and VCAM-1 (~500 bp) were as expected.

As illustrated in Figure 7, RT-PCR analysis showed that purified, multi-  
5 differentiated MPCs express both critical hematopoietic growth factor/cytokines, such as G-CSF and SCF as well as matrix receptors/hematopoietic cell adhesion molecules, i.e. ICAM-1, VCAM-1, and ALCAM.

## EXAMPLE 2

*Comparison of the Ability to Support in vitro Hematopoiesis by Purified MPCs vs.*

10 *Unfractionated Bone Marrow Stromal Cells*

CD34+ positive cells (hematopoietic progenitor cells) were purified (Dynal kit) and cocultured with irradiated stromal monolayers for five weeks, followed by performance of standard colony assays for hematopoietic progenitors using methylcellulose medium supplemented with colony stimulating factors (using  
15 MethoCult medium from Stem Cell Technologies, Inc, Canada). Unfractionated bone marrow stromal cells and purified MPCs were prepared in the same manner as in Example 1. Data in Figure 8 represents results from three experiments. Purified MPC provides increased preservation of hematopoietic progenitor cells compared to unfractionated stromal cells.

20

## EXAMPLE 3

*Animal Model for Enhanced Engraftment Capacity of MPCs*

The Severe Combined Immunodeficiency Disease (SCID) mouse model is an ideal system in which to investigate MPC function. Engraftment of human hematopoietic progenitors in SCID mice requires either coadministration of  
25 exogenous human cytokines, or cotransplantation of human bone marrow plugs or bone fragments.

There has been discovered a convenient, new source for human bone marrow stromal cells for enhancing transplantation that does not require cytokines, bone fragment, or marrow. Unlike prior methods, the isolated cells of the present  
30 invention support human hematopoiesis in the SCID mouse model as effectively as whole marrow stroma. The transplantation of human marrow mononuclear cells combined with purified MPCs results in dramatically vigorous engraftment of human cells in spleen, bone marrow, liver, pancreas, lungs, stomach, and paravertebral

neuronal ganglia of SCID mice. By contrast, mice receiving human bone marrow mononuclear cells alone or MPCs alone expectedly showed no detectable evidence of human hematopoietic cell engraftment. Also notably, the mortality rate was highest in mice that received unfractionated whole marrow stroma whereas purified MPC increased the survival rate which can be due to reduction in GvHD.

*Transplantation of human cells in SCID mice:*

Homozygous CB-17 scid/scid mice, six to eight weeks of age, were used. Lyophilized anti-asialo GM1 rabbit antibody (Wako Chemicals) was suspended in 1 ml sterile ddH<sub>2</sub>O, followed by pretreatment of mice with an IP injection of 20 ml (600 mg) ASGM1 antibody (to specifically deplete mouse macrophages and NK cells). Alternatively, one could use NOD/SCID mice lacking NK cell function, however, in light of highly promising preliminary results it was elected to continue use of scid/scid mice. The antibody treatment schedule included four-hour pre-engraftment and every seven days thereafter for the duration of the experiment. On the day of transplantation, the mice were irradiated with 200 or 300 cGy gamma-irradiation from a <sup>137</sup>Cs source. Approximately  $2.5 \times 10^6$  MPCs suspended in 0.5 ml McCoy's medium and/ or  $25 \times 10^6$  MNCs suspended in 0.2 ml were injected per mouse, intraperitoneally. Hematopoietic cell engraftment was assessed after five weeks by harvesting and analyzing representative hematopoietic and nonhematopoietic organs including blood, spleen, bone marrow (from two femurs and tibia) from euthanized mice.

*Flow Cytometric Evidence*

Figure 9A and 9B are flow cytometric evidence of human hemopoietic cells in a SCID mouse cotransplanted with marrow MPC. Figure 9A shows the presence of CD45+/CD34+ progenitors in the marrow. Figure 9B shows CD45/CD34- mature hematopoietic cells circulating in the mouse's blood.

*Photomicrographs of Cells*

Figures 10A-H shows engraftment of human hematopoietic cells in a SCID mouse cotransplanted with the purified marrow MPCs of the present invention. Figure 10A shows a serial section of a mouse spleen stained with H & E. Figure 10B shows a serial section of a mouse spleen stained with immunoperoxidase stain for CD45. Figure 10C shows bone marrow stained for CD45. Figure 10D shows a serial section of the mouse liver stained with H&E depicting involvement of periportal

areas. Figure 10E shows a serial section of the mouse stomach stained with H&E showing transmural infiltration. Figure 10F shows a serial section of the mouse lung stained with H&E showing involvement of peribronchial area. Figure 10G shows a serial section of the mouse pancreas stained with H&E. Figure 10H shows a serial  
5 section of the mouse paravertebral ganglia stained with H&E.

Figure 11A is a photomicrograph of a serial section of the spleen of a normal BALB/C mouse showing white pulp populated by darkly staining lymphocytes (H&E). Figure 11B is a photomicrograph of the spleen of a SCID mouse showing white pulp largely consisting of lightly staining stromal framework (H&E). Figure 11C  
10 is a photomicrograph of the spleen of a SCID mouse cotransplanted with human bone marrow MNC and the purified bone marrow MPCs of the present invention showing homing (engraftment) of human B cells to white pulp.

#### *Southern Blotting Data*

15 Hybridization of sample DNA using a DNA probe specific for human chromosome 17 alpha satellite DNA (p17H8) shows linear signal intensity with a 2.7 Kb band (arrow; autoradiogram exposed for only 45 minutes) (Figure 12A). Lanes 1-10 contain human DNA starting 1000 ng to 100 ng admixed with 0 ng 900 ng of mouse DNA, total amount DNA loaded in each lane being 1 ug, allowing  
20 construction of a standard curve. The reported limit of detection with this technique is 0.05% human cells, which is more reliable than flow cytometry in detecting very low levels of human cell engraftment.

Figure 12B is a Southern blot of EcoR1 digest of thymic genomic DNA from SCID mice. Lanes 1-5 were loaded with 500 through 100 ng human DNA.  
25 Lanes 6, 9-11 were loaded with DNA from mice which received unfractionated bone marrow stroma plus bone marrow mononuclear cells. Lanes 7, 8, 14, 15 were loaded with DNA from mice that received MPCs plus bone marrow mononuclear cells. Lanes 12, 13 were loaded with DNA from mice that received bone marrow mononuclear cells only. There is evidence of human cell engraftment in the mouse  
30 thymus in lanes 9 and 11 and lanes 14 and 15 evidenced by the 2.7 Kb band. There was no evidence of engraftment in mice that only received only bone marrow mononuclear cells, lanes 12 and 13.



Figure 12C is EcoRI digest of Lymph Node genomic DNA from SCID mice. Lanes 1-5 were loaded with 500 through 100 ng human DNA. Lanes 6, 9-11 were loaded with DNA from mice which received unfractionated bone marrow stroma plus bone marrow mononuclear cells. Lanes 7, 8, 14, 15 were loaded with DNA from mice that received MPCs plus bone marrow mononuclear cells. Lanes 12, 13 were loaded with DNA from mice that received bone marrow mononuclear cells only. While there was evidence of engraftment of human cells in the mouse lymph nodes for mice that received unfractionated bone marrow stromal cells and MPCs, there was no evidence of engraftment in mice that only received only bone marrow mononuclear cells, lanes 12 and 13.

*Increased Survival and Evidence of MPC Effect on GvHD*

Figure 13A and Figure 13B show graphs comparing the survival rate and engraftment of human hematopoietic cells in SCID mice cotransplanted with the purified bone marrow MPCs of the present invention versus unpurified bone marrow stromal cells. Mice in Figure 13A received 300 cGy irradiation dose and mice in Figure 13B received 200 cGy of irradiation. Figure 13A and Figure 13B show comparable engraftment of human hematopoietic cells in SCID mice cotransplanted with purified MPCs versus unpurified bone marrow stromal cells and the markedly enhanced survival of mice receiving purified MPCs. Notably, no engraftment was observed in mice receiving bone marrow mononuclear cells alone.

The highest mortality rate, Figure 13B, was observed in mice receiving the unpurified stromal cells and the bone marrow mononuclear cells. The increased mortality observed can be related to the presence of highly immunogenic macrophages and consequent GvHD. The mice with the highest survival rate, as shown in Figure 13A, were the mice receiving purified MPCs and bone marrow mononuclear cells.

Figures 14A-C demonstrate apoptosis by TUNEL assay in organs of SCID mice that died after transplantation with human bone marrow mononuclear cells and unpurified bone marrow stromal cells. Figure 14A shows a serial section of the liver of the mouse that survived. Figure 14B shows a serial section of the liver of the mouse that died. Figure 14C shows a serial section of the spleen of the mouse that survived. Figure 14D shows a serial section of the spleen of the mouse that died. Hematoxylin counterstain was applied to sections in Figure 14A and Figure

14C. Methylgreen counterstain was applied to sections in Figure 14B and Figure 14D.

Notably, there is discrete TUNEL-positive nuclei in the liver of the expired mouse in Figure 14B and complete absence of staining in the liver of the surviving mouse Figure 14A. While some ill-defined globules of staining are observed in the spleen of the mouse that survived, the nuclear integrity of most of the cells is well preserved suggesting minimal or no apoptosis (Figure 14C). By contrast, the dead mouse spleen (Figure 14D) showed extensive TUNEL positivity precluding accurate interpretation. Control mouse liver and spleen showed results similar to those of the mouse that survived.

The size of the spleens from the mice that survived and the mice that died were compared. The dead mice were observed to have small and atrophic spleens correlating with lymphoid cell depletion and apoptosis.

The above results indicate that purified MPC can support human hematopoiesis in SCID mice as effectively as whole marrow stroma. Equally important is that the purified MPCs increased the survival rate. Evidence suggests that the increased survival can be due to a reduction in GVHD.

#### EXAMPLE 4

##### *Administration of Bone Marrow Cells and Mesenchymal Progenitor Cells to Breast Cancer Patients Treated with Chemotherapy*

A breast cancer patient undergoes a diagnostic posterior iliac crest bone marrow aspiration and biopsy using a local anesthetic. A small portion (2 to 3 ml) of the aliquot (10 to 20 ml) of marrow is submitted for routine histologic testing and determination of the presence of tumor cells using immunoperoxidase testing. The remainder of the cells are Dexter cultured for MPCs as described above in Example 1.

The patient also undergoes placement of a pheresis central venous catheter, and receives subcutaneous injections of G-CSF (filgrastin) 10µg/kg/day as described in Peters, et al, Blood, Vol. 81, pgs. 1709-1719 (1993); Chao, et al, Blood, Vol. 81, pgs. 2031-2035 (1993); Sheridan, et al, The Lancet, Vol. 2, pgs. 891-895 (1989); and Winter, et al, Blood, Vol. 82, pg. 293a (1993). G-CSF injections begin at least three days before the first pheresis is initiated. G-CSF therapy is withheld if the

white blood cell count rises above 40,000/ $\mu$ L and is resumed once the white blood cell count drops to less than 20,000/ $\mu$ L.

If the patient is receiving only G-CSF as the vehicle for "mobilization" of peripheral blood progenitor cells, the patient must not have received chemotherapy within four weeks of the planned pheresis. If the patient has received both  
5 conventional chemotherapy and G-CSF treatment for mobilization, the patient must not have received chemotherapy within ten days of the planned pheresis, and the white blood cell count must be at least 800/ $\mu$ L and the platelet count at least 30,000/ $\mu$ L.

10 Daily pheresis procedures are performed using a Cobe Spectra instrument (Cobe, Lakewood, Col.), and each cellular collection is cryopreserved using a controlled-rate liquid nitrogen freezer, until at least  $15 \times 10^8$  mononuclear cells/kg are collected (Lazarus, et al., Bone Marrow Transplant, Vol. 7, pgs. 241-246 (1991)). Each peripheral blood progenitor cell is processed and cryopreserved  
15 according to previously published techniques. (Lazarus, et al., J. Clin. Oncol., Vol. 10, pgs. 1682-1689) (1992); Lazarus et al., (1991)).

Eight days before the patient is infused with the autologous peripheral blood progenitor cells, the patient receives chemotherapy over a period of 96 hours (four days), with the following chemotherapy agents: 1) Cyclophosphamide in a total  
20 dosage of 6 g/m<sup>2</sup> (1.5 g/m<sup>2</sup> /day for four days) is given via continuous intravenous infusion at 500 mg/m<sup>2</sup> in 1,000 ml normal saline every eight hours; 2) Thiotepa in a total dosage of 500 mg/ m<sup>2</sup> /day for four days) is given via continuous intravenous infusion at 125 mg/ m<sup>2</sup> in 1,000 ml normal saline every 24 hours; and 3) Carboplatin in a total dosage of 1,800 mg/m<sup>2</sup> (200 mg/m<sup>2</sup> /day for four days) is given via continuous  
25 intravenous infusion at 200 mg/m<sup>2</sup> in 1,000 ml of 5% dextrose in water every 24 hours.

The patient also receives 500 mg of Mesna in 50 ml normal saline IV over 15 minutes every four hours for six days (144 hours), beginning with the first dose of cyclophosphamide.

30 At least 72 hours after the completion of the chemotherapy, the MPCs are harvested from the Dexter culture(s). MPCs are collected and purified as described in Example 1. Cells are resuspended at approximately  $10^6$  cells/ml, and

injected slowly intravenously over 15 minutes to provide a total dosage of from 10 to about  $5 \times 10^6$  cells.

MPCs can also be frozen and thawed to use when needed. For example, unfractionated cells from a Dexter culture are frozen. Upon thawing the cells are plated for about two days. The MPCs are then purified as in Example 1 above. The MPCs are then replated with serum or in a serum free media and can remain stable for up to six days.

The day after the patient receives the MPCs, the frozen autologous peripheral blood progenitor cells are removed from the liquid nitrogen refrigerator, transported to the patient in liquid nitrogen, submersed in a 37°C to 40°C sterile water bath, and infused rapidly intravenously without additional filtering or washing steps. GM-CSF in an amount of  $250 \mu\text{g}/\text{m}^2$  then is given as a daily subcutaneous injection, beginning three hours after completion of the autologous blood progenitor cell infusion. The GM-CSF is given daily until the peripheral blood neutrophil count exceeds  $1,000/\mu\text{L}$  for three consecutive days.

#### EXAMPLE 5

##### *Genomic Changes Observed in Leukemia Associated MPCs*

The following is one example of how normal hematopoiesis might be compromised in leukemic conditions. The cellular interactions that underlie leukemic bone marrow involve stromal cells, leukemia/ lymphoma cells, and normal hematopoietic progenitors (including those of myelopoiesis, erythropoiesis and megakaryocytopoiesis). In addition to displacing normal hematopoietic cells, the leukemia/ lymphoma cells can potentially cause direct damage to the hematopoietic supportive stromal cells by inducing unwanted gene expression profiles and adversely affecting the normal hematopoiesis. The cellular interactions can be schematized as:

Leukemia/lymphoma cells                            stromal cells                            normal hematopoietic progenitors.

The point of this scheme is that regardless of whether stromal cell lesions are primary or secondary to leukemogenesis, the normal hematopoietic function is invariably compromised in leukemic conditions, though different leukemias affect myelopoiesis, erythropoiesis and megakaryocytopoiesis differentially. Contrary to the prevailing notion (see Marini, F *et al.*, Mesenchymal Stem Cells from Patients with Chronic Myelogenous Leukemia Patients can be

Transduced with Common Gene Transfer Vectors at High Efficiency, and are Genotypically Normal, 42<sup>nd</sup> Annual Meeting of the American Society of Hematology, Dec. 1-5, 2000 Poster # 665), there has been observed extensive and striking gene expression changes in leukemia-associated bone marrow MPCs by using high-resolution genomics. Therefore, one embodiment of the present invention is to use transplantation of tissue-culture expanded, purified normal MPCs to improve granulopoiesis, erythropoiesis and thrombopoiesis, in for example MDS (most of MDS patients do not die from blast transformation but from complications related to

5    cypopenias, i.e., hematopoietic failure).

10           The studies targeted acute myeloid leukemia (AML), chronic myeloid leukemia (CML) and multiple myeloma (MM), one case of each. The AML patient was a 57 year-old woman with 52% myeloblasts in the bone marrow with immunophenotype confirmed by flow cytometry and a karyotypic abnormality of 45, XX, -7(6)/46, XX [6]. Together with morphology, the diagnosis was AML arising in a

15    background of myelodysplasia. The CML patient was a 35 year-old man with 2% blasts in the bone marrow and karyotypic abnormalities of Philadelphia chromosome and BCR/ABL gene rearrangement. Together with morphology, the diagnosis was CML in chronic phase. The MM patient was a 61 year-old woman with a IgA myeloma. The serum IgA level was 2.4 g/dl and the marrow plasma cell count was

20    37%. None of the patients was treated prior to obtaining marrow samples used in this study, to avoid any therapy-induced changes complicating the disease-associated changes.

          The leukemic samples consisted of marrow aspirates that remained unused after clinical diagnostic studies were preformed. A bone marrow sample

25    obtained from an adult healthy male who had consented to donate bone marrow for standard marrow transplantation was simultaneously studied. The normal bone marrow sample consisted of residual cells recovered from the filters after complete filtration of the marrow sample. Setting up of Dexter-type stromal cell cultures and isolation of MPC were as described in Example 1. The normal stromal cells were

30    studied without and after stimulation with TNF $\alpha$  because TNF $\alpha$  (and IL-4) are regarded as negative regulators of hematopoiesis. Notably these cytokines, especially TNF  $\alpha$ , are elevated in marrow plasma of patients with myelodysplastic syndromes (MDS), the clinical hallmarks of which are anemia, leukopenia and

thrombocytopenia (i.e., pancytopenia). TNF $\alpha$  and IL-4 are considered possible mediators of hematopoietic dysregulation typical of MDS.

*A stepwise genomics strategy encompassed:*

Preparation of total RNA from MPC samples  $\rightarrow$  generation of cDNA  $\rightarrow$   
5 preparation of ds DNA  $\rightarrow$  *in vitro* transcription into cRNA  $\rightarrow$  fragmentation of cRNA  
 $\rightarrow$  hybridization of target RNA to a microarray of known genes (Affymetrix genechip  
containing DNA from ~12,000 known human genes, e.g., U95A oligonucleotide  
microarray)  $\rightarrow$  analysis of differentially expressed genes using an appropriate  
software (GeneSpring) to discern the patterns of gene expression or genomic  
10 signatures by a given MPC type.

*Cluster analysis showing gene expression patterns in bone marrow MPC isolated  
from a normal individual and patients with different leukemic conditions.*

*Genes with correlated expression across bone marrow MPC types:*

GeneSpring was used for cluster analysis. Prior to application of an agglomerative  
15 hierarchical clustering algorithm, microarray signals were normalized across  
experiments (i.e., from one MPC type to another) making the median value of all of  
measurements unity, so different experiments are comparable to one another. The  
signals were also normalized across genes in order to remove the differing intensity  
signals from multiple experimental readings. Genes that are inactive across all  
20 samples were eliminated from analysis. Notably, 7398 genes out of 12,626 genes  
(present on the Affymetrix genechip used) passed the filter of a normalized signal  
intensity of at least 0.1 across at least one of the five experiments performed.  
Cluster analysis was performed with standard correlation (same as Pearson  
correlation around zero) as the distance metric, a separation ratio of 0.5 and a  
25 minimum distance of 0.001 as provided by the software application. A closer  
relationship between CML- and MM-associated MPCs was observed, which in turn  
are related to AML-associated MPC, thus transforming global patterns of gene  
expression into potentially meaningful relationships.

*Two-dimensional cluster analysis of tissue vs. gene expression*  
30 *vectors:* A gene tree was constructed. Genes cluster near each other on the "gene  
tree" if they exhibit a strong correlation across MPC experiments and MPC tree  
branches move near each other if they exhibit a similar gene expression profile. The  
data indicated that the two-way clustering readjusted the location of a number of

genes resulting in accentuation of genomic signatures of each cell type. Investigators can usefully catalog genes composing any unique or signature cluster of interest by creating a gene list and disclosing their identities.

*Self-organizing map (SOM) clusters (6x5) show differential gene expression in bone marrow MPC isolated from different hematopoietic conditions.*

Generation of SOM clusters involved prior normalization and filtering of the data. SOM algorithm was applied as provided by GeneSpring. Visualization of SOM clusters in combination with hierarchical clustering (i.e., MPC tree) revealed correlated meaningful patterns of gene expression. Predicated on the basis of SOM operating principle, the related SOM clusters tend to be located physically close to each other. For example, the juxtaposition of the SOM clusters with the common denominator containing genes that are up-regulated in AML/MDS-associated MPC. Whole or part of any SOM cluster can be selected to make a gene list providing the identities of the genes involved.

*Genes highly expressed in normal MPC but absent or minimally expressed in leukemia-associated MPC*

Lists of genes that are down-regulated in leukemia-associated MPC (AML/MDS, CML and MM) were created in comparison to normal MPC. A Venn diagram was made using these three gene lists. GeneSpring allows creation of sublists of genes corresponding to union, intersection and exclusion. Transcriptional profiles of any of these sublists of genes can be visualized across MPC samples of interest. The following is one such sublist of genes containing genes that are highly expressed in normal MPC and down-regulated in leukemia-associated MPCs revealing the identity of the subset of genes of interest: putative, wg66h09.x1 Soares Homo sapiens cDNA clone, Homo sapiens mRNA for CMP-N-acetylneuraminic acid hydroxylase, Homo sapiens cDNA clone DKFZp586G0421 (symptom: hute1), Human mRNA for histone H1x, Putative monocarboxylate transporterHomo sapiens gene for LD78 alpha precursor, Interacts with SH3 proteins; similar to c-cbl proto-oncogene product, wg82b12.x1 Soares Homo sapiens cDNA clone, Human atrial natriuretic peptide clearance receptor (ANP C-receptor) mRNA, Human 71 kDa 2'5' oligoadenylate synthetase (p69 2-5A synthetase) mRNA, Homo sapiens hMmTRA1b mRNA, Human G0S2 protein gene, Preproenkephalin, Human guanylate binding protein isoform I (GBP-2) mRNA, Human gene for

hepatitis C associated microtubular aggregate protein p44, 17-kDa protein, Human insulin-like growth factor binding protein 5 (IGFBP5) mRNA, GS3686, Human monoamine oxidase B (MAOB) mRNA, Insulin-like growth factor II precursor, Human insulin-like growth factor binding protein 5 (IGFBP5) mRNA, Similar to ribosomal protein L21, X-linked mental retardation candidate gene, and Homo sapiens mRNA; cDNA DKFZp434A202. *Genes not expressed in normal MPC but highly expressed in leukemia-associated MPC*

Lists of genes that are upregulated (instead of down-regulated) in leukemia-associated MPCs (AML/MDS, CML and MM) were created in comparison to normal MPC and a Venn diagram was made. The following is one such sublist of genes containing genes that are inactive in normal MPC but up-regulated in leukemia-associated MPCs revealing the identity of the subset of genes of interest: Beta- tropomyosin, Homo sapiens clone 24659 mRNA sequence, Human mRNA for DNA helicase Q1, OSF; contains SH3 domain and ankyrin repeat, ym22b12.r1 Soares infant brain 1NIB Homo sapiens cDNA clone, Human mRNA for pre-mRNA splicing factor SRp20, Human mRNA for golgi alpha-mannosidaseII, OSF-2os, Homo sapiens gene for Proline synthetase, hk02952 cDNA clone for KIAA0683, wi24g10.x1 Homo sapiens cDNA clone, Lysosomal enzyme; deficient in Sanfilippo B syndrome, CTP synthetase (AA 1-591), WD repeat protein; similar to petunia AN11, Human mRNA for 5'-terminal region of UMK, complete cds, Homo sapiens chemokine exodus-1 mRNA, complete cds, Human GPI-H mRNA, complete cds, Homo sapiens mRNA encoding RAMP1, Transforming growth factor-beta-2 precursor, and Homo sapiens mRNA for KIAA0763 protein.

*Visualizing expression of phenotypically & functionally relevant genes across samples of normal & disease-associated BM MPC.*

Although GeneSpring is a highly flexible and user-friendly software application, it lacks the facility to create functionally relevant gene lists containing user-defined key words. This limitation was overcome by devising the following method via Microsoft Excel. A stepwise protocol to create such a gene list using Excel includes: Open the annotated microarray genome file (e.g., Affymetrix U95A) in Excel → select the column with gene names → select Data from pull-down menu → Filter → AutoFilter → Custom → enter key words (e.g., cell adhesion or cell cycle) → OK → generates a new Excel worksheet with the list of genes containing the key



words. Copy and paste the list of genes containing the key words into GeneSpring and save the gene list with a meaningful name. Twenty-two (22) such functionally relevant gene lists (Table 2) were created.

The resulting approach is a simple and powerful way to peer into the expression profiles of focused sets of functionally relevant genes across samples of interest. For example, the human vascular cell adhesion molecule-1 (VCAM-1) gene is completely down-regulated in AML/MDS and the human insulin-like growth factor binding protein (hIGFBP.1) gene is up-regulated in AML compared to all other samples. Similarly, *Homo sapiens* gene for LD78 alpha precursor is down-regulated in all of leukemia-associated MPCs. Finally, the lineage markers CD45 and CD68 are essentially absent from the leukemia-associated MPCs attesting to the high degree of purity achieved by the sample preparation technique of the present invention.

### Results

The genomic changes observed in leukemia-associated MPCs are striking. As shown in Table 2, the changes (up-regulation and/ or down-regulation) involved hundreds of genes. These changes were most dramatic in MPC associated with AML arising in a background of MDS and involved multiple classes of genes (Tables 1-2). Expectedly, the TNFa-induced changes were extensive. Given the high level of purity of MPC preparations, the enormous genomic changes observed are reflective of the underlying pathologic lesions in the MPCs themselves (and not due to the contaminating leukemic cells and/ or macrophages). These studies strongly support the hypothesis that stromal cells in a leukemic patient are functionally defective and therefore purified MPCs are of value in restoring the loss of hematopoietic function in leukemic patients.

**Table 2. Magnitude of global gene expression changes in leukemia-associated and TNFa-stimulated MPCs in comparison to normal MPC**

	AML/MDS MPC	CML MPC	MM MPC	TNFa MPC
# of genes up-regulated	234	112	108	279
# of genes down-regulated	379	208	251	164

**Table 3. Functional classes of genes analyzed across normal and leukemia-associated MPCs**

Annexins (14) Caspases & apoptosis-related transcripts (33) Cadherins (50) Calmodulins/ calmodulin-dependent kinases (25) Cell adhesion molecules (20) Cathepsins (19) Collagens (71)	Cell division cycle-related transcripts (36) Cytokines (19) Epidermal growth factors and related transcripts (22) Fibroblast growth factors (21) Fibronectins (6) Galectins (6) Growth factors (136)	IGF system (24) Interleukins/ receptors (76) Integrins/ disintegrins (70) Lineage-related markers (19) Laminins (13) Platelet-derived growth factors & receptors (12) TNF alpha-related transcripts (29) TGF beta-related transcripts (25)
---	--	---

5                   The gene lists in Table 3 were created as described above and analyzed using GeneSpring. The numerical value in parenthesis refers to the number of transcripts in the corresponding class of genes analyzed.

#### **Example 6**

10                   The present invention provides the following benefits: a) identification and documentation of BM stromal cell gene expression patterns under varied, normal, and leukemic hematopoietic conditions; b) identification of stromal cell genes that can be therapeutic targets for improvement of normal hematopoietic function that is constantly compromised in leukemic patients, and identification of similar targets for arresting the growth and progression of neoplastic clones since  
15                   stromal cells provide the necessary support for preferential growth of leukemic cells (CLL, MM) within BM and protect the leukemic cells from chemotherapy-induced death (MM); and c) identification of new biological bases and new diagnostic markers for refinement of the classification and diagnosis of leukemia. This present invention can also lead to important insights into the pathogenesis of leukemia. In  
20                   broad terms, analysis of global gene expression or transcriptome (transcriptional profile composed of all transcribed regions of the genome) is considered a nonbiased discovery-driven (as opposed to hypothesis-driven) approach to the analysis of gene expression. A stepwise genomic strategy encompasses preparation of total RNA from cells of interest, to generation of cDNA, to preparation of ds DNA,  
25                   to *in vitro* transcription into cRNA, to fragmentation of cRNA, to hybridization of target RNA, to a microarray of known genes (and/or ESTs), to analysis of

differentially expressed genes using an appropriate software to discern the patterns of gene expression or genomic signatures by a given disease-associated cell type.

Further test utility of sample preparation technology applied to normal EM-derived MPCs (untreated and treated with representative cytokines) and MPCs  
5 derived from patients with representative pre-leukemic and leukemic conditions for performance of high-resolution DNA microarray technology (Affymetrix genechip containing DNA from 12,000 known human genes, e.g., U95A oligonucleotide microarray).

Representative cytokines which are pathologically altered in  
10 hematopoietic conditions and that can be used in this study include TNF- $\alpha$ , TGF- $\beta$  and interferon- $\gamma$ . The pre-leukemic conditions include myelodysplastic syndromes (MDS) and the leukemic conditions include chronic myeloid leukemia (CML), acute myeloid leukemia (AML), acute lymphocytic leukemia (ALL), and multiple myeloma (MM).

15 The front-end strategy of microarray analysis involves the use of Percoll-gradient purified MPCs. As a follow-up strategy, to validate the stromal cell origin of the differentially expressed genes, MPCs obtained from cytopins of BM stromal cells by laser-capture microdissection (LCM) selected on the basis of morphology (Figure 3) are used followed by "real-time" quantitative polymerase  
20 chain reaction (PCR). This can be performed with an LGM system as well as a "real-time" QPCR system. Validation can be performed on at least one sample from each of 6 normal BM M7NC/ MPC types and on one sample from each of 5 leukemia-associated MPC types. Validation is considered successful if the microarray results and PCR results on a given MPC sample match using a suite of 20 genes selected  
25 based on median pattern of microarray results for the given cell type. This approach not only validates the microarray results but also ascertains the stromal cell origin of the expressed genes. The standard published protocols involving LGM and "real-time" quantitative PCR and the instructions accompanying the equipment are used for performing the experiments.

30 Stepwise LCMJ real-time QPCR protocol entails the following. Cytopins are made from BM stromal cells. The cytopins are stained with hematoxylin and MPC is selected for based on morphology. Microdissect up to 1,000 MPC from each sample. RNA is extracted and reverse transcribed into cDNA.

The cDNA is amplified using gene-specific primers and "real-time" quantitative PCR.

By applying the combined power of different analytical techniques (such as hierarchical clustering and self-organizing maps) together with the recently developed sample preparation technology for stromal cells the present invention provides a molecular biological basis that can allow refinement of the classification and diagnosis of leukemias and lymphomas, uncovering the suspected disease heterogeneity. This enables the deciphering of the genomic expression profiles or signatures of bone marrow stromal cells in about 10 different physiologic states and about 20 different leukemic states. In addition to aiding in refinement of the classification and diagnosis of the hematopoietic malignancies, the data provides clues to potential novel drug targets and insights into pathogenesis.

The present invention functions by identifying the MPC genes that are differentially expressed after stimulation with different hematopoietic cytokines implicated in the pathogenesis of pre-leukemic conditions (MDS); in actual pre-leukemic disorders (MDS); and in overt leukemias (CML, AML, CLL, ALL, MM) as well as in lymphomas that have a leukemic phase with involvement of BM.

The present invention is accomplished by first determining the median gene expression profiles for MPCs associated with each disease and stimulated by each cytokine of interest (this objective can be achieved by treating the gene expression vectors of individual cases in each MPC category as replicates; this capability is available in GeneSpring software application). Then the gene groups that are up regulated and down regulated and that are common to all the members in a given MPC category are identified (this is accomplished using a series of Venn diagrams and creating required gene lists via GeneSpring). Finally, the up-regulated and down-regulated gene sets for a given disease-associated or cytokine-stimulated MPC are combined. This allows the identification of gene sets with minimal number of elements that are unique to a given MPC type with a capability to discriminate one MPC type from another (this can also be accomplished by means of a series of Venn diagrams and lists of required genes obtained via GeneSpring). Such gene sets can be of immense diagnostic value as they can be routinely used in an assay simpler than microarray analysis (for example "real-time" quantitative PCR). Such gene sets can additionally provide insights into pathogenesis and possible targets for design of new drugs.

Determine expression profiles of MPC genes which are regulated as a result of exposure of normal MPCs to cytokines that are known to have a hematopoietic support role and/or are abnormally elevated in pre-leukemic/leukemic conditions, i.e., TNF  $\alpha$ ; IL-4; TNF  $\alpha$ + IL-4; interferon  $\gamma$ ; TGF  $\beta$ ; PDGF; FGF; EGF; and calmodulin.

TNF  $\alpha$ , IL-4 and IFN  $\gamma$  are potent negative regulators of hematopoiesis. Notably these cytokines, especially TNF  $\alpha$ , are elevated in marrow plasma of patients with myelodysplastic syndromes (MDS), the clinical hallmarks of which are anemia, leukopenia and thrombocytopenia (i.e., pancytopenia). TNF  $\alpha$  and IL-4 are thus possible mediators of hematopoietic dysregulation typical of MDS. Studies regarding these regulators can uncover the molecular pathways leading to cytopenias in MDS patients. As indicated earlier, myeloproliferative disorders are another, in some ways similar, group of hematopoietic disorders that are clonal in origin but not overtly malignant clinically. These MPDs include polycythemia vera, essential thrombocythemia, idiopathic myelofibrosis (agnogenic myeloid metaplasia) and chronic myelogenous leukemia. These disorders have the potential to change from one to the other at any time, however the signals that trigger such conversion remain enigmatic. Idiopathic myelofibrosis (IMF), in which stromal cells seem to play a profound pathogenetic role, is characterized by fibrosis of the marrow cavity, extramedullary hematopoiesis, splenomegaly, and anemia and leukoerythroblastic features in the peripheral blood. While myeloproliferation is known to be a clonal process, the accompanying stromal cell proliferation and fibrosis are believed to be a polyclonal reactive process that is likely to be due to increased intramedullary activity of a number of cytokines including TGF  $\beta$ , PDGF, FGF, EGF and calmodulin, as shown by other investigators.

Cancer genomics is a rapidly expanding area of investigation. The focus is unique however in emphasizing not the leukemic cells themselves but rather BM stromal cells that provide a haven to various types of pre-leukemia and leukemia cells, non-Hodgkin's lymphomas (NHLs) and metastatic cancers (METs). Pre-leukemic clonal neoplastic conditions include myelodysplastic syndromes (MDSs) and myeloproliferative disorders (MPDs). Stromal cells are known to produce and/or respond to growth factors such as EGF, PDGF, FGF, VEGF, and cytokines such as IL-1 or TNF  $\alpha$ , partially explaining the interactive relationship between stromal cells

and cancer cells, especially in MDS and CML.

In spite of similarities between BM stroma and non-BM stroma, certain sharp distinctions do stand out. Non-BM stromal cells are terminally differentiated fibroblasts, while BM stromal cells represent a unique pluripotent or pluridifferentiated mesenchymal cell type, thus exhibiting preserved developmental "plasticity". Using 5-10 cc BM aspirate samples from adult leukemic patients and 3-5 cc BM samples from pediatric patients with ALL, the study can analyze the BM stroma. One cc of marrow sample can produce at least 1 T-150 flask of stromal cells. One concern is that it can be hard to obtain marrow samples from cases like CML and myelofibrosis. In such cases stromal cells are grown using peripheral blood samples as described in the prior art. At least one flask of stromal cells (i.e., 1 cc marrow) to yield the RNA required for analysis. About 10 cases of each type of leukemia/lymphoma were studied. The study provided important insights into the functioning of the BM microenvironment in normal and leukemic hematopoiesis.

A database including all of the above information and that can include age, gender and associated major illness in terms of clinical/pathologic diagnosis for each subject/patient can be created. This can also include information on cytogenetic, molecular and flow cytometric studies. Finally, also included can be the information on clinical course in terms of disease progression and response to treatment exercising adequate care to protect the identity of individual patients. The study analyzed genomic expression profiles or signatures of bone marrow stromal cells derived from about 12 different normal bone marrow states and about 19 different leukemia/lymphoma states, approximately 10 cases of each as shown in Table 4, accounting for a total of 310 samples.

Using the information of the present invention, those of skill in the art can: a) study select gene or sets of genes as relevant to hematopoietic disease conditions using relatively inexpensive but low-throughput technologies such as Northern blotting, RNase protection assays and/or PCR intended for gene expression analysis; b) reanalyze the primary data by using newer and more powerful bioinformatic tools as they become available; and/or c) identify newer drug targets and diagnostic markers relevant to specific diseases, such as MM or CML etc.

Table 4 Scope of human BM samples targeted for DNA microarray analysis  
(approximately 10 cases of each)

- Normal BM mononuclear cells (NMNC)
- Normal BM stromal cells, unfractionated and unstimulated (NBMS)
- Normal purified mesenchymal progenitor cells, unstimulated (NMPC)
- NMPC stimulated with 9 different cytokines:
- 5 NMPC stimulated with  $\text{TNF}\alpha$  ( $\text{TNF}\alpha$  MPC)
- NMPC stimulated with  $\text{TGF}\beta$  ( $\text{TGF}\beta$  MPC)
- NMPC stimulated with interferon  $\gamma$  ( $\text{IFN}\gamma$  MPC)
- NMPC stimulated with IL-4 (IL-4 MPC)
- NMPC stimulated with  $\text{TNF}\alpha$  + IL-4 ( $\text{TNF}\alpha$  + IL-4 MPC)
- 10 NMPC stimulated with PDGF (PDGF MPC)
- NMPC stimulated with EGF (EGF MPC)
- NMPC stimulated with FGF (FGF MPC)
- NMPC stimulated with calmodulin (calmodulin MPC)
- MDS - Refractory anemia (MDS-RA MPC)
- 15 MDS - Refractory anemia with ringed sideroblasts (MDS-RARS MPC)
- MDS - Refractory anemia with excess blasts (MDS-RAEB MPC)
- MDS - Chronic myelomonocytic leukemia (M1)S-CMML MPC)
- MPD - Polycythemia vera (MPD-PV MPC)
- MPD - Essential thrombocythemia (MPD-ET MPC)
- 20 MPD - Myelofibrosis (MPD-LMF MPC)
- CML (CML MPC)
- AML-M0/M1/M2 (AML-MOJM1JM2 MPC)
- AML-M3 (APL) (AML-M3 MPC)
- AML-M4/M5 (myelomonocytic) (AML-M4iM5 MPC)
- 25 ALL-L1/L2 (lymphoblastic) (ALL-L1L2 MPC)
- ALL-L3 (Burkitt's) (ALL-L3 MPC)
- Multiple myeloma (MM MPC)
- CLL/SLL (CLL/SLL MPC)
- Follicle center cell lymphoma (FCL MPC)
- 30 Mantle cell lymphoma (MCL MPC)
- Lymphoplasmacytic lymphoma (LPL MPC)
- Marginal zone lymphoma (MZL MPC).

### Human Subjects

This study involves the use of bone marrow (BM) samples from human subjects. BM samples can be obtained from normal subjects (male and female 20-45 years) as well as leukemic patients after informed consent is obtained. Leukemic cells can be obtained from diagnostic samples of BM of adult and pediatric patients (in those cases in which cells remain unused after clinical diagnostic studies are

performed; i.e., about 90% of cases).

#### Example 7

In broad terms, global gene expression analysis is considered a nonbiased discovery-driven (as opposed to hypothesis-driven) approach to the analysis of protein expression. A stepwise proteomics strategy encompasses: 5 solubilization of proteins from cells of interest; 2-D gel electrophoresis (IPG DALT); staining and image analysis of gels; excision of protein spots of interest; trypsin digestion of proteins; mass spectrometry (MALDI-TOF MS and/or ESI MS/MS) performed on tryptic fragments; identification of proteins by database searching. The present invention provides a method to analyze the population of expressed proteins 10 (i.e., proteome) of BM MPCs in relation to hematopoiesis in collaboration with a state-of-the-art mass spectrometry facility.

The large-format 2-D gel electrophoretic system is used for reproducible separation of MPC proteins and to prepare 2-D PAGE protein maps for 15 normal bone marrow-derived MPCs (untreated and treated with representative cytokines, e.g., TNF  $\alpha$  and/or IL-4) and for MPCs derived from patients with representative pre-leukemic/premalignant and leukemic/malignant conditions. The pre-leukemic conditions include myelodysplastic syndromes (MDS) and the leukemic conditions include chronic myeloid leukemia (CML), acute myeloid leukemia (AML), 20 chronic lymphocytic leukemia (CLL), acute lymphocytic leukemia (ALL), and multiple myeloma (MM). The protein samples can consist of culture supernatants/secreted proteins; extracellular matrix (ECM) proteins; plasma membrane proteins solubilized using a three-step differential extraction protocol, employing conditions of progressively increasing solubility; and whole cell lysate proteins similarly solubilized 25 using the three-step differential extraction protocol. This subproteome approach not only simplifies the 2-D PAGE electrophoretic protein patterns but also reveals additional proteins, which would otherwise have gone undetected.

The system of the present invention can be used to differentially express MPC proteins (i.e., those that increased or decreased in intensity as 30 compared to 2-D PAGE protein maps of normal, unstimulated MPCs) using mass spectrometry (MALDI-MS and/or nanoelectrospray ionization MS/MS) and/or Western blotting and/or Western-ligand blotting.

Using high-resolution proteomics with the added power of high-



throughput robotics, enables the system to identify on a larger (semi-comprehensive) scale the MPC proteins that are differentially expressed in conditions that simulate pre-leukemic bone marrow (following stimulation with different cytokines); and in actual pre-leukemic disorders (MDS) as well as in overt  
5 leukemias (CML, AML, CLL, ALL, MM).

The system of the present invention enables the identification of MPC proteins whose expression is regulated as a result of exposure of normal MPCs to cytokines that are known to have a hematopoietic support role and/or are abnormally elevated in pre-leukemic/leukemic conditions, i.e., TNF  $\alpha$ ; IL-4; TNF  $\alpha$  + IL-4;  
10 interferon  $\gamma$ ; TGF  $\beta$ ; PDGF; FGF; EGF; and calmodulin.

The system of the present invention also enables the identification of MPC proteins for which expression is altered as a result of exposure of normal MPCs to agents that are clinically used for mobilization of hematopoietic stem cells from BM into peripheral blood to facilitate easy collection and subsequent transplantation,  
15 e.g., G-CSF and G-CSF plus cyclophosphamide.

Further, the system of the present invention enables the identification of Identify the MPC proteins whose expression is pathologically altered in hematopoietic disease states such as: MDS, CML, AML, CLL, ALL and MM by matching the 2-D PAGE protein maps of disease-associated MPCs with the 2-D  
20 PAGE database of normal MPCs. If a protein of interest does not exist in the normal MPC proteome, or if it exists in the normal MPC proteome but has not yet been characterized, then such proteins can be identified by MALDI-MS and/or Nano ESI MS/MS.

The system facilitates understanding of the pathogenetic mechanisms  
25 by identifying the phosphoproteins involved in cell signaling pathways. The systems immunoblots the whole cell lysate proteins of normal MPCs, untreated and treated with respective cytokines, using antibodies to phosphotyrosine, phosphoserine, and phosphothreonine. The system then locates the corresponding putative phosphoprotein spots on the gel and identifies the proteins by MALDI-MS and/or  
30 Nano ESI MS/MS. Similarly, the system can locate the altered phosphoproteins by immunoblotting the whole cell lysate proteins of untreated MPCs derived from leukemic patients. If a protein of interest does not exist in the normal MPC proteome, or if it exists in the normal MPC proteome but has not yet been identified,

then MALDI-MS and/or Nano ESI MS/MS can identify the protein.

**Bone marrow MPCs derived from a leukemia background express distinctively different patterns of cell adhesion molecules from normal MPCs.**

5                   BM stromal cells provide the background required for homing and subsequent proliferation and differentiation of hematopoietic stem cells. BM stromal cells also provide a rich microenvironment for metastases and growth of various leukemias. Based on the hypothesis that homing of normal hematopoietic cells and leukemic cells to marrow utilize the same adhesion mechanisms, it was questioned  
10 whether there are fine regulatory distinctions in terms of quantitative differences in the expression of the adhesion molecules in normal vs. leukemic BM microenvironments. In a pilot study 11 cell adhesion molecules (CAMs) and several lineage-associated markers for Northern blot analysis were targeted. Dexter-type cultures were grown under standard stromal cell culture conditions using bone  
15 marrow samples from a normal individual and from one patient diagnosed with and treated for acute myelogenous leukemia (AML). Representative cultures were treated with cytokines such as TNF  $\alpha$  alone, IL-4 alone, and TNF  $\alpha$  plus IL-4. MPCs from unstimulated and cytokine-treated cultures were purified using Percoll gradient techniques disclosed above. Total RNAs were extracted by a standard method and  
20 analyzed by Northern blotting. This study demonstrated expression by MPCs of several CAMs, heretofore unsuspected of expression by BM stroma. These include an embryonic endothelial cell protein Dell (developmental endothelial locus 1), galectin-I, human milk fat globule protein (RMFG, lactadherin), and epithelial membrane protein I (EMP 1). Secondly, MPCs from the AML patient expressed  
25 significantly lower levels of mRNA for three CAMs Del- 1, galectin- 1, and collagen type 1 as well as for the adipocyte marker adipsin, and to a minor degree the muscle-associated protein caldesmon. On the other hand, mRNA for CAMs like TGF beta-inducible BiGH3, HMFG, osteoblast-specific cadherin 11, and VCAM1 were dramatically increased in AML-associated MPCs. CAMs such as integrin beta 5,  
30 fibronectin, EMP 1 and the muscle-associated molecule transgelin are variably increased in diseased MPCs and appear to be unaffected by treatment with cytokines tested. ICAM I was undetectable at basal level in either patient or normal samples, but was slightly elevated by TNF  $\alpha$  and markedly elevated by TNF  $\alpha$  plus

IL-4. VCAM1 was mildly up regulated by TNF  $\alpha$  alone or IL-4 alone, but markedly up regulated by TNF  $\alpha$ /IL-4 in combination. Also, the MPCs from the patient were much more sensitive to stimulation by these inflammatory cytokines than were the normal MPCs. These studies establish that stromal cells in a leukemic patient are  
5 functionally defective.

**Role of leptin receptor in hematopoiesis using human marrow stromal cells as a model.**

The receptor for the product of the obesity gene, leptin, is widely distributed in tissues ranging from central nervous system to reproductive system to  
10 hematopoietic system. Within hematopoietic system, OB-R is reportedly expressed on diverse cell types ranging from early CD 34+ hematopoietic stem cells to circulating monocytes. Leptin acts on monocytes to induce production of TNF  $\alpha$  and IL-6, which are powerful regulators of hematopoiesis. However, literature reports on the expression of leptin or its receptor on stromal cells are infrequent. To date, one  
15 particular report suggests that leptin acts on the stromal cells to enhance their differentiation into osteoblasts and to inhibit differentiation into adipocytes. Because leptin is an adipocyte-generated hormone and because marrow stromal cells represent a unique pluridifferentiated mesenchymal cell type expressing some adipocytic features, the expression of the leptin receptor by these cells was  
20 investigated in the hope of revealing its role in hematopoiesis.

By Northern blotting marrow stromal cells showed abundant expression of OB-R, consistent with their adipocytic nature. In terms of regulation, exposure of the stromal cultures to different cytokines revealed an interesting pattern of OB-R. As shown, G-CSF and TNF  $\alpha$  down-regulated OB-R while IL-4 up-  
25 regulated OB-R expression by stromal cells. Simultaneous treatment of stromal cultures with TNF  $\alpha$  and IL-4 nearly abolished OB-R expression. The expression of OB-R was also analyzed at the protein level by a high-resolution, high capacity 2-D PAGE system, followed by Western blotting.

More specifically, the method provides the identification of leptin  
30 receptor in human BM stromal cell membrane protein extracts using 2-D Western blotting. The expression of OB-R was investigated at protein level using 2-D PAGE, followed by Western blotting. Two isoforms differing in molecular weight of 2.2 kDa (60.2; 62) and an isoelectric point of 0.2 pH unit (5.78; 5.98, respectively) have been

identified (the pH was determined by using the values specified by the IPG strip manufacturer). The ability to subsequently stain the same Western blot with gold stain allowed precise localization of the immunoreactive protein spots of interest on the blot. The gold staining of the blot, by revealing other protein spots in addition to  
5 the immunoreactive spots, has provided the necessary landmarks in turn facilitating subsequent alignment with the silver-stained gel using an appropriate 2-D analysis software program (Melanie 3).

This technique has identified two OB-R isoforms that differ in molecular mass by 2.2 kDa (60.2; 62.4) and differ in their isoelectric point by 0.2 pH units  
10 (5.78; 5.98). The level of macrophage contamination is determined by two macrophage markers, CD68 and cathepsin B. The studies include the determination of OB-R expression in a) unfractionated stromal cells vs. isolated pluri-differentiated mesenchymal progenitor cells; b) unstimulated cultures vs. cultures stimulated with a variety of cytokine/hormones including leptin itself. The studies also include mass  
15 spectrometric characterization of the two OB-R isoforms detected by Western blotting in order to establish their exact structural differences.

**Proteome analysis of 2-D PAGE separated human BM stromal cell membrane proteins.**

BM stromal cells support the growth and development of normal blood  
20 cells as well as providing a haven for malignant leukemia/lymphoma cells. Focusing on stromal cell-surface proteins as potentially playing a role in cell-to-cell communication in normal as well as in abnormal hematopoiesis, the mixtures of stromal-cell plasma membrane, and plasma membrane-associated proteins were analyzed by a high-resolution, high-capacity 2-D gel electrophoresis. The 2-D  
25 system described utilizes an immobilized pH gradient gel (pH 4-7) in the first dimension and a mini nondenaturing but high-resolution lithium dodecyl sulfate-polyacrylamide gel electrophoresis (LDS-PAGE) in the second dimension. As identified by silver staining, this system has resolved greater than 800 protein spots in a pH interval of 2.5 units (4.25-6.75, the isoelectric pH range for most of plasma  
30 membrane proteins to migrate) and a molecular mass range of 10-150 kDa. Equally important, the system is compatible with high sample loads (up to 1.5 — 2.0 mg of total protein in up to 350- $\mu$ l sample volume). All the protein species identifiable by a silver stain that is compatible with subsequent mass spectrometric analysis have

been analyzed by a 2-D gel software with respect to isoelectric point, molecular weight and mass abundance. The lectin-binding status of these proteins has also been determined by lectin blotting. Lectin blots and Western blots have subsequently been stained by a gold stain for detection of total proteins on the same PVDF membrane. Although gold-staining of the Western blot is not as sensitive as silver-staining of the gel, gold-staining of the Western blot generates the necessary landmarks for alignment with the silver stained gel, facilitating excision of spots of interest from the gel for identification by MALDI-MS. Representative protein spots were excised from gel and subjected to mass spectrometric profiling (MALDI-MS) and/or sequencing (Nano ESI MS/MS) with subsequent database searching, resulting in a productive identification of ten proteins. The protein digests are then submitted in a near-ready state for mass spectrometry. Upon receiving the MS data the group performs the database searching. MALDI/MS has been used, which identifies a protein on the basis of its characteristic mass sizes, as well as MS/MS studies that provide amino acid sequences of selected masses to identify proteins with enhanced specificity and confidence level. This work represents the first systematic attempt to analyze BM stromal cell proteins by high-resolution 2-D gel electrophoresis and provides the basis for a full-scale proteome mapping of the marrow stromal cells. The present work can facilitate the long-term goal of deciphering the hematopoietic support functions of BM stromal cells.

#### **Modulation of stromal cell plasma membrane protein expression by TNF $\alpha$ /IL-4.**

The effects of TNF  $\alpha$ /TM on bone marrow stromal cell plasma membrane protein expression has been tested using the described system. TNF  $\alpha$  and IL-4 are regarded as negative regulators of hematopoiesis. Notably these cytokines, especially TNF  $\alpha$ , are elevated in marrow plasma of patients with myelodysplastic syndromes (MDS), the clinical hallmarks of which are anemia, leukopenia and thrombocytopenia (i.e., pancytopenia). TNF  $\alpha$  and IL-4 are thus possible mediators of hematopoietic dysregulation typical of MDS. TNF  $\alpha$ /IL-4 treatment of the stromal cultures induced dramatic changes in the protein profile. Initial studies using plasma membrane protein samples show reduced expression of at least 7 proteins and enhanced expression of 13 proteins.

#### **Analyzing the insulin-like growth factor system in human marrow stromal cells**

**by 2-D PAGE analysis of BM stromal cell culture supernatants.**

Proliferation and development of normal and leukemic hematopoietic cells within bone marrow is regulated by interplay of various classes of molecules. These include cell adhesion molecules (CAMs), colony stimulating factors (CSFs), and cytokines as well as growth factors including insulin-like growth factors 1 and 2 (IGF 1 and IGF 2), which are small peptide homologs of prolinsulin. IGF 1 has known erythropoietic activity, whereas the function of IGF 2 is less clear. IGF 1 and 2 exert their activities through two types of receptors. The type I IGF receptor, a tyrosine kinase receptor highly homologous to the insulin receptor, binds to IGF 1 and IGF 2 with high affinity. The type II IGF receptor, a mannose 6-phosphate receptor that lacks intrinsic kinase activity, binds IGF 2 with high affinity and IGF 1 with low affinity. The type and number of receptors expressed on a target cell determine the strength of the IGF signal. One important key to understanding the IGFs' role in hematopoiesis is to appreciate how biological effects of receptors are modulated by larger soluble proteins, the IGF binding proteins (IGFBPs), which share no homology with the IGF receptors. Because IGFs and IGFBPs play important roles in cell growth and proliferation in many tissues, and because marrow stromal cells support hematopoietic growth and development, the patterns of expression of the IGF system components by marrow stromal cells cultured under serum-free conditions is necessary. To this end, unfractionated and purified stromal cells were analyzed, side-by-side, by Northern blotting, under varied stimulatory conditions for expression of IGFs and IGFBPs with surprising results. IGF 2 is constitutively expressed at a high level by macrophages in Dexter cultures; it is down regulated markedly by TNF  $\alpha$  alone; moderately by TNF  $\alpha$  plus IL-4; and unaffected by IL-4 alone. On the other hand, IGF 2 is minimally expressed by unstimulated MPCs, but is markedly up regulated by TNF  $\alpha$  alone or IL-4 alone; and moderately up regulated by combined TNF  $\alpha$  and IL-4. IGFBP4 is abundantly expressed both by macrophages and MPCs and is unaffected by cytokine treatment. In contrast, IGFBPs 5, 7, and 10, selectively expressed by MPCs, show no evidence of expression by macrophages and are unaffected by cytokine treatments. IGF 1 and the precursor to IOFBP 3 are not expressed in either macrophages or MPCs, either constitutively or after stimulation with TNF  $\alpha$ , IL-4 or both. In initial studies, bone marrow mononuclear cells expressed none of the IGFs or IGFBPs tested. These

results provide important insights into the operation of the IGF system in stromal cells and it is likely that potentially novel IGFBPs can be uncovered by ligand blotting studies.

The present invention provides a large-format 2-D gel electrophoretic system for reproducible separation of MPC proteins and to prepare 2-D PAGE protein maps for normal bone marrow-derived MPCs (untreated and treated with representative cytokines, e.g. TNF  $\alpha$  or IL-4) and for MPCs derived from patients with representative pre-leukemic and leukemic conditions. The pre-leukemic conditions include myelodysplastic syndromes (MDS) and the leukemic conditions include chronic myeloid leukemia (CML), acute myeloid leukemia (AML), chronic lymphocytic leukemia (CLL), acute lymphocytic leukemia (ALL), and multiple myeloma (MM). The protein samples can consist of culture supernatants/secreted proteins; extracellular matrix (ECM) proteins; plasma membrane proteins solubilized using a three-step differential extraction protocol employing conditions of progressively increasing solubility; and whole cell lysate proteins similarly solubilized using the three-step differential extraction protocol. This subproteome approach not only simplifies the 2-D PAGE electrophoretic protein patterns but also reveals additional proteins, which would otherwise have gone undetected.

**Molecular analysis assay involving the high-resolution 2-D PAGE and mass spectrometric identification of gel-separated proteins.**

The completion of human genome project has provided a huge proteome database including the theoretical mass databases generated on the basis of site-specific cleavage employing proteolytic enzymes, such as trypsin and others. The availability of highly sensitive biological mass spectrometers together with the capability of bioinformatics to search extremely large amounts of data and identify the relevant proteins matching the mass spectrometry data provides the basis for the current excitement in proteomics. The focus of the interest is the BM MPC proteome as expressed under varied functional and disease states. The goal of the present invention is to identify BM MPC proteins that have possible functional and/or pathologic significance, that is, those proteins that show altered levels of expression in response to cytokine treatments and various leukemic states.

Until recently, the focus of the laboratory has centered on isolation and characterization of BM stromal cell adhesion molecules using a novel 2-D cell

blotting technique. For this purpose, applicants have established an analytical 2-D mini gel system that separates stromal cell plasma membrane proteins using 18-cm long 4-7 pH range IPG strips in the 1<sup>st</sup> D (Amersham Pharmacia Biotech). Subsequent to IEF, the IPG strip is cut into appropriately small pieces and subjected to 2 D separation using nondenaturing lithium dodecyl sulfate-polyacrylamide gel electrophoresis (LDSPAGE) and mini gels. The reason for using mini gels in the 2<sup>nd</sup> D is that they are compatible with a downstream functional assay involving cell adhesion. The stromal cell membrane proteins are blotted on to a PVDF membrane and assayed for hematopoietic cell-binding proteins directly on the blotting membrane. The system can be extended using 17-cm long 3-10 pH range IPG strips (Bio-Rad) for separation of stromal cell culture supernatants, ECM proteins, and whole cell lysates. As detected by silver staining of the gels, and analyzed by appropriate software (GelLab II or Melanie 3) this 2-D system has resolved greater than 800 membrane protein spots within a pH interval of 2.5 units (4.25-6.75) and a MW range of 10-150 kDa. Similarly, the ECM samples showed 475 spots; and conditioned media from BM stromal cell cultures grown under serum free conditions showed 524 spots. Not surprisingly, the total cell lysate of BM stromal cultures showed only 553 spots, most likely representing the abundant housekeeping proteins and masking detection of many functionally relevant proteins. These observations provide the rationale for the proposed subproteome approach involving the use of differential solubilization of sample proteins and multiple large gels. Membrane proteins thus far identified by mass spectrometry followed by database searching; proteins are identified by standard Western blotting. Select IGF binding proteins were identified by ligand Western blotting. The blotting shows the identification of IGF-binding proteins (IGFBPs) using 2-D ligand blotting. The conditioned media from BM stromal cultures grown under serum-free conditions were concentrated using Microcon concentrator, and proteins were fractionated using a high-resolution 2-D PAGE. The separated proteins were electroblotted onto PVDF membrane and subjected to Western ligand-blotting assays using 1-125 labeled IGF-2, resulting in the identification of a series of IGFBPs (up to 30 spots). Notably, TNF  $\alpha$  treatment of the cultures down-regulated two LGFBPs and up-regulated IGFBP labeled 6.

By necessity the protein work began on BM stromal cells using a



nondenaturing (LDS-PAGE) mini gel system that contained no reducing/alkylating agents. To preserve the function of 2-D gel separated proteins many otherwise powerful sample preparation methodologies designed for proteomic studies (such as multiple surfactant solution, MSS) were avoided. While mini gels are convenient and allow comparison and information transfer to large-format gels, they are less sensitive.

#### **Subproteomes according to sample prefractionation.**

In order to be able to identify the low-abundance proteins implicated in the regulatory and pathologic processes, a number of approaches to prefractionation of the whole cell lysates have been described. Applicant studied the subproteomes of secreted proteins from BM stromal cell culture supernatants as well as ECM proteins. Notably, the ECM protein samples can be a rich source of functionally relevant cytokines and chemokines since the latter are known to mediate function by binding to ECM. In addition, the plasma membrane and whole cell samples were subjected to the 3-step sequential solubilization protocol shown. The solubilizing solutions can be prepared in-house or purchased commercially (Bio-Rad). The first step involves the use of Tris base, which can solubilize the peripheral membrane proteins and cytosolic proteins. These proteins are lyophilized and subsequently solubilized prior to 2-D PAGE in a standard solubilizing medium (the modified O'Farrell cell lysis solution containing urea, CHAPS, DII, Iris, ampholytes and appropriate protease inhibitors). The resulting pellet can also be solubilized in the standard 2-D solubilizing medium and subjected to 2-D PAGE. Because the standard solution cannot solubilize some proteins, the membrane-rich pellet is finally solubilized in a potent multiple surfactant solution (MSS) consisting of urea, thithea, CI-LAPS, zwittergent 3-10 and tributyl phosphine (TBP) in addition to Iris base and ampholytes that is compatible with subsequent IEF. The MSS has been shown to solubilize the hydrophobic proteins with as many as 12 transmembrane regions (TMRs), facilitating their 2-D analysis. Another final step incorporating 1% SDS in boiling sample buffer can be used to test by 1-D SDS-PAGE if any proteins remained unsolubilized after these extractions (notably, SDS extract is unsuitable for 2-D PAGE analysis since SDS interferes with IEF). The prefractionation step clearly reduces the complexity of the sample. Thus, the serial extractions not only simplify the gel images and reduce spot overlapping frequently encountered in single-step

extractions but also correlate closely with the cellular location of specific proteins, providing clues to their function. The prefractionation strategy can be extended to enriching low-abundance proteins in culture supernatants by selective removal of contaminating albumin using an Albumin Depletion Kit (containing Cibachron Blue  
5 resins) (Genomic Solutions, Inc.). Similarly membrane glycoproteins can be enriched by a Glycoprotein Enrichment Kit (containing lectins) prior to 2-D PAGE analysis (Genomic Solutions, Inc.).

#### **Subproteomes according to overlapping pH gradients.**

Using a series of medium-range and partially overlapping pH gradients  
10 (3-6, 5-8, 7-10, each 17-cm long) (Bio-Rad) can enhance reproducibility and resolution by creating "virtual" gels with up to 40 cm equivalent of PI separation across a pH 3-10 range. Alternatively, a combination of two pH gradients, pH 4-7 and pH 6-11, each 24 cm-long (Amersham Pharmacia Biotech) can be used, also providing a "virtual" separation distance of 40 cm across a pH range of 4-11. These  
15 strips accept micropreparative sample loads (1-2 mg). Notably, a given sample of cells yields a total of 8 protein samples. These samples include one protein sample composed of conditioned medium, one protein sample comprising of ECM proteins, three protein samples derived from plasma membrane lysates and three protein samples derived from total cell lysates, following application of a three-step protein  
20 extraction protocol to purified plasma membranes and total cells. Eight protein samples can thus translate into 24 large format (18 cm) gels corresponding to three overlapping 1st D gels; or 16 extra large format gels (24 cm) corresponding to two overlapping 1st D gels. Proteomics is no longer considered a single 2-D gel study. Taking advantage of the common spots in the 2nd D corresponding to overlapping  
25 regions, PDQUEST software can allow "stitching together" of the constituent gels, creating the so-called "cyber gel" providing a composite map for each protein sample. The data generated can be stored in an internet-accessible 2-D PAGE database in the form of 8 submaps. Three of these submaps correspond to plasma membrane proteins representing 3-step solubilization; one of them corresponds to  
30 secreted proteins; one of them corresponds to ECM proteins; and 3 of them correspond to total cell lysate proteins representing 3-step solubilization. These submaps can be linked to a master synthetic gel, a conglomerate of the submaps, representing the so-called "cyberproteome" of MPCs. Given the ability to run up to

12 IPG strips per 1st D gel (using IPGPhor) and 10 to 12 large or extra large SDS-PAGE gels per 2nd D gel run (using Hoefer DALI and Ettan DALI II, respectively), the resulting number of gels can be well within the manageable workload of one person (36). Although not easily accessible now, some innovative technological developments are on the horizon, e.g., development of fluorescence 2-D difference gel electrophoresis (DIGE), which could minimize the tedium. Unlike the current practice of running different protein samples on separate gels, and then staining and comparing the gels, DIGE technology uses matched, spectrally resolvable dyes (e.g., Cy2, Cy3 and Cy5) to label protein samples prior to 2-D separation. Differentially labeled protein samples are mixed and co-separated by 2-D electrophoresis, allowing analysis of at least three samples on a single gel. Gels are scanned and proteins are subjected to image analysis using appropriate software. Alternatively, one can use a highly sensitive silver stain to visualize the proteins after electrophoretic separation. Notably, the silver stain is compatible with subsequent mass spectrometry analysis.

**Follow-up strategy for 2-D PAGE using the so-called ultrazoom LPG gels with narrow-range pH gradients.**

Commercially available narrow-range IPG strips include pH 3.54.5; 4.0-5.0; 4.5-5.5; 5.0-6.0; 5.5-6.7. These are available as 18 cm and 24 cm-long strips, consequently allowing spanning of 1 pH unit over a distance of 18-24 cm and providing extraordinary resolution. By using narrow pH gradients (1pH unit) up to 10mg of protein would be loaded onto a single IPG gel strip, either by repeated sample cup application or by in-gel rehydration without incurring vertical or horizontal streaking. Employing a combination of such narrow-range overlapping IPG strips, one study utilized up to 40 2-D gels for analysis of a single protein sample. The preference is not to follow such extreme approach but rather to use these gradients as a backup in situations where a functionally relevant protein is first detected by the front-end strategy but could not be studied by mass spectrometry for lack of adequate resolution or due to overlapping spots. The 24-cm long narrow IPG strips can be subjected to 2nd D using correspondingly extra large slab gels (the required precast, plastic-backed gels can be purchased from Amersham Pharmacia Biotech). However, the "giant 2-DE" 30 X 40cm size gels are impractical to handle. The situations for the use of narrow range pH gradients include situations like detection

of proteins by Western blotting using anti-phosphotyrosine antibodies or Western ligand blotting using labeled IGF 1 or 2, which are probably more sensitive than silver staining. Consequently, these assays identify the functionally relevant proteins but without providing the actual identity of the individual proteins. Because the front-end strategy can at least provide the range of the phosphoprotein or the IGF-binding protein identified, on the basis of this information samples can be subjected 2-D PAGE using the appropriate ultrazoom IPG strip, which as indicated above can permit loading of several mg of protein sample. Extra large precast slab gels (26x20 cm) with plastic backing suitable for running the 24-cm long ultrazoom IPG strips and the appropriate electrophoretic system (Ettan DALI II 2 dimension electrophoresis system) that runs up to 12 of these gels are commercially available (Amersham Pharmacia Biotech).

#### **Summary of subproteome strategy.**

The subproteome approach involves: 1) Cellular fractionation involving isolation of purified MPCs. 2) Subcellular fractionation involving preparation of functionally relevant protein sets. These include: 2a) secreted proteins such as colony stimulating factors (CSFs), cytokines, etc in the conditioned media; 2b) ECM proteins such as cell adhesion molecules (CAMs), etc; 2c) plasma membrane proteins such as various receptor molecules, CAMs and components of cell signaling systems, etc; 2d) finally, whole cell lysate proteins that include some of these proteins plus cytosolic and nuclear proteins. The cytosolic and nuclear proteins can be a rich source of target proteins for phosphorylation with a regulatory function.

#### **2-D PAGE data capture and analysis**

2-D PAGE data capture and analysis can be performed using standard equipment and protocols. Silver-stained gels can be scanned using an imaging densitometer and processed with QuantOne software (Bio-Rad) whereas gels stained with fluorescent Sypro Ruby (with 450 nm in the excitation range) can be scanned using a STORM 860 gel and blot imaging system and processed with ImageQuant Solutions software (Amersham Pharmacia Biotech). A number of factors, including differences in sample preparation and loading, staining and image acquisition can influence the reproducibility of 2-D gel protein separation. Quantitative data are reported as spot volumes (integrated spot densities). In

experiments comparing replicate 2-DE patterns of the same sample or 2-DE patterns of samples from different individuals, the spot volumes in each pattern are scaled to correct for differences in the total amount of protein loaded onto each gel. These variations are compensated by accurately comparing the quantity of any spot across multiple gels. These operations can be performed using a dedicated 2-D gel analysis software, Melanie 3. This program can analyze such variations by scatter analysis and can compensate for varying staining absorption across proteins by normalizing protein expression change. Varying stain intensities and sample sizes can be compensated for by relative spots quantification. The Melanie 3 software also has the capability to merge several gel electrophoretic patterns from the same sample into a composite gel, providing fine control over the included proteins. Finally, the software can compensate for gel distortions caused by variations in protein migration through alignment of the gels.

#### **Mass spectrometric instrumentation.**

Examples of such mass spectrometers include, but are not limited to, Voyager DE Pro (Applied Biosystems, formerly Perceptive Biosystems, Inc.) and QSTAR (Applied Biosystems). Voyager DE Pro is a matrix-assisted laser desorption time-of-flight mass spectrometer (MALDI-IOF) that can be operated in a linear mode for the analysis of large biomolecules or in a reflector mode for high-resolution analysis of smaller molecules, i.e., peptides. The MALDI-TOF instrument also utilizes delayed extraction technology that results in greatly increased resolution, sensitivity and mass accuracy. This is the instrument of choice for high throughput analysis, with a capacity of up to 100 samples per sample plate. On the other hand, the QSTAR is a hybrid quadrupole-quadrupole-time-of-flight mass spectrometer. Samples are introduced in solution and are ionized by electrospray. For samples requiring the highest sensitivity, Dr. Jackson utilizes a low flow rate (25 nl min<sup>-1</sup>) electrospray called nanoelectrospray, typically requiring only 1-2  $\mu$ l of a solution for sample analysis. The QSTAR instrument yields data quite similar to those obtained from the MALDI-TOF instrument, except that the QSTAR data analysis is somewhat more complex due to the multiple charging of peptides by the electrospray process compared to the single charging applied to peptides on the MALDI-TOF instrument. One important additional characteristic of the QSTAR is its ability to determine structural information from sample molecules by tandem MS/MS. This is achieved by

effectively "purifying" selected molecules within the mass spectrometer's first quadrupole section. For analysis of peptides produced by tryptic digestion, a single MS experiment is initially performed to determine the masses of components present in the mixture. Next, MS/MS experiments are carried out to select specific peptides for *de novo* amino acid sequence determination. Typically 2 µl of peptide mixture is sufficient for determining the sequences of ten to twelve peptides.

#### Mass spectrometric analysis by MALDI

The scheme for mass spectrometric analysis of in-gel tryptic digests of proteins for the purpose of protein identification consists of several steps. First, the peptides extracted from the gel must be cleaned and concentrated. The cleanup is necessary to remove residual detergent and other non-peptide materials that can interfere with the analysis of the tryptic peptides. This step involves binding of the peptides to a Microcon-SCX adsorptive microconcentrator. This is a cation exchange membrane held within a microcentrifuge device. At low pH, the peptides bind to the negatively charged membrane, while uncharged or negatively charged molecules pass through. After a brief wash, the peptides are eluted from the membrane in two 25-µl steps of 1.5 N ammonium hydroxide in 1:1 methanol/water. The samples are then speed-vac dried for 10 minutes, and fresh solvent is added for additional treatment to concentrate the sample prior to MS analysis. Initially, all samples can be analyzed by MALDI-TOF MS. For this analysis, the sample from the Microcon-SCX elution can be dissolved in 0.1% trifluoroacetic acid (TFA) in water and loaded on a ZipTipC 18 Pipette tip. The tip is then washed with the same solution and the peptides are then eluted directly onto the MALDI-TOF sample plate with 2 µl matrix solution (cyano-4-hydroxy-cinnamic acid, 10 mg/ml in 0.1% TFA in 1:1 acetonitrile/water). The spotted sample is dried at room temperature for at least five minutes before the sample plate is loaded in the instrument. The instrument calibration is performed externally by the addition of a calibration mixture to the sample plate. Samples are calibrated internally if the known tryptic autodigestion peptides are observed in the sample. This can be used as long as the specific type of trypsin used in the proteolytic digestion step is known. After data collection, the data can be further processed in two ways. First, the data can be treated by noise reduction software and second, it can be deisotoped. Software for both operations of these programs are standard features of the Data Explorer system provided with the

Voyager DE Pro mass spectrometer. The obtained peptide mass data can be subjected to peptide fingerprint analysis utilizing one of the protein database search sites on the Internet, such as Mascot or MS-Fit. While each of these search sites has access to several databases, one can initially select either OWL or NCBI nr. One  
5 can search the database with a standard set of criteria without using a species filter. The practice is to select three variable modifications to allow for conversion of peptide N-terminal glutamine to pyroglutamate, and oxidation of methionine residues; allowing for up to one missed cleavage. Neither the protein MW nor the PI can be used as a search parameter (these, however, can be used for subsequent  
10 validation of the matched protein). Also important is that expected peptide masses of known potential "contaminants" such as keratin and trypsin can be excluded from analysis. Finally, the peptide mass tolerance can be set to  $\pm 0.15$  Da relative to the monoisotopic MW of the singly charged peptide ion. Positive database hits are scored with a MOWSE number. The higher the number of hits the greater the  
15 confidence level. The database search algorithm relates the significance level for a given search. If a high MOWSE score is obtained indicating an unambiguous match, one can consider the protein positively identified, otherwise the sample can be subjected to analysis by use of the QSTAR mass spectrometer.

#### **Mass spectrometric analysis by Nano ESI MS/MS.**

20 Samples that require analysis utilizing the QSTAR, following cleanup by Microcon-SCX adsorptive microconcentrator, can be concentrated by binding the peptide mix to a small amount of POROS R12 reversed-phase C18 chromatographic support packed into a nanopurification capillary. The packed capillary column volume is ~ 10-15 nl. The sample, dissolved in 10- $\mu$ l of 5% acetic acid in water, is  
25 applied to the capillary by use of a ten- $\mu$ l gel loading pipette tip. A brief centrifugation forces the liquid down the capillary so that the peptides can bind to the support. The support is then washed with 10-15  $\mu$ l of 0.5% acetic acid in 1:50 methanol/water. The peptides are eluted from the purification capillary into a nanospray capillary by the addition of 2  $\mu$ l of 0.5% acetic acid in 1:1 methanol/water followed by brief  
30 centrifugation with the nanospray capillary stacked just below the purification capillary in a micropurification holder (MDS Protana). Initially, data for a single MS run is collected. The peak masses are labeled and peptides are selected for potential MS/MS sequencing by locating those that appear to be doubly charged.

Most peptides resulting from a tryptic digest can have a significant doubly charged form, which is ideal for MS/MS sequencing. The first quadrupole of the QSTAR is tuned to pass a 2 Dalton window for the pre-selected doubly charged peptide ions, one at a time, for fragmentation by collision with low-pressure argon gas in the second quadrupole. Collision energy is adjusted for each peptide to obtain the best possible MS/MS spectra. Data are collected long enough to get good quality spectra. After MS/MS spectra are collected for all selected peptides, the data are manually interpreted. Internet protein database searches are performed similar to that for MALDI-TOF peptide fingerprint, except that the search is a partial amino acid sequence search with mass information (i.e., Mascot, employing Sequence Query format). The search criteria cannot screen for a species or a protein MW or PI (which, however, can be used for subsequent validation of the protein matched). Also important is that expected peptide masses of known potential "contaminants" such as keratin and trypsin can be excluded from MS/MS analysis. One missed cleavage can be allowed and two variable modifications can be selected, carbamidomethylation of cysteine and oxidation of methionine. The tolerance of the peptide monoisotopic mass can be set to  $\pm 1-0.3$  and the MS/MS tolerance can be set at  $\pm 1-0.2$ . This type of search generally requires only two or three peptide sequences consisting of three of the amino acids per peptide to obtain a statistically significant match (a high MOWSE score). Once a match is identified, a list of the matched peptide's theoretical MS/MS fragments can be generated to compare with the observed fragments to further confirm the correctness of the match.

**Establishment of large-format 2-D PAGE protein maps for MPCs derived from normal BM.**

The normal cell samples include, A) Untreated normal MPCs; B) Normal MPCs treated with TNF  $\alpha$ ; C) Normal MPCs treated with TNF- $\alpha$  and IL-4. Each cell sample can generate a total of 8 protein samples, 1) culture supernatants/secreted proteins (1 protein sample); 2) extracellular matrix (ECM) proteins (1 protein sample); 3) plasma membrane proteins solubilized using a three-step differential extraction protocol employing conditions of progressively increasing solubility (3 protein samples); 4) whole cell lysate proteins similarly solubilized using a 3-step differential extraction protocol (3 protein samples). Each protein sample can generate 3 large format 2 D gels (corresponding to 3 medium-range, overlapping



IPG gradient gels, pH 3-6; 5-8; 7-10). This means each cell sample can generate 24 large format 2 D gels, leading to generation of at least 72 large format gels for analysis of normal MPCs. To account for duplicate or triplicate samples, the gel number falls in the range of 200-300.

5    **Establishment of large-format 2-D PAGE protein maps for MPCs derived from BM involved with representative pre-leukemic and leukemic conditions.**

The disease-associated MPCs include those from MDS, CML, AML, CLL, ALL, and MM. As above, each MPC sample can generate 24 large-format 2 D gels. With 6 such diseases being studied, the gel number can reach 144. To account  
10    for duplicate or triplicate samples, the gel number falls within the range of 400-500. The use of IPGPhor, together with ready-made IPG strips, permits sample in-gel re-hydration and performance of unattended IEF overnight by adding automation to the 2-D procedure.

Using high-resolution proteomics and with the added power of high-  
15    throughput robotics, identify on a larger (semi-comprehensive) scale the MPC proteins that are differentially expressed in conditions that simulate pre-leukemic bone marrow (following stimulation with different cytokines); and in actual pre-leukemic disorders (MDS) as well as in overt leukemias (CML, AML, CLL, ALL, MM).

20        A robotically guided system facilitates excision of protein spots (by a spot cutter or picker) from 2-D PAGE gels, transfer of protein samples to 96-well microplates, and automated protein digestion in the microwells. Such a system reduces the time and labor relative to manual procedures and provides high throughput while minimizing keratin contamination from human skin, a frequent  
25    problem in proteomics research. The preferred method is to excise all spots from a gel but to process only the spots of interest, storing the remaining excised proteins frozen at -70°C for a later use. The robotic components can include MALDI slide spotter in addition to an automated protein spot picker and digestion station.

**Example 8**

30    **Methods**

The present study involved microarray analysis of 23 samples and a corresponding number of chips. The samples were obtained from 4 normal healthy adult human subjects, consisting of mixtures of unfractionated stromal cells

(collective USCs or cUSCs, 8 samples), Percoll gradient-purified MPCs (collective MPCs or cMPCs, 5 samples) and single-cell MPCs (sMPCs, 10 samples) obtained by laser-capture microdissection (LCM). The study design allowed for adequate controls and replicates appropriate for a comprehensive gene expression profiling of normal BM stromal cells. The isolated single stromal cells were selected on the basis of morphology. Wright-Giemsa stained cytopsin preparation revealed characteristically large cells with a relatively irregular nucleus and cytoplasm compartmentalized into ectoplasm and endoplasm. Subsequently, applicant identified a hematoxylin stain as a substitute for Wright-Giemsa stain. The hematoxylin stain is simpler to use and provides morphologic detail sufficient to allow recognition and isolation of these cells by laser capture microdissection and does not interfere with the downstream microarray testing (see details under Materials & Methods). The photomicrographs of 10 stromal cells that have been subjected to microarray testing are shown in Figure 15. To serve as controls and facilitate comparison, applicant analyzed side-by-side 8 samples of unfractionated stromal cells that are "contaminated" by up to 35% macrophages and 5% hematopoietic cells (referred to collective USC, or cUSC), and 5 samples of Percoll-gradient purified stromal cells, up to 95% pure (referred to collective MPC, or cMPC to distinguish from sMPC). RNA isolated from sMPC samples was subjected to 2 rounds of amplification using RiboAmp kit (Arcturus, Inc) prior to *in vitro* transcription (IVT). In contrast, RNA samples isolated from cUSCs and cMPCs were used without amplification for IVT. The subsequent steps of microarray testing were standard for all 3 types of samples and are schematized as follows: Preparation of total RNA → generation of cDNA → preparation of ds cDNA → *in vitro* transcription into cRNA → fragmentation of cRNA → hybridization of target RNA to a microarray of known genes (Affymetrix U95Av2 oligonucleotide microarray, with 12,625 probe sets) → Signal quantification and first-tier analysis using the microarray quantification software, Microarray Suite (MAS v. 5, Affymetrix, Inc). The presence of a gene within a given a sample was determined at a detection p-value of <0.05, according to the statistical expression analysis algorithm employed by MAS v.5, and was graded absent (A), marginal (M) or present/ positive (P).

#### **Assessment of RNA amplification method**

Since single-cell microarrays are relatively novel, applicant critically reviewed the

data with respect to two important statistics that would reflect on the reliability of RNA amplification assay procedure employed before analysis involving data-mining techniques. **a) 3': 5' ratios of housekeeping control genes:** As shown in Table 9, these ratios were close to 1 in the standard unamplified samples, whereas, they were increased in the amplified samples. Although this is to be expected due to preferential amplification toward 3' end, since amplification may not proceed all the way up to 5' end, applicant wanted to exclude possible sample degradation. For reasons unclear, in the case of ACTB (beta actin), the 3': 5' ratios were highly variable across single cell MPC samples. In any event, the 3': 5' ratios in case of GAPD (glyceraldehyde 3-phosphate dehydrogenase) were relatively tight, suggesting no evidence of sample degradation. Furthermore, both GAPD and ACTB gene probes that were employed as part of the standard gene probe set yielded relatively stable signals across replicates in each sample type, which is further evidence of intactness of RNA samples targeted for microarray analysis. **b)**

**Number of genes present or detected:** As outlined in Table 9, the amplified single cell MPC RNA samples expectedly showed significantly lower number of genes compared to the standard RNA samples (on average 34% vs. 46% of the genes etched on the array). The fact that the number is relatively constant across single cell replicate samples is further indication of the reliability of the data. Notwithstanding the shortcomings of the amplification procedure, it is important to bear in mind that the conclusions are based only on those stromal cell genes that are detected commonly across unamplified cMPCs and cUSCs as well as in amplified sMPCs (but do not include the genes undetected or the genes selectively detected in sMPCs).

**25 Data mining and reproducibility of overall procedures**

The thrust of the present invention is to identify genes that are relatively uniformly expressed across normal untreated bone marrow stromal cell samples, regardless whether they are of single cell type or collective cell samples, purified or unpurified. As detailed under Materials & Methods, GeneSpring was used to achieve the following data-analysis objectives: a) Filtering for genes reliably detected in each sample group by eliminating the genes with weak expressions that are statistically close to the background estimate. b) Filtering for genes that are active or "present" across replicates in each sample group. c) Exclusion of genes

with weak expressions from genes "present" in each sample group. d) Preparation of master stromal cell gene list by intersecting gene lists from step (c) (as shown in Figure 16). These steps have led to identification of a list of 2755 genes that are detected in at least 7 of 8 cUSC samples AND 4 of 5 cMPC samples AND 9 of 10 sMPC samples, i.e., in at least 20 of 23 stromal cell samples investigated. The main conclusions of the present report are based on this "stromal cell gene list" that is broadly representative of all 3 types of stromal cell samples investigated, and not on a gene list that is selective to sMPCs. A hallmark of the quality of microarray data can be discerned from hierarchical cluster analysis of replicates, which involves the principles of vector algebra. An array of numbers representing expression levels of a particular gene in terms of normalized signal intensity in a group of samples is considered a gene expression vector. Likewise, an array of numbers showing expression levels of a group of genes by a particular tissue sample is considered a tissue expression vector. In the case, applicants have 2755 gene expression vectors and 23 tissue or sample expression vectors. These vectors are amenable to algebraic treatment, facilitating calculation of similarity between any two gene- or tissue-expression vectors on the basis of a correlative metric or a similarity-measure employed, e.g., Euclidean angle. Grouping together of two samples on the basis of these principles signifies that they are most closely related out of all the samples in terms of their overall pattern of gene expression. Construction of a bone marrow stromal cell hierarchical tree has enabled visualization of global gene expression patterns across replicates and conditions. As shown in Figure 17, stromal cell genes that are expressed at a relatively lower level in amplified samples (sMPCs) are clustered to the left of gene tree, genes that are more strongly expressed in sMPCs are prominently figured in the middle of gene tree, and genes that are expressed approximately at same level as in unamplified samples (cMPCs and cUSCs) are clustered to right of gene tree. Even more important as noticeable on the sample or experiment tree, hierarchical clustering segregated the members of each sample type into a separate group (cMPC, cUSC and sMPC). Note within each sample type, corresponding subject replicates clustered together with minor exceptions. This is a reflection on the reproducibility of the overall assay-procedures employed, which encompass a variety of stages and steps in addition to target RNA amplification prior to *in vitro* transcription (see Materials & Methods for details).

Finally, it is important to keep in mind that the measured level of a transcript following amplification does not necessarily provide a quantitative estimate of gene expression, but only provides a qualitative indication that the gene is transcriptionally active, which by itself is sufficient grounds for the conclusions arrived at in the present report. As shown in Figure 18, the expression of genes within the stromal cell gene list ranges from 0.2 to 6 (on the log scale) in unamplified samples (cMPC and cUSC) and from 0.02 to 36 in amplified samples (sMPC), thus showing much greater variability in the amplified samples. For illustration purpose, the coloring of gene expression curves (following the linear color bar shown on the right) was based on the gene expression pattern of a particular single-cell sample, SCA1. Note that the genes that are detected at a low level in this sample (as indicated in blue) are not necessarily expressed at a low level in unamplified samples (as read by the log scale on Y-axis). In fact, a significant number of them are expressed at a high level in the unamplified samples. This finding together with the observation that amplified samples detected about 34% of genes as opposed to unamplified samples detecting about 46% of genes tested (Table 9), strikes a cautious note that some genes do not amplify at all by the method used, and other genes amplify to a sufficient degree to be detectable (shown in blue), while some other genes amplify to a degree equal to (in yellow) or surpassing (in red) the amounts in the collective samples. (The curve shown in white is the housekeeping gene, GAPD.) The statistical algorithm as implemented in the latest version of Microarray Analysis Suite (MAS v.5) determined that a gene within a given sample as positive, regardless of grading. To overcome the limitations of the amplification procedure employed, applicant focused only on genes that were positive in at least 20 of the 23 stromal cell samples investigated.

A stromal cell gene list is expected to be representative of typical stromal cell gene expression profile. Such master gene list forms the basis for derivation of all other stromal cell gene lists, organized in accordance with lineage or functional categories. As depicted in Figure 19A & 19B, and listed in Tables 10 through Table 17, that were prepared according to lineage/ functional assignment, the findings show that isolated single cells simultaneously express genes associated with diverse mesenchymal cell lineages, namely osteoblasts, muscle cells, fibroblasts, adipocytes, epithelial cells, endothelial cells, nerve cells and glial cells,

providing confirmation of the existence of a pluridifferentiated progenitor cell type. By definition the stromal cell genes are present in at least 4 of 5 collective MPC samples AND 7 of 8 collective USC samples AND 9 of 10 single cell MPC samples; consequently, they are active in at least 20 of 23 samples tested, representing a  
5 typical genomic profile of stromal cells. The following gene lists are sub-lists of the master stromal cell gene list consisting of 2,755 genes. The stromal cell gene list contains a number of genes that are capable of causing endothelial differentiation and vasculogenesis within the marrow microenvironment; however, these genes themselves are not necessarily endothelial cell markers. In fact, stromal cells  
10 express a gene, EDF1, the expression of which inversely correlates with endothelial cell differentiation within the stromal cells. Of the 67AFFX control genes present on the U95A v2 chip, 22 genes are detected in at least 7 of 8 cUSC samples, 24 genes are detected in 4 of 5 cMPC samples and 19 genes are detected in at least in 9 of 10 sMPC samples. Thirteen of these genes are present in the stromal cell gene list,  
15 i.e., in 20 of the 23 samples investigated.

As evident from these gene lists, note that an isolated single stromal cell simultaneously expresses transcripts for epithelial and neuroectodermal cell types as well. Departing even further from the initial thinking, the findings add to the evidence that the MPCs within the Dexter system might represent a form or stage of  
20 the progenitor cell that is common to nonhematopoietic and hematopoietic cells. As depicted in Figure 20, and listed in Table 18 through Table 21, the isolated single stromal cells express transcripts that are typical of hematopoietic cells, in particular precursor B cells. That BM stromal cells express CD10 (CALLA) is not novel since BM stromal cells as well as endometrial stromal cells and normal breast  
25 myoepithelial cells are known to express CD10. However, the expression of CD19, CD79A and immunoglobulin enhancer binding factors E12/E47 (proto-oncogene TCF3) by BM stromal cells is unforeseen, and forms the basis for postulating the existence of a common progenitor with B cell lineage. B-cell progenitors typically display the phenotype, (CD45 +/-, CD34 +/-, CD20 +/-), (CD10 +, CD19 +, CD79A +,  
30 HLA-Dr +), which as reported here is also displayed by isolated single stromal cells at least at the transcriptome level.

CD45 positivity by cMPC and cUSC samples is attributable to coexisting or contaminating hematopoietic cells in these samples as evidenced by

concurrent positivity for myelomonocytic markers CD13, CD33 and CD14 (Table 21). However, a similar explanation cannot hold true in case of isolated single stromal cells. The protein products or transcripts for CD45 and CD19 are most likely present in stromal cells at a basal level that is beyond the detection limits of conventional techniques, e.g., immunocytochemistry and Northern blotting, respectively. Conceivably, two rounds of amplification prior to IVT sufficiently increased their transcript levels to be detected by microarray analysis. In fact, the CD45 levels were several-fold lower in cMPC and cUSC compared to CD45 levels in sMPC, and CD19 was undetectable in unamplified samples. Finally, note that CD45 and CD19 are not isolated examples in this regard since applicant has identified at least 200 other genes that are uniquely present across sMPC samples but undetectable in cMPC and cUSC (Figure 16).

#### **The issue of stromal cell – B cell connection**

Although no anlage of Bursa of Fabricius exists in mammals, bone marrow is generally regarded as the site of B-cell generation. While the Dexter type stromal cell culture system was devised for investigation of hematopoiesis, specifically myelopoiesis (see Introduction), Whitlock and Witte developed another system for the study of B-lymphopoiesis. Whitlock-Witte cultures, like Friedenstein cultures, are grown in the absence of hydrocortisone and horse serum. When stromal cell layers in W-W cultures are seeded with fresh bone marrow as a source of B cell precursors or with purified B cell precursors, the latter then differentiate into mature B cells. On the other hand, although Dexter cultures do not promote B cell maturation, Dexter cultures do contain B cell precursors, which upon switching of culture conditions from those of Dexter to Whitlock-Witte, differentiate into mature B cells. While BM stromal cells in one form or another are definitely known to support B-lymphopoiesis, it has not been so clear as to whether stromal cells actually give rise to B-cell precursors. Evidence for a progenitor cell common to stromal cells and hematopoietic cells has been coming to light piecemeal in the form of isolated reports. 1) Singer JW et al in 1984 in the course of investigating bone marrow cultures from human patients with clonal myeloproliferative disorders showed that the nonhematopoietic stromal cells were derived from the same clonal progenitors that were involved by the hematopoietic neoplasm, as revealed by G6PD marker analysis. 2) Huss R et al in 1995 in the course of investigating a canine BM stromal

cell line showed that the adherent stromal cells had "turned" into nonadherent hematopoietic cells, especially when the latter were cultured in presence of stem cell factor. 3) Pessina et al in 1997 showed that a particular murine stromal cell line upon stimulation with bFGF, expressed a B-cell phenotype, including CD45R and surface immunoglobulin. Although not by design, applicant shows for the first time that isolated single stromal cells express transcripts that are typically associated with hematopoietic lineage, namely, CD45 and CD19, as well as relevant proto-oncogenes and transcription factors. These results are strongly supportive of the existence of a progenitor cell common to bone marrow stromal cells and hematopoietic cells, particularly the bone marrow-derived (B) lymphocytes. Note that the study involves no feeder cells, no embryonic stem cells, no cell lines and no colonies of cells. Contrasting with the existing literature, the present study embarks on a new path of investigation entailing gene expression analysis of single, primary, normal human stromal cells that suggest a broad capacity for multilineage differentiation. On this model, progenitor cells express genes that are characteristic of any of the lineage fates that these cells are capable of adopting.

#### **Perspective on pluripotentiality vs. pluridifferentiation**

The present investigation involves isolated single stromal cells, consisting of 10 cells from 4 different individuals (Figure 15). The cell culture system has been earlier characterized at light microscopic level, ultrastructural level and by karyotypic analysis, showing no evidence to suggest the artifacts discussed. Spontaneous cell fusion most likely involves monocytes/macrophages, forming multinucleated giant cells; however applicant observed no expression of myelomonocytic marker genes by isolated single stromal cells (Table 12). Keep in mind that the readout of *in vivo* transdifferentiation studies involves localization of different lineage cells in different tissues or organs; such a situation only requires fusion between two cell types (one donor cell and one recipient cell) for the investigators to believe the artifact as transdifferentiation. In contrast, applicant shows here presence of genes for a variety of cell-lineages simultaneously within the same cell. The probability of an array of different cell types fusing into one cell which then masquerading as a pluridifferentiated cell, and that too happening with 10 of 10 cells investigated, is in the opinion close to zero. There has never before been an opportunity to assess the extent of differentiation within these multipotential



progenitor cells in molecular terms at the single-cell level. Theoretically, a) A stem cell can directly become a terminally differentiated cell, or b) A stem cell can enter a phase of multilineage differentiation prior to becoming a single-lineage, mature cell. To the knowledge, this study is the first systematic attempt to answer these questions at the single cell level by using the marrow stromal cells as a model. Although numerous forward-looking reviews exist on the topic of single-cell genomics, only a rare report is available on the actual application of this technology. Applicant has applied this frontier technology to show that a phase of multilineage differentiation indeed exists at least in Dexter-type stromal cells. Pluripotentiality of the bone marrow mesenchymal stromal cells in terms of their ability to become muscle cells, bone cells, fat cells and fibroblasts under select culture conditions has been described by other investigators. Instead of documenting another example of the phenomenon per se, the results provide an independent validation of the studies on transdifferentiation by casting light at the molecular basis of cellular plasticity. Finally, to borrow a concept from the clinical practice setting, a morphologically "poorly" differentiated neoplasm expressing hematopoietic markers is classified as a leukemia/ lymphoma and treated as such. Similarly, a morphologically "undifferentiated" neoplasm marking for epithelial gene expression is diagnosed as a carcinoma and treated according to the protocols designed for a carcinoma. It is in this sense that applicant uses the term "pluridifferentiated" as opposed to "pluripotent" to characterize the BM stromal cells. Notwithstanding the semantics, applicant shows that the pluripotent stromal cells are pluridifferentiated, at least at the molecular level.

### Conclusions

The findings of the present study clarify the on-going controversy as to the co-existence of multiple stromal cell types vs. one stromal cell type with co-expression of multiple phenotypes within the Dexter system of BM stromal cell cultures. An isolated single stromal cell from these cultures simultaneously expresses an array of phenotypes, i.e., osteoblasts, fibroblasts, muscle cells, adipocytes, epithelial cells, endothelial cells, neural cells/glia cells and even hematopoietic cells, in particular, B-lymphoid progenitors, thus documenting its wide differentiation repertoire. The significance of the findings is three-fold, 1<sup>st</sup>) They validate the hypothesis that the BM stromal cells express a pluridifferentiated

progenitor cell phenotype, providing insight into the molecular basis of cellular plasticity as well as establishing the utility of single-cell genomics, 2<sup>nd</sup>) They provide evidence for a common progenitor for mesenchymal progenitors and BM-derived (B) lymphoid progenitors, 3<sup>rd</sup>) By establishing a comprehensive phenotype of cultured  
5 bone marrow stromal cells at single cell level for the first time, the findings pave the road for ultimate identification and investigation of these cells in fresh samples of marrow, normal as well as diseased, in which they occur at a low frequency.

## Materials & Methods

### Second-tier data-analysis/ data mining

10 The microarray data outputted by MAS v.5 (in the form of tab delimited text files) were imported into GeneSpring<sup>TM</sup> software version 4.2.1 (Silicon Genetics, Redwood City, CA). Following instructions accompanying GeneSpring, each gene was normalized to itself (per-gene normalization) by using the median of the gene's expression values over all the samples of an experimental group (or groups) and  
15 dividing each measurement for that gene by the corresponding median value, assuming that it was at least 0.01. The ratios were then log transformed to base e. No per-sample normalization was performed in GeneSpring since it was already accomplished as part of MAS v.5 analysis. The purpose of the above data transformations, including scaling and normalization, was to remove systematic error  
20 within and across conditions or experimental groups prior to further analysis. GeneSpring was used to achieve the following data-analysis objectives: **a) Filtering for reliably present genes by eliminating the genes with weak expressions that are statistically close to the background estimate.** As per the instructions accompanying GeneSpring, random error was estimated from control strength or  
25 median measurement level using the two-component global error model of Rocke-Lorenzato that assumes variability between replicates as being similar for all genes showing similar measurement level. The formula for the error model of normalized expression levels can be written as follows:

$$S(norm)^2 = a^2/C^2 + b^2$$

30 Where, S = standard error of normalized expression data, a & b are the two error components, a = an absolute or fixed error component impacting at lower measurement values, b = a relative or proportional error component impacting at higher measurement levels, and C = control strength. According to the

manufacturer, a curve is fitted for each group of replicates, with standard error of normalized data on Y-axis vs. control strength on X-axis. At lower end of control strength, the normalized standard error would be high and as the control strength increases, the standard error would decrease reaching a point where the curve flattens and data become more reliable. Control strength for each condition or sample group at which the above-referred two error components contribute equally, was calculated as follows, for collective MPCs,  $C = 128.68$ ; collective USCs,  $C = 253.52$ ; single-cell MPCs,  $C = 348.32$ . Each condition was filtered for genes expressing signals greater than the respective control strength, thus eliminating the genes with weak expressions from each group. Note 7,196 genes (out of 12,625 gene probes tested) passed the restriction in case of cMPCs, 7,287 genes in case of cUSCs and 5,937 in case of sMPCs. Corresponding gene lists were created. **b) Filtering for genes "present" across replicates in each sample group.** GeneSpring's "Add data file restriction" feature was used to prepare the respective lists of genes that were present (or expressed or active) in a least 7 of 8 cUSC samples, 4 of 5 cMPC samples, and 9 of 10 sMPC samples. Note 5,204 genes (out of 12,625 gene probes tested) passed the restriction in case of cMPCs, 4,763 genes in case of cUSCs, and 3,124 genes in case of sMPCs. Corresponding gene lists were created. **c) Exclusion of genes with weak expressions from genes "present" in each sample group.** Respective gene-lists for each sample group from steps (a) and (b), were intersected via Venn diagrams. Note 5,204 genes passed the restriction in case of cMPCs, 4,761 genes in case of cUSCs, and 3,124 genes in case of sMPCs, which are almost identical to the numbers obtained as under step (b), except for a difference of 2 genes in case of cUSCs, thus providing no significant improvement in restricting the data beyond under step (b). This is a reflection of the high stringency of the criterion employed under step (b). The 2 genes in case of cUSCs that passed the restriction under step (b) but failed the combined restriction under step (c) did show weak expressions (raw signals ranging, 142-331). Corresponding gene lists were created. **d) Preparation of master stromal cell gene list.** Respective gene lists for the three sample groups from step (c) were intersected via Venn diagrams, resulting in identification of a list of 2,755 genes that are uniformly present or expressed in at least 20 of 23 stromal cell samples investigated. The stromal cell gene list thus arrived at contained genes that

are representative of diverse mesenchymal lineages. Parenthetically, intersecting of gene lists corresponding to the three sample groups from step (b) resulted in a stromal cell gene list consisting of 2,756 genes, thus differing by 1 gene from the "official" master stromal cell gene list. **e) Two-way hierarchical clustering of 2755 stromal cell genes based on expression profiles in 23 stromal cell samples.**

Only the data that were "cleaned up" of genes with weak expressions as outlined under step (a) were used for hierarchical clustering. This necessitated further processing of data in Microsoft Access prior to analysis by GeneSpring. Note that the data for each individual sample as outputted by MAS v.5 contained probe IDs, quantitative and qualitative data, as well as other information such as annotations and are readily recognizable by GeneSpring. In contrast, the gene list, resulting from step (a), contained only probe IDs and could not contain the data associated with each individual sample and was not recognizable by GeneSpring for inputting as part of an Experiment. Therefore, the microarray data for each group of individual samples (in Excel format) as well as the corresponding gene list for that group from step (a) (also in Excel format) were imported into an Access database. The genes that did not pass the test under step (a) were deleted from the microarray data for each individual sample by querying and intersecting with the appropriate post-clean-up gene list. The resulting data files were saved first as Excel files, then re-saved as tab delimited text files and then imported into GeneSpring. Per-gene normalization and log transformation were applied as described above. "Gene Tree" and "Experiment Tree" were constructed by applying a method similar to that of Eisen et al as implemented in GeneSpring and by using the stromal cell gene list and the following parameters: standard correlation as similarity measure; a minimum distance of 0.001; and a separation ratio of 0.5 in case of Gene Tree and 1.0 in case of Experiment Tree. **f) Preparation of stromal cell gene lists as relevant to different cellular phenotypes and/ or functions.** The gene lists associated with distinct mesenchymal cell lineages or phenotypes, i.e., osteoblasts, fibroblasts, muscle cells and adipocytes, etc, were prepared using a combination of methods. These include 1) Visually inspecting the entire stromal-cell gene list for relevant key words. 2) Directly searching the stromal cell gene list by using key words of interest via "Advanced Find Genes" feature under Edit menu in GeneSpring and by selecting "Search Only Current Gene List". 3) Intersecting the stromal cell gene list with gene

lists of interest from Gene Ontology lists, e.g., list of oncogenes, via Venn diagrams.

**g) Visualization of gene-expression plots.** The expression pattern of a gene across a given group (or groups) of samples of interest was pictured via Gene Inspector window, utilizing desired display options.

5                    Throughout this application, various publications, are referenced by author and year. Full citations for the publications are listed below. The disclosures of these publications in their entireties are hereby incorporated by reference into this application in order to more fully describe the state of the art to which this invention pertains.

10                   The invention has been described in an illustrative manner, and it is to be understood that the terminology which has been used is intended to be in the nature of words of description rather than of limitation.

                    The preceding descriptions of the invention are merely illustrative and should not be considered as limiting the scope of the invention in any way. From the  
15   foregoing description, one of ordinary skill in the art can easily ascertain the essential characteristics of the instant invention, and without departing from the spirit and scope thereof, can make various changes and/or modifications of the inventions to adapt it to various usages and conditions. As such, these changes and/or modifications are properly, equitably, and intended to be, within the full range of  
20   equivalence of the following claims.

## Tables

Table 5.

Summary of bone marrow stromal cell samples targeted for microarray analysis  
with an outline of the corresponding indicators of assay quality performance

	Unfractionated stromal cells (Collective USC, 8 replicates)	Percoll gradient-purified stromal cells (Collective MPC, 5 replicates)	LCM-dissected single cell samples (Single Cell MPC, 10 replicates)
Subject A	UNFR A	MPC A	SCA1, SCA2, SCA3
Subject B	UNFR B, UNFR B R1, UNFR B R2	MPC B R2	SCB1, SCB3
Subject C	UNFR C R1, UNFR C R2	MPC C R2	SCC1, SCC3
Subject D	UNFR D R1, UNFR D R2	MPC D R1, MPC D R2	SCD1, SCD2, SCD3
Amplification of RNA before IVT	No	No	Two rounds
Number of genes present (% of 12,625)	Mean: 46.63 SD: 5.95	Mean: 46.54 SD: 3.66	Mean: 33.93 SD: 3.94
3':5' ratio, GAPD M33197 (Probe used as part of housekeeping control gene probe set)	Mean: 0.89 SD: 0.33	Mean: 1.23 SD: 0.53	Mean: 6.76 SD: 2.97
GAPD signal 35905_s_at (Probe used as part of standard gene probe set)	Mean: 130,723 SD: 36,990	Mean: 164,593 SD: 40,204 (See Figure 5B.)	Mean: 43,235 SD: 14,413 (See Figure 5B.)
3':5' ratio, ACTB X00351 (Probe used as part of housekeeping control gene probe set)	Mean: 1.44 SD: 0.60	Mean: 2.29 SD: 1.57	Mean: 57.92 SD: 67.82
ACTB signal 32318_s_at (Probe used as part of standard gene probe set)	Mean: 86,104 SD: 18,458	Mean: 100,383 SD: 28,427 (See Figure 5B.)	♦ Mean: 4,445 ♦ SD: 884 (See Figure 5B.)

## Footnote to Table 5

Replicate samples shown under each sample type as indicated correspond to each subject. The replicates of collective USC and collective MPC represent cell-culture or biological replicates of stromal cells grown in parallel flasks (instead of technical replicates). We started with 27 samples of which 2 collective MPC samples and 2 single cell MPC samples failed either at the test chip stage or produced unusual results in terms of the number of genes present and/or 3':5' ratios and were therefore excluded as outliers. Only those samples that were targeted for the data mining analysis are represented in this table. The statistics shown (means and SDs) were based on the number of sample replicates indicated in the top row of the table except for ACTB-signal for single cell MPCs (noted in the table by ♦), which were based on 9 replicates instead of 10.

Table 6: Osteoblast/ bone cell/ bone disorders (Shi, B)

Systematic	Common	Genbank	Description	Phenotype/ Function
38112_g_at	CSPG2	X15998	chondroitin sulfate proteoglycan 2 (versican)	OMIM Notes: c-fos restricted to perichondrial growth regions of the cartilaginous skeleton.
38111_at	CSPG2	X15998	chondroitin sulfate proteoglycan 2 (versican)	
38126_at	BGN	J04599	biglycan	
36976_at	CDH11	D21255	cadherin 11, type 2, OB-cadherin (osteoblast)	
37315_f_at	BM036	AI057607	uncharacterized bone marrow protein BM036	
36996_at	OS-9	U41635	amplified in osteosarcoma	
41202_s_at	OS4	AF000152	conserved gene amplified in osteosarcoma	
671_at	SPARC	J03040	secreted protein, acidic, cysteine-rich (osteonectin)	
2087_s_at	CDH11	D21254	cadherin 11, type 2, OB-cadherin (osteoblast)	
1916_s_at	c-fos	V01512	Human cellular oncogene c-fos (complete sequence).	
1915_s_at	c-fos	V01512	Human cellular oncogene c-fos (complete sequence).	?Osteoporosis, involutional; Rickets, vitamin D-resistant
1388_g_at	VDR	J03258	vitamin D (1,25- dihydroxyvitamin D3) receptor	
1451_s_at	OSF-2	D13666	osteoblast specific factor 2 (fascin-like)	
32094_at	CHST3	AB017915	carbohydrate (chondroitin 6) sulfotransferase 3	Ehlers-Danlos syndrome, type VIIA2; Marfan syndrome, atypical; Osteogenesis imperfecta, 3 clinical forms, 166200, 166210; Osteoporosis, idiopathic
32307_s_at	COL1A2	V00503	collagen, type I, alpha 2	
32306_g_at	COL1A2	J03464	collagen, type I, alpha 2	



32305_at	COL1A2	J03464	collagen, type I, alpha 2	Ehlers-Danlos syndrome, type VIIA2; Marfan syndrome, atypical; Osteogenesis imperfecta, 3 clinical forms, 166200, 166210; Osteoporosis, idiopathic
34321_i_at	GS3786	D87120	predicted osteoblast protein	
34342_s_at	SPP1	AF052124	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)	
34763_at	CSPG6	AF020043	chondroitin sulfate proteoglycan-6 (bamacan)	
222_at	EXT1	S79639	exostoses (multiple) 1	Chondrosarcoma; Exostoses, multiple, type 1
36822_at	WAC	U51334	WW domain-containing adapter with a coiled-coil region	Chondrosarcoma, extraskeletal myxoid
41202_s_at	OS4	AF000152	conserved gene amplified in osteosarcoma	
40790_at	BHLHB2	AB004066	basic helix-loop-helix domain containing, / transcription factor class B, 2; OMIM Notes: Alternative title, DEC1, expressed primarily in differentiated chondrocytes.	

Table 7: Muscl / muscle disorders (Seshi, B)

Syst matic	Common	Genbank	Description	Phenotype/ Function
38251_at 38923_at	MLC1SA FRG1	AI127424 L76159	myosin light chain 1 slow a FSHD (Facioscapulohumoral muscular dystrophy) region gene 1	
37012_at	CAPZB	U03271	capping protein (actin filament) muscle Z-line, beta	
37279_at	GEM	U10550	GTP binding protein overexpressed in skeletal muscle	/ GTPase
36791_g_at	TPM1	M19267	tropomyosin 1 (alpha)	Cardiomyopathy, familial hypertrophic, 3
36790_at	TPM1	M19267	tropomyosin 1 (alpha)	Cardiomyopathy, familial hypertrophic, 3
36792_at	TPM1	Z24727	tropomyosin 1 (alpha)	
36678_at	TAGLN2	D21261	transgelin 2	
36641_at	CAPZA2	U03851	capping protein (actin filament) muscle Z-line, alpha 2	
36931_at	TAGLN	M95787	transgelin	
37631_at	MYO1E	U14391	myosin IE	
41439_at	MYO1B	AJ001381	myosin IB	
40910_at	CAPZA1	U56637	capping protein (actin filament) muscle Z-line, alpha 1	/ binds barbed ends of actin filaments
41187_at	MLC-B	U26162	myosin regulatory light chain	
41747_s_at	MEF2A	U49020	Human myocyte-specific enhancer factor 2A (MEF2A) gene, last coding exon, and complete cds.	
41738_at	CALD1	M64110	caldesmon 1	
41739_s_at	CALD1	M83216	caldesmon 1	
39791_at	ATP2A2	M23114	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	Darier disease
39790_at	ATP2A2	M23115	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	Darier disease
39378_at	BECN1	U17999	beclin 1 (coiled-coil, myosin-like BCL2 interacting protein)	
40488_at	DMD	M18533	dystrophin (muscular dystrophy, Duchenne and Becker types)	Becker muscular dystrophy; Cardiomyopathy, dilated, X-linked; Duchenne muscular dystrophy
40438_at	PPP1R12A	D87930	protein (myosin) phosphatase 1, regulatory (inhibitor) subunit 12A	OMIM Notes: Regulates the interaction of actin and myosin downstream of the guanosine triphosphatase Rho.

32838_at	smooth muscle myosin heavy chain isoform SMemb	S67247	Homo sapiens cDNA: FLJ23324 fis, clone HEP12482, highly similar to HUMMYOHC Human nonmuscle myosin heavy chain-B (MYH10) mRNA	
32755_at	ACTA2	X13839	actin, alpha 2, smooth muscle, aorta	
33994_g_at	MLC	M22919	Human nonmuscle/smooth muscle alkali myosin light chain gene, complete cds.	
33447_at	MLCB	X54304	myosin, light polypeptide, regulatory, non-sarcomeric (20kD)	
32313_at	TPM2	M12125	tropomyosin 2 (beta)	OMIM Notes: Fibroblast and muscle isoforms result from alternative splicing on exons 6 and 9.
35362_at	MYO10	AB018342	myosin X	
34306_at	MBNL	AB007888	muscleblind-like (Drosophila)	
36989_at	DAG1	L19711	dystroglycan 1 (dystrophin-associated glycoprotein 1)	
40022_at	FCMD	AB008226	Fukuyama type congenital muscular dystrophy (fukutin)	?Walker-Warburg syndrome; Muscular dystrophy, Fukuyama congenital
39031_at	COX7A1	AA152406	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)	
35729_at	MYO1D	AB018270	myosin ID	
32378_at	PKM2	M26252	pyruvate kinase, muscle	
40375_at	EGR3	X63741	early growth response 3; OMIM Notes: Expressed in developing muscle spindles.	
1637_at	MAPKAPK3	U09578	mitogen-activated protein kinase-activated protein kinase 3; OMIM Notes: Expressed especially high in heart and skeletal muscle.	
40399_r_at	MEOX2	A1743406	mesenchyme homeobox 2 (growth arrest-specific homeobox). OMIM Notes: Important regulator of myogenesis.	
39565_at	BMPR1A	Z22535	bone morphogenetic protein receptor, type IA. OMIM Notes: Alternative title, activin receptor-like kinase 3; ALK3. Expressed almost exclusively in skeletal muscle with weak expression in heart and placenta.	Polyposis, juvenile intestinal
41449_at	SGCE	AJ000534	sarcoglycan, epsilon	Dystonia, myoclonic

Table 8: Fibroblast (Seshi, B)

Systematic	Common	Genbank	Description	Phenotype/ Function
39333_at	COL4A1	M26576	Human alpha-1 collagen type IV gene, exon 52.	
37037_at	P4HA1	M24486	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I	
36666_at	P4HB	M22806	precursor; Human prolyl 4-hydroxylase beta-subunit and disulfide isomerase (P4HB) gene, exon 11, clones 6B-(1,3,5,6).	
41504_s_at	MAF	AF055376	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	
39757_at	SDC2	J04621	syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan)	
39945_at	FAP	U09278	fibroblast activation protein, alpha	OMIM Notes: Expressed in fetal normal mesenchymal tissues and stromal fibroblasts within common types of epithelial tumors.
32835_at	MAFF	AA725102	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	
32535_at	FBN1	X63556	fibrillin 1 (Marfan syndrome)	Ectopia lentis, familial; Marfan syndrome; MASS syndrome; Shprintzen-Goldberg syndrome; Jackson-Weiss syndrome; Pfeiffer syndrome
2057_g_at	FGFR1	M34641	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)	
1380_at	FGF7	M60828	fibroblast growth factor 7 (keratinocyte growth factor)	OMIM Notes: May play a role in mesenchymal stimulation of epithelial cell proliferation.
32313_at	TPM2	M12125	tropomyosin 2 (beta)	OMIM Notes: Fibroblast and muscle isoforms result from alternative splicing on exons 6 and 9.
31720_s_at	FN1	M10905	fibronectin 1	
31719_at	FN1	X02761	fibronectin 1	
35835_at	PDL-108	AB019409	periodontal ligament fibroblast protein	
34390_at	P4HA2	U90441	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide II	

Table 9: Adipocyte (Seshi, B, et al)

Prob ID	Gene Name	Genbank ID	Description	OMIM Notes
34378_at	ADRP	X97324	adipose differentiation-related protein (adipophilin) / lipid-droplet binding/ adipocyte-specific	mRNA levels are induced rapidly and maximally after triggering adipocyte differentiation. High level of expression in fat.
40282_s_at	DF	M84526	D component of complement (adipsin)	
33337_at	DEGS	AF002668	degenerative spermatocyte homolog, lipid desaturase (Drosophila)	
39673_i_at	ECM2	AB011792	extracellular matrix protein 2, female organ and adipocyte specific	
39674_r_at	ECM2	AB011792	extracellular matrix protein 2, female organ and adipocyte specific	
31504_at	HDLBP	M64098	high density lipoprotein binding protein (vigilin)	
37542_at	LHFPL2	D86961	lipoma HMGIC fusion partner-like 2	
36073_at	NDN	U35139	necdin homolog (mouse)/ Prader-Willi syndrome	
37122_at	PLIN	AB005293	Perilipin (Did not meet the criteria to be included in stromal cell gene list because it was positive in 5 of 5 cMPC and 9 of 10 sMPCs, but only 6 of 8 cUSc instead of 7 of 8 cUSC samples).	

Table 10: Epithelial cell/ carcinoma (Shi, B)

Systematic	Common	Genebank	Description	Phenotype/ Function
38590_r_at	PTMA	M14630	prothymosin, alpha (gene sequence 28)	
38589_i_at	PTMA	M14630	prothymosin, alpha (gene sequence 28)	
38610_s_at	KRT10; KPP	X14487	unnamed protein product; Human gene for acidic (type I) cytokeratin 10.	Epidermolytic hyperkeratosis
37326_at	A4	U93305	integral membrane protein; swiss-prot accession: O04901; may play role in cell differentiation in intestinal epithelium	
36812_at	BCAR3	U92715	breast cancer anti-estrogen resistance 3	
36953_at	MADH4	U44378	MAD, mothers against decapentaplegic homolog 4 (Drosophila)	Pancreatic cancer; Polyposis, juvenile intestinal
36852_at	N33	U42349	Putative prostate cancer tumor suppressor	
36851_g_at	N33	U42360	39 kDa protein; Human N33 protein form 2 (N33) gene, exon 11 and complete cds.	?Prostate cancer, susceptibility to
37762_at	EMP1	Y07909	epithelial membrane protein 1	/ receptor
37731_at	EPS15	Z29064	epidermal growth factor receptor pathway substrate 15	
40856_at	SERPINF1; PEDF; EPC-1	U29953	PEDF; Human pigment epithelium-derived factor gene, complete cds.	
41431_at	ICK	AB023153	intestinal cell kinase	
39363_at	BC-2	AF042384	putative breast adenocarcinoma marker (32kD)	
39631_at	EMP2	U52100	epithelial membrane protein 2	
39542_at	ENC1	AF059611	ectodermal-neural cortex (with BTB-like domain)	/ associates with p110(RB)
40454_at	FAT	X87241	FAT tumor suppressor homolog 1 (Drosophila)	
32781_f_at	BPAG1	AA058762	bullous pemphigoid antigen 1 (230/240kD)	
32780_at	BPAG1	AB018271	bullous pemphigoid antigen 1 (230/240kD)	
32329_at	KRTHB6	X99142	keratin, hair, basic, 6 (monilethrix)	Monilethrix
34005_at	PIGR	X73079	polymeric immunoglobulin receptor, expressed in glomerular epithelial cells.	/ Binds and transports polymeric immunoglobulin
1846_at	LGALS8	L78132	lectin, galactoside-binding, soluble, 8 (galectin 8); OMIM Notes: Expressed in prostate carcinoma cells but only rarely in prostatic hypertrophy.	

Table 11: Endothelial cell (Seshi, B)

Systematic	Common	Genbank	Description	Phenotype/ Function
32755_at	ACTA2	X13839	actin, alpha 2, smooth muscle, aorta	
39315_at	ANGPT1	D13628	angiopoietin 1	/ ligand for the TIE2 receptor
1929_at	ANGPT1	U83508	angiopoietin 1	
40387_at	EDG2	U80811	endothelial differentiation, lysophosphatidic acid (LPA) G-protein-coupled receptor, 2	
40874_at	EDF1	AJ005259	endothelial differentiation-related factor 1; OMIM Notes: EDF1 level inversely correlates with the level of endothelial differentiation. Inhibition of EDF1 expression promotes endothelial cell differentiation. It is postulated that EDF1 may function as a bridging molecule that interconnects regulatory proteins and the basal transcriptional machinery, thus modulating the transcription of the genes involved in endothelial differentiation.	
37907_at	F8A; DXS522E	M34677	Factor VIII-associated gene 1; CpG island protein; Human nested gene protein gene, complete cds.	
41433_at	VCAM1	M73255	Human vascular cell adhesion molecule-1 (VCAM1) gene, complete CDS.	
36988_at	TNFAIP1	M80783	tumor necrosis factor, alpha-induced protein 1 (endothelial); OMIM Notes: Involved in the primary response of the endothelium to TNF.	
583_s_at	VCAM1	M30257	vascular cell adhesion molecule 1	
1953_at	VEGF	AF024710	vascular endothelial growth factor	
36100_at	VEGF	AF022375	vascular endothelial growth factor	
37268_at	VEGFB	U43368	vascular endothelial growth factor B	
159_at	VEGFC	U43142	vascular endothelial growth factor C	/ ligand and activator of the receptor tyrosine kinase Flt4

Table 12: Nerve cell/ neuro endocrine/ neurologic disorders (Seshi, B)

Systematic	Common	Genebank	Description	Phenotype/ Function
37298_at	GABARAP	AF044671	GABA(A) receptor-associated protein diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme	
37692_at	DBI	AI557240	A binding protein)	
35767_at	GABARAPL2	AI565760	GABA(A) receptor-associated protein-like 2	
35785_at	GABARAPL1	W28281	GABA(A) receptor-associated protein like 1	
38406_f_at	PTGDS	AI207842	prostaglandin D2 synthase (21kD, brain)	
38657_s_at	CLTA	M20471	clathrin, light polypeptide (Lca), brain-specific insertion sequences	
38653_at	PMP22	D11428	peripheral myelin protein 22.	Charcot-Marie-Tooth disease with deafness; Charcot-Marie-Tooth neuropathy-1A; Dejerine-Sottas disease; Neuropathy, recurrent, with pressure palsies
38291_at	PENK	J00123	preproenkephalin (; Human enkephalin gene: exon 3 and 3'flank.	
39072_at	MXI1	L07648	MAX interacting protein 1	Neurofibrosarcoma; Prostate cancer, susceptibility to/ transcription factor; forms heterodimers with Max protein
38841_at	GDBR1	AF068195	putative glioblastoma cell differentiation-related	
38818_at	SPTLC1	Y08685	serine palmitoyltransferase, long chain base subunit 1	Neuropathy, hereditary sensory and autonomic, type 1
36990_at	UCHL1	X04741	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase), neuron-specific. OMIM Notes: Highly specific to neurons and to cells of the diffuse neuroendocrine system and their tumors.	Parkinson disease, familial
37005_at	NBL1	D28124	neuroblastoma, suppression of tumorigenicity 1	
37286_at	NRCAM	AB002341	neuronal cell adhesion molecule	
36667_at	PYGB	U47025	phosphorylase, glycogen; brain	
36965_at	ANK3	U13616	ankyrin 3, node of Ranvier (ankyrin G)	/ peripheral proteins believed to act as membrane-cytoskeleton linker molecules



38040_at	SPF30	AF107463	splicing factor 30, survival of motor neuron-related	
37958_at	BCMP1	AL049257	brain cell membrane protein 1	
41221_at	PGAM1	J04173	phosphoglycerate mutase 1 (brain)	
40936_at	CRIM1	AI651806	cysteine-rich motor neuron 1	
41091_at	FALZ	U05237	fetal Alzheimer antigen. OMIM Notes: Abnormally expressed in fetal brain. The corresponding antibody ALZ50 recognizes neurofibrillary pathology associated with Alzheimer's disease.	
41136_s_at	APP	Y00264	amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease)	Alzheimer disease-1, APP-related; Amyloidosis, cerebroarterial, Dutch type; Schizophrenia, chronic
763_at	GMFB	AB001106	glia maturation factor, beta	
641_at	PSEN1	L76517	presenilin 1 (Alzheimer disease 3)	Alzheimer disease, familial, with spastic paraparesis and unusual plaques; Alzheimer disease-3
39793_at	GBAS	AF029786	glioblastoma amplified sequence	
40023_at	BDNF	X60201	brain-derived neurotrophic factor	
39687_at	E46L	AI524873	like mouse brain protein E46	
39686_g_at	E46L	AL050282	like mouse brain protein E46	
39542_at	ENC1	AF059611	ectodermal-neural cortex (with BTB-like domain)	/ associates with p110(RB). OMIM Notes: Expressed highest in brain.
40193_at	ENO2	X51956	Human ENO2 gene for neuron specific (gamma) enolase.	
40121_at	HIP2	U58522	huntingtin interacting protein 2	
40467_at	SDHD	AB006202	succinate dehydrogenase complex, subunit D, integral membrane protein	Parangliomas, familial central nervous system; Parangliomas, familial nonchromaffin, 1, with and without deafness; Pheochromocytoma
40281_at	NEDD5	D63878	neural precursor cell expressed, developmentally down-regulated 5	
32824_at	CLN2	AF039704	deficient in late-infantile neuronal ceroid lipofuscinosis; Homo sapiens lysosomal pepstatin insensitive protease (CLN2) gene, complete cds.	Ceroid-lipofuscinosis, neuronal 2, classic late infantile
32607_at	BASP1	AF039656	brain abundant, membrane attached signal protein 1	

33817_at	D10S102	S63912	FBRNP; heterogeneous ribonucleoprotein homolog; This sequence comes from Fig. 3; D10S102=FBRNP (human, fetal brain, mRNA, 3043 nt).	
33942_s_at	STXBP1	AF004563	syntaxin binding protein 1	/ implicated in vesicle trafficking and neurotransmitter release
1659_s_at	RHEB2	D78132	Ras homolog enriched in brain 2	
1695_at	NEDD8	D23662	neural precursor cell expressed, developmentally down-regulated 8	
2053_at	CDH2	M34064	cadherin 2, type 1, N-cadherin (neuronal)	
216_at	PTGDS	M98539	Human prostaglandin D2 synthase gene, exon 7, brain	
32102_at	SACS	AB018273	spastic ataxia of Charlevoix-Saguenay (sacsin)	Spastic ataxia, Charlevoix-Saguenay type
31896_at	NAG	AL050281	neuroblastoma-amplified protein	
35681_r_at	ZFHX1B	AB011141	zinc finger homeobox 1b. OMIM Notes: SMAD-interacting protein 1 (SMADIP1) appears to be essential to embryonic neural and neural crest development.	Hirschsprung disease-mental retardation syndrome; Hirschsprung disease-mental retardation syndrome without Hirschsprung disease
35268_at	AXOT	AL050171	axotrophin	
36190_at	CDR2	M63256	cerebellar degeneration-related protein (62kD)	
36609_at	SLC1A3	D26443	solute carrier family 1 (glial high affinity glutamate transporter), member 3	
35973_at	HYPH	AB023163	Huntingtin interacting protein H	
36142_at	SCA1	X79204	spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1)	Spinocerebellar ataxia-1
34817_s_at	A2LP	U70671	ataxin 2 related protein	
34777_at	ADM	D14874	adrenomedullin	
34394_at	ADNP	AB018327	activity-dependent neuroprotector	
32606_at	BASP1	AA135683	brain abundant, membrane attached signal protein 1	
38233_at	HOMER-3	AF093265	Homer, neuronal immediate early gene, 3	
36998_s_at	SCA2	Y08262	spinocerebellar ataxia 2 (olivopontocerebellar ataxia 2, autosomal dominant, ataxin 2)	Spinocerebellar ataxia-2
35150_at	TNFRSF5	X60592	tumor necrosis factor receptor superfamily, member 5	Immunodeficiency with hyper-IgM, type 3
34166_at	SLC6A7	S80071	solute carrier family 6 (neurotransmitter transporter, L-proline), member 7	

34265_at	SGNE1	Y00757	secretory granule, neuroendocrine protein 1 (7B2 protein)	Neurofibrosarcoma; Prostate cancer, susceptibility to/ transcription factor; forms heterodimers with Max protein
654_at	MXI1	L07648	MAX interacting prot in 1	
37945_at	BACH	U91316	brain acyl-CoA hydrolase	
39685_at	E46L	AL050282	like mouse brain protein E46	
33769_at	MPZL1	AF087020	myelin protein zero-like 1	
39356_at	NEDD4L	AB007899	neural precursor cell expressed, developmentally down-regulated 4-like	
38800_at	STMN2	D45352	stathmin-like 2; OMIM Notes: Neuronal growth-associated protein SCG10.	Neuropathy, hereditary motor and sensory, Lom type
36933_at	NDRG1	D87953	N-myc downstream regulated gene 1	
40140_at	ZFP103	D76444	zinc finger protein 103 homolog (mouse); OMIM Notes: Alternative title, KF1, expressed in normal cerebellum and Alzheimer disease cerebral cortex, but not in normal cerebral cortex.	OMIM Notes: is highly expressed in the cranial neural crest cells, somite, dorsal limb bud mesenchyme, motor neurons, Schwann cell progenitors, and T-lymphocyte lineage.
1452_at	LMO4	U24576	LIM domain only 4	
1058_at	WASF3	S69790	WAS protein family, member 3	

Table 13: Drosophila and/ or homeotic genes (S shi, B)

Systematic	Common	Genbank	D scription	Ph notype/ Function
38288_at	SNAI2	U69196	snail homolog 2 (Drosophila). OMIM Notes: Neural crest transcription factor SLUG. A zinc finger protein that plays an important role in the transition of epithelial to mesenchymal characteristics within the neural crest.	
39037_at	MLLT2	L13773	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 2	
39070_at	SNL	U03057	singed-like (fascin homolog, sea urchin) (Drosophila). OMIM Notes: Positive in dendritic cells of lymph nodes and Reed-Sternberg cells.	
39164_at	ARIH2	AF099149	ariadne homolog 2 (Drosophila). OMIM Notes: Upregulated during retinoic acid-induced granulocytic differentiation of APL cells.	
38750_at	NOTCH3	U97669	Notch homolog 3 (Drosophila). OMIM Notes: Promotes the differentiation of astroglia from multipotent progenitors.	Cerebral (autosomal dominant) arteriopathy with subcortical infarcts and leukoencephalopathy (CADASIL)
38944_at	MADH3	U68019	MAD, mothers against decapentaplegic homolog 3 (Drosophila)	OMIM Notes: SMAD3 signal transduction important in the regulation of muscle-specific genes.
37693_at	NUMB	L40393	numb homolog (Drosophila)	OMIM Notes: Numb directs neuronal cell fate decisions.
40004_at	SIX1	X91868	sine oculis homeobox homolog 1 (Drosophila)	OMIM Notes: Expressed in adult skeletal muscle, and in multiple tumors including mammary carcinoma.
39610_at	HOXB2	X16665	homeo box B2	OMIM Notes: Essential for motor neuron development. Within the hematopoietic compartment, expressed specifically in erythromegakaryocytic cell lines.

40575_at	DLG5	AB011155	discs, large (Drosophila) homolog 5	OMIM Notes: Expressed in prostate gland epithelial cells.
40570_at	FOXO1A	AF032885	forkhead box O1A (rhabdomyosarcoma)	Rhabdomyosarcoma, alveolar. OMIM Notes: Activates myogenic transcription program.
40127_at	PMX1	M95929	paired mesoderm homeo box 1	OMIM Notes: Expressed in cardiac, skeletal and smooth muscle tissues.
40454_at	FAT	X87241	FAT tumor suppressor homolog 1 (Drosophila)	OMIM Notes: Expressed in many epithelial, some endothelial and smooth muscle cells.
40328_at	TWIST	X99268	twist homolog (acrocephalosyndactyly 3; Saethre-Chotzen syndrome) (Drosophila)	Saethre-Chotzen syndrome. OMIM Notes: Required for cranial neural tube morphogenesis.
33222_at	FZD7	AB017365	frizzled homolog 7 (Drosophila)	OMIM Notes: Highest expression adult skeletal muscle and fetal kidney. FZD7 dependent PKC signaling controls cell sorting behaviour in the mesoderm.
32696_at	PBX3	X59841	pre-B-cell leukemia transcription factor 3	
33337_at	DEGS	AF002668	degenerative spermatocyte homolog, lipid desaturase (Drosophila); adipocyte associated.	
1857_at	MADH7	AF010193	MAD, mothers against decapentaplegic homolog 7 (Drosophila)	OMIM Notes: MAD proteins were originally defined in Drosophila as essential components of the signaling pathways of the TGF-beta receptor family (e.g., TGFBR1). MADH7 and MADH6 as shown by IHC and ISH are predominantly expressed in vascular endothelium.
1955_s_at	MADH6	AF035528	MAD, mothers against decapentaplegic homolog 6 (Drosophila)	/ inhibitor of BMP signaling

1013_at	MADH5	U59913	MAD, mothers against decapentaplegic homolog 5 (Drosophila)	OMIM Notes: SMAD5 plays a critical role in the signaling pathway by which TGF-beta inhibits the proliferation of human hematopoietic progenitor cells.
1453_at	MADH2	U68018	MAD, mothers against decapentaplegic homolog 2 (Drosophila)	
1433_g_at	MADH3	U68019	MAD, mothers against decapentaplegic homolog 3 (Drosophila)	OMIM Notes: SMAD2/SMAD3 signal transduction appears to be important in the regulation of muscle-specific genes.
35681_r_at	ZFHX1B	AB011141	zinc finger homeobox 1b. OMIM Notes: SMAD-interacting protein 1 (SMADIP1) appears to be essential to embryonic neural and neural crest development.	Hirschsprung disease-mental retardation syndrome; Hirschsprung disease-mental retardation syndrome without Hirschsprung disease
35226_at	EYA2	U71207	eyes absent homolog 2 (Drosophila)	OMIM Notes: Expressed in extensor tendons, and in lens fibers and participates in connective tissue patterning.
36308_at	ZIC1	D76435	Zic family member 1 (odd-paired homolog, Drosophila)	OMIM Notes: Specifically expressed in nervous tissue and in particular cerebellar granule cells, potential biomarker for cerebellar granule cell lineage and medulloblastoma.
34306_at	MBNL	AB007888	muscleblind-like (Drosophila)	OMIM Notes: Expressed in skeletal muscle myoblasts, also in lymphoblastoid cell lines.
33710_at	C3F	U72515	putative protein similar to nessy (Drosophila)	OMIM Notes: Expressed in fibroblasts and hepatocytes.

Table 14: B-cell/ B-cell neoplasms (Seshi, B)

Systematic	Common	Genbank	Description	Phenotype/ Function
41562_at	BMI1	L13689	B lymphoma Mo-MLV insertion region (mouse)	/ proto-oncogene
37294_at	BTG1	X61123	B-cell translocation gene 1, anti-proliferative	
38418_at	CCND1	X59798	cyclin D1 (PRAD1: parathyroid adenomatosis 1)	Centrocytic lymphoma; Leukemia/lymphoma, B-cell, 1; Multiple myeloma; Parathyroid adenomatosis 1
37730_at	p100	U22055	EBNA-2 co-activator (100kD); OMIM Notes: EBNA-2 activates transcription of specific genes and is essential for EBV-mediated B-lymphocyte transformation.	/ associates with the EBV nuclear protein 2 acidic domain
466_at	GTF2I	U77948	general transcription factor II, I; OMIM Notes: Alternative title, BTK-associated protein, 135kD (BAP135). Bruton's tyrosine kinase (BTK) is essential for B-cell activation and phosphorylates BAP135 in B cells.	
36875_at	IBTK	AL050018	inhibitor of Bruton's tyrosine kinase	
38438_at	NFKB1	M58603	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	
39730_at	ABL1	X16416	v-abl Abelson murine leukemia viral oncogene homolog 1	Leukemia, chronic myeloid
38743_f_at	RAF1	X06409	v-raf-1 murine leukemia viral oncogene homolog-1	
36645_at	RELA	L19067	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian)	
41436_at	ZNF198	AJ224901	zinc finger protein 198; OMIM Notes: ZNF198 involves T- or B-cell lymphoblastic lymphoma, myeloid hyperplasia, and eosinophilia and evolves toward AML. This multilineage involvement suggests the malignant transformation of primitive hematopoietic stem cell.	Stem-cell leukemia/lymphoma syndrome
40091_at	BCL6	U00115	B-cell CLL/lymphoma 6 (zinc finger protein 51); OMIM Notes: BCL6 is predominantly expressed in the B-cell lineage, especially mature B cells (centrocytes and centroblasts).	Lymphoma, B-cell, Diffuse Large
32776_at	RALB	M35416	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein)	
32696_at	PBX3	X59841	pre-B-cell leukemia transcription factor 3	
33791_at	DLEU1	Y15227	deleted in lymphocytic leukemia, 1	

34005_at	PIGR	X73079	polymeric immunoglobulin receptor	/ Binds and transports polymeric immunoglobulin
1636_g_at	ABL	U07563	ABL is the cellular homolog proto-oncogene of Abelson's murine leukemia virus and is associated with the t9:22 chromosomal translocation with the BCR gene in chronic myelogenous and acute lymphoblastic leukemia.	Leukemia, chronic myeloid
1728_at	BMI1	L13689	B lymphoma Mo-MLV insertion region (mouse)	/ proto-oncogene
2020_at	CCND1	M73554	cyclin D1 (PRAD1: parathyroid adenomatosis 1)	Centrocytic lymphoma; Leukemia/lymphoma, B-cell, 1; Multiple myeloma; Parathyroid adenomatosis 1
1295_at	RELA	L19067	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian)	
1377_at	NFKB1	M58603	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	
1461_at	NFKBIA	M69043	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	/ Ikb-like activity
1389_at	MME	J03779	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)	
35350_at	GALNAC4 S-6ST	AB011170	B cell RAG associated protein	
35992_at	MSC	AF087036	musculin (activated B-cell factor-1, ABF1); OMIM Notes: Downstream target of B-cell receptor signal transduction pathway. Also expressed in proliferating undifferentiated myeloblasts.	/ basic helix-loop-helix transcription factor
34344_at	IKBKAP	AF044195	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein	Dysautonomia, familial
34350_at	RSN	X64838	restin (Reed-Sternberg cell-expressed intermediate filament-associated protein); Note R-S cell is a form of B-cell.	
36204_at	PTPRF	Y00815	protein tyrosine phosphatase, receptor type, F; OMIM Notes: Alternative title, Leukocyte antigen-related tyrosine phosphatase (LAR). Both LAR and LCA (CD45) map to chromosome 1. LCA is protein-tyrosine phosphatase, receptor-type C, PTPRC, whereas LAR is PTPRF.	
34391_at	IGBP1	Y08915	immunoglobulin (CD79A) binding protein 1.	IGBP1, a marker for early B-cells



1373_at	TCF3	M31523	proto-oncogene or transcription factor 3 TCF3 (E2A immunoglobulin enhancer binding factors E12/E47); OMIM Notes: E2A mutant mice will have selective failure to develop B cells, all other hematopoietic cell lineages being intact. The block to B cell development occurs before immunoglobulin D(H)-J(H) rearrangement.	Leukemia, acute lymphoblastic. A homeobox gene contributing the DNA binding domain of the t(1;19) translocation protein in precursor B-cell ALL.
35150_at	TNFRSF5	X60592	tumor necrosis factor receptor superfamily, member 5; OMIM notes: Alternative title, B- cell associated molecule CD40; expressed on the surface of all mature B cells, most mature B-cell malignancies and some early B-cell ALL.	Immunodeficiency with hyper-IgM, type 3
38740_at	ZFP36L1	X79067	zinc finger protein 36, C3H type-like 1; OMIM Notes: Alternative title, BERG36 (B- cell early response gene encoding a 36 kD protein).	
37026_at	COPEB	AF001461	core promoter element binding protein; OMIM Notes: Alternative title, B-cell-derived 1, BCD1. The expression of BCD1 was limited to two tissues, CD19+ B-cells and testis of normal individuals. B-cell maturation is associated with BCD1+ expression.	/ transcription factor involved in hepatic wound healing
38050_at	BTF	D79986	Bcl-2-associated transcription factor	
32696_at	PBX3	X59841	pre-B-cell leukemia transcription factor 3	

Table 15: Myeloid cell/ myeloid leukemia (Seshi, B)

Systematic	Common	Genbank	Description	Phenotype/ Function
39037_at	MLLT2	L13773	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 2	Leukemia, acute myeloid; Leukemia, acute T-cell lymphoblastic
37486_f_at	MEIS3	U68385	Meis1, myeloid ecotropic viral integration site 1 homolog 3 (mouse)	
37685_at	PICALM	U45976	phosphatidylinositol binding clathrin assembly protein	
41220_at	MSF	AB023208	MLL septin-like fusion; a fusion partner gene of MLL	Leukemia, acute myeloid, therapy-related; Ovarian carcinoma
41175_at	CBFB	L20298	core-binding factor, beta subunit	Myeloid leukemia, acute, M4Eo subtype
943_at	RUNX1	D43968	runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene)	Leukemia, acute myeloid; Platelet disorder, familial, with associated myeloid malignancy
39730_at	ABL1	X16416	v-abl Abelson murine leukemia viral oncogene homolog 1	Leukemia, chronic myeloid
33146_at	MCL1	L08246	myeloid cell leukemia sequence 1 (BCL2-related)	Leukemia, chronic myeloid
1636_g_at	ABL	U07563	ABL is the cellular homolog proto-oncogene of Abelson's murine leukemia virus and is associated with the t(9;22) chromosomal translocation with the BCR gene in chronic myelogenous and acute lymphoblastic leukemia.	
277_at	MCL1	L08246	myeloid cell leukemia sequence 1 (BCL2-related)	
41388_at	MEIS2	AF017418	Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse)	Leukemia, acute nonlymphocytic
40189_at	SET	M93651	SET translocation (myeloid leukemia-associated, M2/M4 AML); SET stands for suppressor of variegation, enhancer of zeste and trithorax.	
38992_at	DEK	X64229	DEK oncogene (DNA binding)	
36941_at	AF1Q	U16954	ALL1-fused gene from chromosome 1q	Leukemia, acute myelomonocytic

Table 16: T cell/ NK cell (Seshi, B)

Systematic	Common	Genbank	Description	Phenotype/ Function
37685_at	PICALM	U45976	phosphatidylinositol binding clathrin assembly protein	Leukemia, acute myeloid; Leukemia, acute T-cell lymphoblastic
498_at	TAX1BP1	U33821	Tax1 (human T-cell leukemia virus type I) binding protein 1	
40822_at	NFATC3	L41067	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3	
34003_at	CD4	U47924	major receptor for HIV-1; member of immunoglobulin supergene family; T cell surface glycoprotein T4	/ T-cell coreceptor; involved in antigen recognition; participant in signal transduction pathway
32602_at	RAP1GDS1	X63465	RAP1, GTP-GDP dissociation stimulator 1	Lymphocytic leukemia, acute T-cell (T-ALL)
35279_at	TAX1BP1	U33821	Tax1 (human T-cell leukemia virus type I) binding protein 1	
34234_f_at	NKTR	A1688640	natural killer-tumor recognition sequence; OMIM Notes: The protein product of the NKTR gene is present on the surface of LGLs and facilitates their binding to tumor targets.	
39426_at	TCERG1	AF017789	transcription elongation regulator 1 (CA150)	/ HIV-1 Tat transcriptional coactivator
32602_at	RAP1GDS1	X63465	RAP1, GTP-GDP dissociation stimulator 1	Lymphocytic leukemia, acute T-cell

Table 17  
 Stromal cells showing expression of genes that are typically affiliated with B-cell progenitors

Gene	Probe ID	GenBank ID	cMPC	cUSC	sMPC
CD45	40518_at		Positive in 4/5 samples	Positive in 8/8 samples	Positive in 6/10 samples
CD34	538_at		4/5	5/8	4/10
CD19	1116_at		0/5	0/8	10/10
CD20	619_at		1/5	0/8	3/10
CD22	38521_at		0/5	2/8	1/10
*CD10 (CALLA) Common acute lymphoblastic leukemia antigen.	1389_at		5/5	8/8	10/10
*Transcription factor 3 (E2A) Immunoglobulin enhancer binding factors E12/E47	1373_at		5/5	8/8	9/10
*CD79A (IGBP1) Immunoglobulin binding protein 1, a marker for early B- cells	34391_at		5/5	8/8	9/10
*HLA class II, Dr alpha	37039_at		5/5	8/8	9/10

*HLA class II, Dr beta 1	33261_at		5/5	8/8	10/10
*B2M Beta-2 microglobulin	34644_at		5/5	8/8	10/10
CD2	40738_at		1/5	2/8	2/10
CD5	32953_at		0/5	0/8	0/10
CD7	771_s_at		0/5	0/8	0/10
CD13	39385_at		5/5	8/8	0/10
CD33	36802_at		2/5	4/8	0/10
CD14	36661_at		3/5	8/8	0/10

Footnote to Table 17

Genes marked with asterisk (\*) have met the criteria for inclusion in stromal cell gene list.

# REFERENCES

- Agarwal R, Doren S, Hicks B, Dunbar CE: Long-term culture of chronic myelogenous leukemia marrow cells on stem cell factor-deficient stroma favors benign progenitors. *Blood* 85:1306-1312, 1995
- 5 Agarwal, R., Doren, S., Hicks, B. & Dunbar, C. E. (1995) *Blood* 85, 1306-12.
- Ahizadeh AA, Eisen MB, Davis RE, Ma C, Lossos IS, Rosenwald A, Boldrick IC, Sabet H, Iran I, Yu X, Powell LL, Yang L, Marti G-, Moore I, Hudson J, Lu L, Lewis DB, Libshirani R, Sherlock O, Chan WC, Greiner IC, Weisenburger DD, Armitage JO, Wamke R, Staudt LM, et al.: Distinct types of diffuse large B-cell lymphoma identified by gene expression profiling. *Nature* 403:503-511, 2000
- 10 Alaiya, A. A., Franzen, B., Auer, G. & Linder, S. (2000) *Electrophoresis* 21, 1210-7.
- Alexandrakis M, Coulocheri S, Xylouri I, Ganotakis E, Ehiakis P, Karkavitsas N, Eliopoulos GD: Elevated serum TNF- $\alpha$  concentrations are predictive of shortened survival in patients with high-risk myelodysplastic syndromes. *Haematologia (Budap)* 29:13-24, 1998
- 15 Alexandrakis, M., Coulocheri, S., Xylouri, I., Ganotakis, E., Eliakis, P., Karkavitsas, N. & Eliopoulos, G. D. (1998) *Haematologia (Budap)* 29, 13-24.
- Alon U, Barkai N, Notterman DA, Gish K, Ybarra S, Mack D, Levine AJ: Broad patterns of gene expression revealed by clustering analysis of tumor and normal colon tissues probed by oligonucleotide arrays. *Proc Natl Acad Sci U S A*, 96:6745-6750, 1999
- 20 Appel, R. D., Bairoch, A., Sanchez, J. C., Vargas, J. R., Golaz, O., Pasquali, C. & Hochstrasser, D. F. (1996) *Electrophoresis* 17, 540-6.
- 25 Appel, R. D., Hoogland, C., Bairoch, A. & Hochstrasser, D. F. (1999) in *2-D Proteome Analysis Protocols*, ed. Link, A. 3. (Humana Press, Totowa, NJ), pp. 411-416.
- Auerbach R: Patterns of tumor metastasis: organ selectivity in the spread of cancer cells. *Lab Invest* 58:361-364, 1988
- 30 Auerbach, R. (1988) *Lab Invest* 58, 361-364.
- Bennett JM, Catovsky D, Daniel MI, Flandrin G, Galton DA, Grignani HS, Sultan C: Proposals for the classification of the myelodysplastic syndromes. *Br J Haematol* 51:189-199, 1982
- Bhatia R, McGlave PB, Dewald GW, Blazar BR, Verfaillie CM: Abnormal function of the bone marrow microenvironment in chronic myelogenous leukemia: role of malignant stromal macrophages. *Blood* 85:3636-3645, 1995
- 35 Bjornson CR, Rietze RL, Reynolds BA, Magli MC, Vescovi AL: Turning brain into blood: a hematopoietic fate adopted by adult neural stem cells in vivo [see comments]. *Science* 283:534-537, 1999
- 40 Budak-Alpdogan I, Alpdogan O, Akoglu I: Morphological and functional characteristics of short-term and long-term bone marrow cultures in chronic myelogenous leukemia. *Am J Hematol* 62:212-220, 1999
- Bustin SA: Absolute quantification of mRNA using real-time reverse transcription polymerase chain reaction assays. *J Mol Endocrinol* 25:169-193, 2000
- 45 Celis JE, Kruhoffer M, Gromova I, Frederiksen C, Ostergaard M, Thykjaer I, Gromov P, Yu J, Palsdottir H, Magnusson N, Orntoft IF: Gene expression profiling: monitoring transcription and translation products using DNA microarrays and proteomics. *FEBS Lett* 480:2-16, 2000
- Celis, J. E., Kruhoffer, M., Gromova, I., Frederiksen, C., Ostergaard, M.,

- Thykjaer, T., Gromov, P., Yu, Z., Palsdottir, H., Magnusson, N. & Orntoft, I. F. (2000) *FEBS Lett* 480, 2-16.
- Celis, J. E. & Gromov, P. (1999) *Curr Opin Biotechnol* 10, 16-21.
- Chambers, G., Lawrie, L., Cash, P. & Fray, G. I. (2000) *J Pathol* 192, 280-288.
- 5 Chen D, Chang RE, Huang YL: Breast cancer diagnosis using self-organizing map for sonography. *Ultrasound Med Biol* 26:405-411, 2000
- Clark EA, Golub IR, Lander ES, Hynes RO: Genomic analysis of metastasis reveals an essential role for RhoC. *Nature* 406:532-535., 2000
- Cordwell, S. J., Nouwens, A. S., Verrills, N. M., McPherson, J. C., Hams, P. G., van Dyk, D. D. & Walsh, B. J. (1999) *Electrophoresis* 20, 3580-8.
- 10 Cordwell, S. J., Nouwens, A. S., Verrills, N. M., Basseal, D. J. & Walsh, B. J. (2000) *Electrophoresis* 21, 1094-103.
- Crino PB, Trojanowski JQ, Dichter MA, Eberwine 1: Embryonic neuronal markers in tuberous sclerosis: singlecell molecular pathology. *Proc Natl Acad Sci U S A* 93:14152-14157., 1996
- 15 Damiano IS, Cress AE, Hazlehurst LA, Shtil AA, Dalton WS: Cell adhesion mediated drug resistance (CAMDR): role of integrins and resistance to apoptosis in human myeloma cell lines. *Blood* 93:1658-1667, 1999
- Damiano IS, Dalton WS: Integrin-mediated drug resistance in multiple
- 20 myeloma. *Leuk Lymphoma* 38:71-81, 2000
- Damiano, J. S. & Dalton, W. S. (2000) *Leuk Lymphoma* 38, 71-81.
- Damiano, J. S., Cress, A. E., Hazlehurst, L. A., Shtil, A. A. & Dalton, W. S. (1999) *Blood* 93, 1658-67.
- Deeg HJ, Beckham C, Loken MR, Bryant E, Lesnikova M, Shulman HM,
- 25 Gooley J: Negative regulators of hemopoiesis and stroma function in patients with myelodysplastic syndrome. *Leuk Lymphoma* 37:405-414, 2000
- Deeg, H. J., Beckham, C., Loken, M. R., Bryant, E., Lesnikova, M., Shuhnan, H. M. & Gooley, J. (2000) *Leuk Lymphoma* 37, 405-14.
- Dexter TM, Allen ID, Lajtha LG: Conditions controlling the proliferation of
- 30 haemopoietic stem cells in vitro. 1 *Cell Physiol* 91:335-344, 1977
- Dexter, T. M., Allen, T. D. & Lajtha, L. G. (1977) *J Cell Physiol* 91, 335-44.
- Diana C, Dominici M, Lanza F, Punturieri M, Pauhi S, Tieghi A, Dabusti M, Scapoli O, O. C: Impairment of stromal cells compartment in hypoplastic myelodysplastic syndromes (Abstract). *Blood* 96:357a, 2000
- 35 Eaves AC, Eaves CJ: Maintenance and proliferation control of primitive hemopoietic progenitors in long-term cultures of human marrow cells. *Blood Cells* 14:355-368, 1988
- Eaves, A. C. & Eaves, C. J. (1988) *Blood Cells* 14, 355-68.
- Eglitis MA, Mezey E: Hematopoietic cells differentiate into both microglia and
- 40 macroglia in the brains of adult mice. *Proc Natl Acad Sci U S A* 94:4080-4085, 1997
- Eisen MB, Spellman PT, Brown PO, Botstein D: Cluster analysis and display of genome-wide expression patterns. *Proc Natl Acad Sci US A* 95:14863-14868, 1998
- Emmert-Buck MR, Bonner RE, Smith PD, Chuaqui RE, Zhuang Z, Goldstein
- 45 SR, Weiss RA, Liotta LA: Laser capture microdissection. *Science* 274:998-1001., 1996
- Felley-Bosco, E., Demalte, I., Barcelo, S., Sanchez, J. C., Hochstrasser, D. F., Schlegel, W. & Reymond, M. A. (1999) *Electrophoresis* 20, 3508-13.
- Findenstein, A. J., Gorska, J. F. & Kulagina, N. N. (1976) *Exp Hematol* 4,
- 50 267-74.

- Frantza, S., Hershkovich, R., Kam, N., Lichtenstein, N., Vaday, G. G., Alon, R. & Lider, O. (2000) *J Immunol* 165, 2738-47.
- Friedenstein AJ, Gorskaja iF, Kulagina NN: Fibroblast precursors in normal and irradiated mouse hematopoietic organs. *Exp Hematol* 4:267-274, 1976
- 5 Gartner S, Kaplan HS: Long-term culture of human bone marrow cells. *Proc Natl Acad Sci U S A* 77:4756-4759, 1980
- Gartner, S. & Kaplan, H. S. (1980) *Proc Natl Acad Sci USA* 77, 4756-9.
- Gazitt, Y., Freytes, C. O., Callander, N., Tsai, I. W., Alsina, M., Anderson, J., Holle, L., Cruz, J., Devore, P., McGrath, M., West, G., Alvarez, R. & Montgomery, W. (1999) *J Hematother* 8, 173-83.
- 10 Gianni, A. M., Siena, S., Bregni, M., Tarella, C., Stern, A. C., Pileri, A. & Bonadonna, G. (1989) *Lancet* 2, 580-5.
- Godovac-Zimmermann, J., Soskic, V., Poznanovic, S. & Brianza, F. (1999) *Electrophoresis* 20, 952-6 1.
- 15 Golub TR, Slonim DK, Tamayo P, Huard C, Gaasenbeek M, Mesirov JP, Coller H, Loh ML, Downing JR, Cahigiuri MA, Bloomfield CD, Lander ES: Molecular classification of cancer: class discovery and class prediction by gene expression monitoring. *Science* 286:531-537., 1999
- Gorg, A., Obermaier, C., Boguth, G., Harder, A., Scheibe, B., Wildgruber, R. & Weiss, W. (2000) *Electrophoresis* 21, 1037-1053
- 20 Greenberg P, Anderson J, de Witte T, Estey E, Fenaux P, Gupta P, Hamblin I, Hellstrom-Lindberg E, List A, Muftic G, Neuwirthova, Ohnishi K, Oscier D, Sanz M, Willmann C: Problematic WHO reclassification of myelodysplastic syndromes. Members of the International MDS Study Group. *J Clin Oncol* 18:3447-3452., 2000
- 25 Greenberger JS: Sensitivity of corticosteroid-dependent insulin-resistant lipogenesis in marrow preadipocytes of obese-diabetic (db/db) mice. *Nature* 275:752-754, 1978
- Greenberger, J. S. (1978) *Nature* 275, 7524.
- 30 Gurney K: Self-organization: An Introduction to Neural Networks (ed First). London, UCL Press Limited, 1997, p 115-146
- Harris NL, Jaffe ES, Diebold J, Flandrin G, Muller-Hermelink HK, Vardiman R, Lister TA, Bloomfield CD: World Health Organization classification of neoplastic diseases of the hematopoietic and lymphoid tissues: report of the Clinical Advisory Committee meeting-Arlie House, Virginia, November 1997. *J Clin Oncol* 17:3835-3849, 1999
- 35 Hidai C, Zupancic I, Penta K, Mikhail A, Kawana M, Quertermous EE, Aoka Y, Fukagawa M, Matsui Y, Platika D, Auerbach R, Hogan BL, Snodgrass R, Quertermous I: Cloning and characterization of developmental endothelial locus 1: an embryonic endothelial cell protein that binds the  $\alpha$ v $\beta$ 3 integrin receptor. *Genes Dev* 12:21-33., 1998
- Hofmann W-K, deVos J, Tsukasaki K, Wachsman W, Pinkus OS, Said SW, Koeffler HP: Altered apoptosis pathways in mantle cell lymphoma detected by oligonucleotide microarray (Abstract). *Blood* 96:468a, 2000
- 45 Hoving, S., Voshol, H. & van Oostrum, J. (2000) *Electrophoresis* 21, 2617-21.
- In L, Thompson CA, Qian X, Kuecker SI, Kuhig E, Lloyd RV: Analysis of anterior pituitary hormone mRNA expression in immunophenotypically characterized single cells after laser capture microdissection. *Lab Invest* 79:511-512., 1999
- Jensen, O. N., Wilm, M., Shevchenko, A. & Mann, M. (1999) in *2-D Proteome Analysis Protocols*, ed. Link, A. J. (Humana Press, Totowa, NJ), pp. 57 1-588.
- 50



- Johnson RA, Wichern DW: Clustering: Applied Multivariate Statistical Analysis (ed Third). Englewood Cliffs, Prentice Hall, 1992, p 573-627
- Kacharina JE, Crino PB, Eberwine 3: Preparation of cDNA from single cells and subcellular regions. *Methods Enzymol* 303:3-18., 1999
- 5 Klose, J. (1975) *Humangenetik* 26, 23143.
- Kohonen I: Self-Organizing Maps (ed Second). New York, Springer-Verlag, 1997
- Lagneaux L, Delforge A, Bron D, De Bruyn C, Stryckmans P: Chronic lymphocytic leukemic B cells but not normal B cells are rescued from apoptosis by contact with normal bone marrow stromal cells. *Blood* 91:2387-2396, 1998
- 10 Lagneaux L, Delforge A, De Bruyn C, Bernier M, Bron D: Adhesion to bone marrow stroma inhibits apoptosis of chronic lymphocytic leukemia cells. *Leuk Lymphoma* 35:445-453, 1999
- Lagneaux, L., Delforge, A., Bron, D., De Bruyn, C. & Stryckmans, P. (1998) *Blood* 91, 2387-96.
- 15 Lagneaux, L., Delforge, A., De Bruyn, C., Bernier, M. & Bron, D. (1999) *LeukLymphoma* 35, 445-53:
- Le Bousse-Kerdiles MC, Martyre MC: Dual implication of fibrogenic cytokines in the pathogenesis of fibrosis and myeloproliferation in myeloid metaplasia with myelofibrosis. *Ann Hematol* 78:437-444, 1999
- 20 Le Bousse-Kerdiles, M. C. & Martyre, M. C. (1999) *Ann Hematol* 78, 437-44.
- Lichtman MA: Myelodysplasia or Myeloneoplasia: Thoughts on the Nosology of Clonal Myeloid Diseases. *Blood Cells Mol Dis* 26:572-581, 2000
- Lichtman MA: The ultrastructure of the hemopoietic environment of the marrow: a review. *Exp Hematol* 9:391-410, 1981
- 25 Lockhart DJ, Winzler EA: Genomics, gene expression and DNA arrays. *Nature* 405:827-836., 2000
- Lokhorst HM, Lamme I, de Smet M, Klein S, de Weger RA, van Oers R, Bloem AC: Primary tumor cells of myeloma patients induce interleukin-6 secretion in long-term bone marrow cultures. *Blood* 84:2269-2277, 1994
- 30 Lokhorst, H. M., Lamme, T., de Smet, M., Klein, S., de Weger, R. A., van Oers, R. & Bloem, A. C. (1994) *Blood* 84, 2269-2277
- Lopez, M. F. (2000) *Electrophoresis* 21, 1082-93.
- Luo L, Salunga RC, Guc tier A, Joy KC, Galindo JE, Xiao H, RoL -i, Wan IS, Jackson MR, Erlender MG: Gene expression profiles of laser-captured adjacent neuronal subtypes. *Nat Med* 5:117-122., 1999
- 35 Manabe A, Coustan-Smith E, Behm FG, Raimondi SC, Campana D: Bone marrow-derived stromal cells prevent apoptotic cell death in B-lineage acute lymphoblastic leukemia. *Blood* 79:2370-2377, 1992
- 40 Manabe, A., Coustan-Smith, E., Behm, F. G., Raimondi, S. C. & Campana, D. (1992) *Blood* 79, 2370-7.
- Marini F, Zompetta C, Wang R-Y, Studeny M, Zoltick P, Wilson I, Andreeff M: Mesenchymal stem cells (MSC) from patients with chronic myelogenous leukemia (CML) patients can be transduced with common gene transfer vectors at high efficiency, and are genotypically normal (Abstract). *Blood* 96:740a, 2000
- 45 Minguell 31, Martinez 1: Growth pattern and function of bone marrow fibroblasts from normal and acute lymphoblastic leukemia patients. *Exp Hematol* 11:522-526., 1983
- Miyazato A, Ohmine K, Ueda M, Ozawa K, Mano H: Identification of myelodysplastic syndrome-specific genes by DNA microarray analysis with "blast
- 50

- bank" samples (Abstract). Blood 96:544a, 2000
- Molloy, M. P., Herbert, B. R., Walsh, B. J., Tyler, M. I., Traini, M., Sanchez, J. C., Hochstrasser, D. F., Williams, K. L. & Gooley, A. A. (1998) *Electrophoresis* 19, 837-44.
- 5 Mundle SD, Ahi A, Cartlidge ID, Reza 5, Alvi 5, Showel MM, Mativi BY, Shetty VT, Venugopal P, Gregory SA, Raza A: Evidence for involvement of tumor necrosis factor-alpha in apoptotic death of bone marrow cells in myelodysplastic syndromes. *Am J Hematol* 60:3647, 1999
- Mundle SD, Reza 5, Ahi A, Mativi Y, Shetty V, Venugopal P, Gregory SA, Raza A: Correlation of tumor necrosis factor alpha (TNF alpha) with high Caspase 3-like activity in myelodysplastic syndromes. *Cancer Lett* 140:201-207, 1999
- 10 Mundle, S. D., Au, A., Cartlidge, J. D., Reza, S., Alvi, S., Showel, M. M., Mativi, B. Y., Shetty, V. T., Venugopal, P., Gregory, S. A. & Raza, A. (1999) *Am J Hematol* 60, 3647.
- Mundle, S. D., Reza, S., Ali, A., Mativi, Y., Shetty, V., Venugopal, P., Gregory, S. A. & Raza, A. (1999) *Cancer Lett* 140, 201-7.
- Nagao I, Yamauchi K, Komatsuda M, Noguchi K, Shimizu M, Yonekura 5, Nozaki H: Inhibition of human bone marrow fibroblast colony formation by leukemic cells. *Blood* 62:1261-1265., 1983
- 20 Nagao I, Yamauchi K, Komatsuda M: Serial in vitro bone marrow fibroblast culture in human leukemia. *Blood* 61:589-592., 1983
- O'Dell DM, McIntosh 1K, Eberwine JH: Single-cell molecular biology: implications for the diagnosis and treatment of neurological disease. *Arch Neurol* 56:1453-1456., 1999
- 25 O'Farrell, P. H. (1975) *JBiol Chem* 250, 4007-21.
- Paget 5: The distribution of secondary growths in cancer of the breast. *Lancet* i:571, 1889
- Paget, S. (1889) *Lancet* 1, 571.
- Peled A, Lee BC, Steinberg D, Toledo 3, Aracil M, Zipori D: Interactions between leukemia cells and bone marrow stromal cells: stroma-supported growth vs. serum dependence and the roles of TGF-beta and M-CSF. *Exp Hematol* 24:728-737., 1996
- Penta K, Varner JA, Liaw L, Hidai C, Schatzman R, Quertermous T: Dell induces integrin signaling and angiogenesis by ligation of alphaVbeta3. *J Biol Chem* 274:11101-11109., 1999
- 35 Perou CM, Jeffrey SS, van de Run M, Rees CA, Eisen MB, Ross DI, Pergamenschikov A, Williams CE, Thu SX, Lee IC, Lashkari D, Shalon D, Brown PO, Botstein D: Distinctive gene expression patterns in human mammary epithelial cells and breast cancers. *Proc Natl Acad Sci U S A* 96:9212-9217., 1999
- 40 Phillips EJL, Ernst RE, Brunk B, Ivanova N, Mahan MA, Deanehan 1K, Moore KA, Overton GC, Lemischka IR:
- Pittenger ME, Mackay AM, Beck SC, Jaiswal RK, Douglas R, Mosca ID, Moorman MA, Simonetti DW, Craig 5, MarshakDR: Multilineage potential of adult human mesenchymal stem cells. *Science* 284:143-147, 1999
- 45 Pittenger, M. F., Mackay, A. M., Beck, S. C., Jaiswal, R. K., Douglas, R., Mosca, J. D., Moorman, M. A., Simonetti, D. W., Craig, S. & Marshak, D. R. (1999) *Science* 284, 143-7.
- Querol, S., Cancelas, 3. A., Amat, L., Capnians, G. & Garcia, 3. (1999) *Haematologica* 84, 493-8.
- 50 Raza A, Mundle 5, Shetty V, Alvi 5, Chopra H, Span L, Parcharidou A, Dar 5,

- Venugopal P, Borok R, Gezer S, Showel J, Loew J, Robin E, Rifkin S, Alston D, Hernandez B, Shah R, Kaizer H, Gregory S: Novel insights into the biology of myelodysplastic syndromes: excessive apoptosis and the role of cytokines. *Int J Hematol* 63:265-278, 1996
- 5 Raza, A., Mundle, S., Shetty V., Alvi, S., Chopra, H., Span, L., Parcharidou, A., Dar, S., Venugopal, P., Borok, R., Gezer, S., Showel, J., Loew, J., Robin, E., Rifkin, S., Alston, D., Hernandez, B., Shah, R., Kaizer, H. & Gregory, S. (1996) *mt J Hematol* 63, 265-78.
- Record, M., Bes, J. C., Chap, H. & Douste-Bla.zy, L. (1982) *Biochim Biophys*  
 10 *Acta* 688, 57-65.
- Reilly IT: Idiopathic myelofibrosis: pathogenesis, natural history and management. *Blood Rev* 11:233-242, 1997
- Reilly, 3. T. (1997) *Blood Rev* 11, 233-42.
- Roberts IA, McMullin ME: A practical miniature long-term bone marrow  
 15 culture system for investigating early myelodysplasia. *Leuk Res* 16:737-741, 1992
- Rowley, S. D. (2000) in *HEMATOLOGY: Basic Principles and Practice*, eds. Hoffman, R., Benz, S., E.J., Shattil, S. J., Furie, B., Cohen, H. J., Silberstein, L. E. & McGlave, P. (Churchill Livingstone, Philadelphia), pp. 1642-1658.
- Santos-Alvarez, J., Goberna, R. & Sanchez-Margalet, V. (1999) *Cell Immunol*  
 20 194, 6-11.
- Sawada K, Sato N, Koike I: Inhibition of GM-CSF production by recombinant human interleukin-4: negative regulator of hematopoiesis. *Leuk Lymphoma* 19:33-42, 1995
- Sawada, K., Sato, N. & Koike, T. (1995) *Leuk Lymphoma* 19, 3342.
- 25 Seshi, B. (1995) *Blood* 86, 309a.
- Seshi B, Kumar S, Sellers D: Human bone marrow stromal cell: coexpression of markers specific for multiple mesenchymal cell lineages. *Blood Cells Mol Dis* 26:234-246, 2000
- Seshi B: Cell adhesion to proteins separated by lithium dodecyl sulfate-polyacrylamide gel electrophoresis and blotted onto a polyvinylidene difluoride  
 30 membrane: a new cell-blotting technique. *J Immunol Methods* 176:185-201, 1994
- Seshi B: Discovery of novel hematopoietic cell adhesion molecules from human bone marrow stromal cell membrane protein extracts by a new cell-blotting technique. *Blood* 83:2399-2409, 1994
- 35 Seshi B: Patterns of progenitor cell adhesion to novel bone marrow stromal CAMs using 2-D cell blotting demonstrate complex adhesive interactions (Abstract). *Blood* 86:309a, 1995
- Seshi B: The dual recognition systems of T lymphocytes: a model. *J Theor Biol* 99:827-830., 1982
- 40 Seshi, B. (1994) *Blood* 83, 2399-409.
- Seshi, B. (1994) *J Immunol Methods* 176, 185-201.
- Seshi, B., Kumar, S. & Sellers, D. (2000) *Blood Cells Mol Dis* 26, 234-246.
- Shain KILT, Landowski TH, Dalton WS: The tumor microenvironment as a determinant of cancer cell survival: a possible mechanism for de novo drug  
 45 resistance. *Curr Opin Oncol* 12:557-563., 2000
- Sherlock O: Analysis of large-scale gene expression data. *Curr Opin Immunol* 12:201-205, 2000
- Shevchenko, A., Wilm, M., Vorm, O. & Mann, M. (1996) *Anal Chem* 68, 850-8.
- Silva IP: Software Review: GeneSpring 3.1: HMS Beagle: The BioMedNet  
 50 Magazine (Issue 7 July, 2000), 2000, p

<http://news.bmn.com,'hmsbeagle/82/reviews/sreview>

Simmons PI, Przepio Thomas ED, Torok-Storb B: Host ori- marrow stromal cells following allogeneic bone marrow transplantation. *Nature* 328:429432, 1987

Soskic, V., Gorlach, M., Poznanovic, S., Boehmer, F. D. & Godovac-

5 Zimmermann, J. (1999) *Biochemistry* 38, 1757-64.

Tamayo P, Slonim D, Mesirov I, Zhu Q, Kitareewan S, Dmitrovsky E, Lander ES, Golub TR: Interpreting patterns of gene expression with self-organizing maps: methods and application to hematopoietic differentiation. *Proc Natl Acad Sci U S A* 96:2907-29 12, 1999

10 Tempst, P., Erdjument-Bromage, H., Posewitz, M. C., Geromanos, S., Freckleton, G., Grewal, A., Lacomis, L., Lui, M. & Philip, J. (2000) in *Mass Spectrometry in Biology & Medicine*, eds. Burlingame, A. L., Can, S. A. & Baldwin, M. A. (Huxnana Press, Totowa, NJ), pp. 121-142.

The genetic program of hematopoietic stem cells. *Science* 288:1635-1640., 2000

15 Thiele DL, Kurosaka M, Lipsky PE: Phenotype of the accessory cell necessary for mitogen-stimulated I and B cell responses in human peripheral blood: delineation by its sensitivity to the lysosomotropic agent, L-leucine methyl ester. *J Immunol* 13 1:2282-2290, 1983

Thiele, D. L., Kurosaka, M. & Lipsky, P. E. (1983) *J Immunol* 131, 2282-90.

20 Thomas, T., Gori, F., Khosla, S., Jensen, M. D., Burguera, B. & Riggs, B. L. (1999) *Endocrinology* 140, 1630-8.

Torok-Storb B: Cellular interactions. *Blood* 72:373-385, 1988

Torok-Storb, B. (1988) *Blood* 72, 373-85.

Unlu, M., Morgan, M. E. & Minden, J. S. (1997) *Electrophoresis* 18, 2071-7.

25 Verfailhe CM: Anatomy and physiology of hematopoiesis, in Hoffman R, Benz 1, E.J., Shattil Si, Furie B, Cohen Hi, Silberstein LE, McGlave P (eds): *HEMATOLOGY: Basic Principles and Practice* (ed 3rd). New York, Churchill Livingstone, 2000, p 139-154

Verfaillie, C. M. (2000) in *HEMATOLOGY Basic Principles and Practice*, eds.

30 Hoffman, R., Benz, J., E.J., Shattil, S. J., Furie, B., Cohen, H. J., Silberstein, L. E. & McGlave, P. (Chuschill Livingstone, New York), pp. 139-154.

Wallace SR, Oken MM, Ness By, Maselhis AM: Abnormalities of bone marrow mesenchymal stem cells in multiple myeloma (Abstract). *Blood* 94:547a, 1999

35 Wallace, S. R., Oken, M. M., Ness, B. V. & Masellis, A. M. (1999) *Blood* 94, 547a.

Whetton, A. D. & Spooncer, E. (1998) *Curr Opin Cell Biol* 10, 721-6.

40 Williams, K. L. & Hochstrasser, D. F. (1997) in *Proteome Research: New frontiers in Functional Genomics*, eds. Wilikins, M. R., Williams, K. L., Appel, R. D. & Hochstrasser, D. F. (Springer, New York), pp. 1-12.

Willman CL: Acute leukemias: a paradigm for the integration of new technologies in diagnosis and classification. *Mod Pathol* 12:218-228., 1999

45 Wilmot I, Schnieke AE, McWhir 1, Kind AJ, Campbell KH: Viable offspring derived from fetal and adult mammalian cells [see comments] [published erratum appears in *Nature* 1997 Mar 13;386(6621):200]. *Nature* 385:810-813, 1997

Wooster R: Cancer classification with DNA microarrays is less more? -Trends Genet 16:327-329., 2000

Yanagida, M., Miura, Y., Yagasaki, K., Taoka, M., Isobe, I. & Takahashi, N. (2000) *Electrophoresis* 21, 1890-8.

50 Young RA: Biomedical discovery with DNA arrays. *Cell* 102:9-15., 2000

### CLAIMS

What is claimed is:

1. Isolated mesenchymal progenitor cells that are pluri-differentiated.
2. A therapeutic composition comprising an isolated pluri-differentiated  
5 mesenchymal progenitor cells and a pharmaceutically acceptable carrier,  
wherein said isolated pluri-differentiated mesenchymal progenitor cells are  
present in an amount effective for treating a disease state in a mammal in need  
thereof.
3. A therapeutic composition comprising isolated pluri-differentiated  
10 mesenchymal progenitor cells and a pharmaceutically acceptable carrier,  
wherein said isolated pluri-differentiated mesenchymal progenitor cells are  
present in an amount effective to enhance hematopoietic progenitor cell  
engraftment in a mammal in need thereof.
4. A therapeutic composition comprising isolated pluri-differentiated  
15 mesenchymal progenitor cells and a pharmaceutically acceptable carrier,  
wherein said pluri-differentiated mesenchymal progenitor cells are present in an  
amount effective to treat GvHD in a mammal about to undergo bone marrow or  
organ transplantation or suffering from GvHD caused by bone marrow or organ  
transplantation.
- 20 5. A method for purifying pluri-differentiated mesenchymal progenitor  
cells comprising the steps of:
  - a) providing a cell culture preparation by the Dexter method;
  - b) treating the cells to obtain a cell suspension;
  - c) removing macrophages;
  - 25 d) fractionating the cells; and
  - e) collecting the fraction of pluri-differentiated mesenchymal progenitor  
cells.
6. A method for enhancing bone marrow engraftment in a mammal in  
need thereof which comprises administering to the mammal (i) isolated pluri-  
30 differentiated mesenchymal progenitor cells and (ii) a bone marrow graft, wherein  
the isolated pluri-differentiated mesenchymal progenitor cells are administered in  
an amount effective to promote engraftment of the bone marrow in the mammal.

7. The method according to claim 6, wherein said administering step includes intravenously injecting or directly injecting the isolated pluri-differentiated mesenchymal progenitor cells to the site of intended activity.

5 8. A gene in an MPC for detecting the presence of cancer or pre-cancer in a cell population.

9. A pharmaceutical for modulating the gene of claim 10.

10 10. A method for enhancing engraftment of cells in a mammal in need thereof which comprises administering to the mammal isolated pluri-differentiated mesenchymal progenitor cells wherein the isolated pluri-differentiated mesenchymal progenitor cells are administered in an amount effective to promote engraftment of the cells in the mammal.

11. The method of claim 10, wherein the isolated pluri-differentiated mesenchymal progenitor cells are administered by intravenous injection or by injecting directly to the site of intended activity.

15 12. The method of claim 10, wherein the isolated pluri-differentiated mesenchymal progenitor cells are administered prior to administration of the hematopoietic progenitor cells.

20 13. The method of claim 10, wherein the isolated pluri-differentiated mesenchymal progenitor cells are introduced in a cell suspension also containing hematopoietic progenitor cells.

14. A SCID mouse model for investigating MPC function.

15. Phenotypic cultured bone marrow stromal cells capable of being analyzed at single cell level.

25 16. A diagnostic test for screening for abnormalities of bone marrow stromal cells.

17. The diagnostic test according to claim 16, wherein said test can be used for screening for various hematologic diseases and other diseases effecting stromal cells

30 18. The diagnostic test according to claim 16, wherein said abnormalities are phenotypic abnormalities that can be discerned at a single cell level.

19. Stromal cells for use in combination with engraftment or other similar procedures for enhancing the effectiveness of the treatment.

20. A method for treating graft-versus-host disease (GvHD) in a mammal about to undergo bone marrow or organ transplantation or suffering from GvHD caused by bone marrow or organ transplantation, by administering to the mammal an effective amount of isolated pluri-differentiated mesenchymal progenitor cells.

- 5 21. A method for diagnosing a disease state comprising the steps of:
- a) establishing gene expression patterns of normal state bone marrow derived isolated pluri-differentiated mesenchymal progenitor cells;
  - b) establishing gene expression patterns of various leukemic state bone marrow derived isolated pluri-differentiated mesenchymal progenitor cells;
  - 10 c) identifying gene sets that are unique to a given state; and
  - d) comparing a profile of bone marrow derived isolated mesenchymal progenitor cell of unknown state to said gene sets.

22. A method for identifying therapeutic targets for treatment of
- 15 hematopoietic function comprising the steps of:
- a) determining the median gene expression profile of bone marrow isolated pluri-differentiated mesenchymal progenitor cells associated with each disease state of interest;
  - b) identifying gene groups that are up-regulated, down regulated, and
  - 20 common to each disease state; and
  - c) identifying gene sets that are unique to a given state.

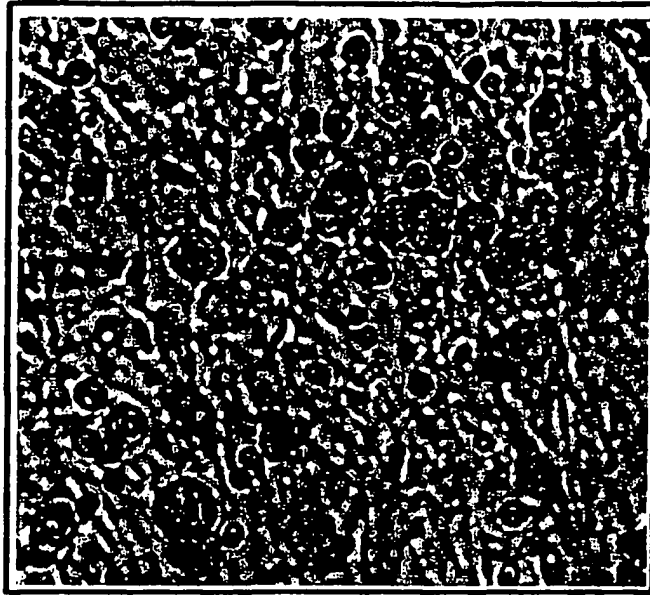
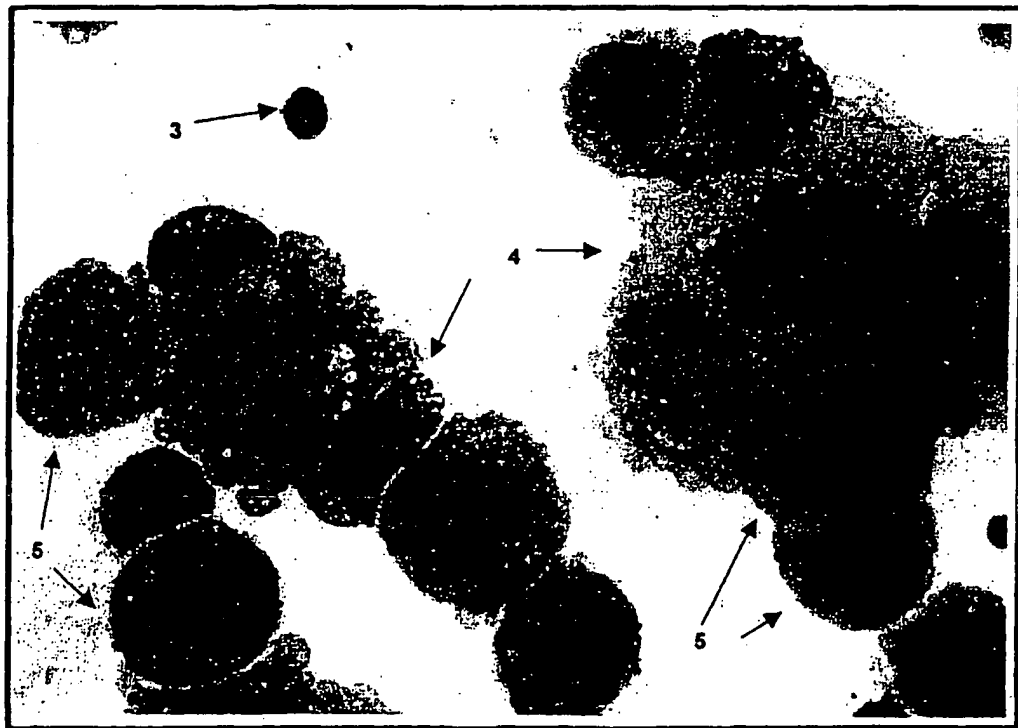
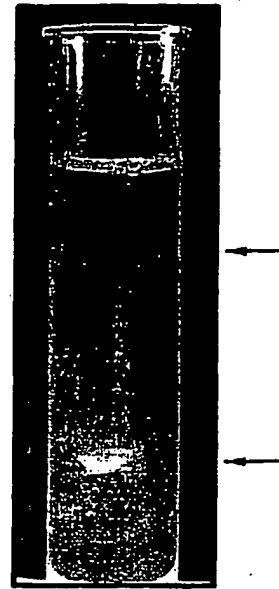
Figure - 1Figure - 2Figure - 3



Figure - 4A



Figure - 4B

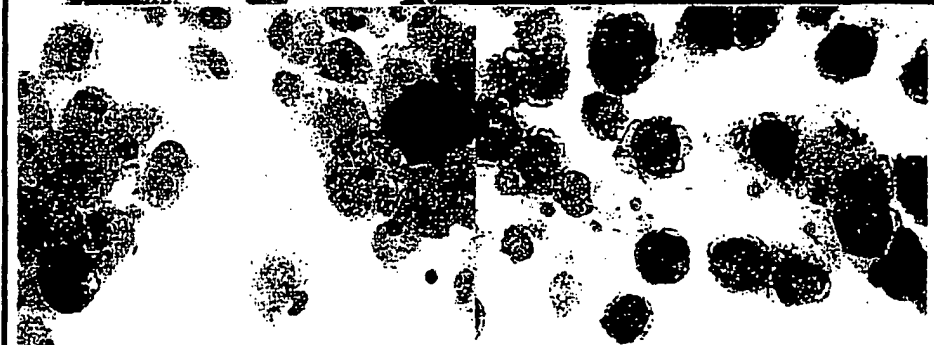


Figure - 4C

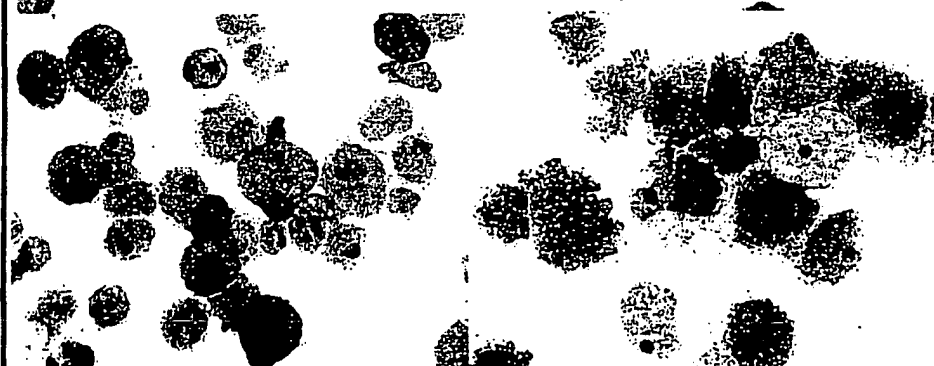


Figure - 4D

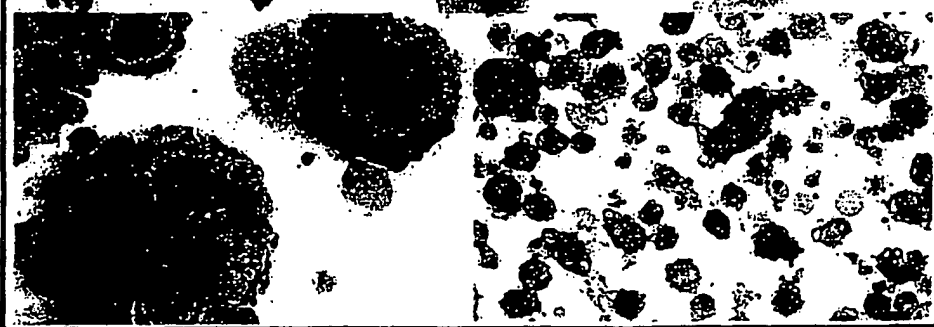


Figure - 4E

Figure - 4F

Figure - 4G

Figure - 4H

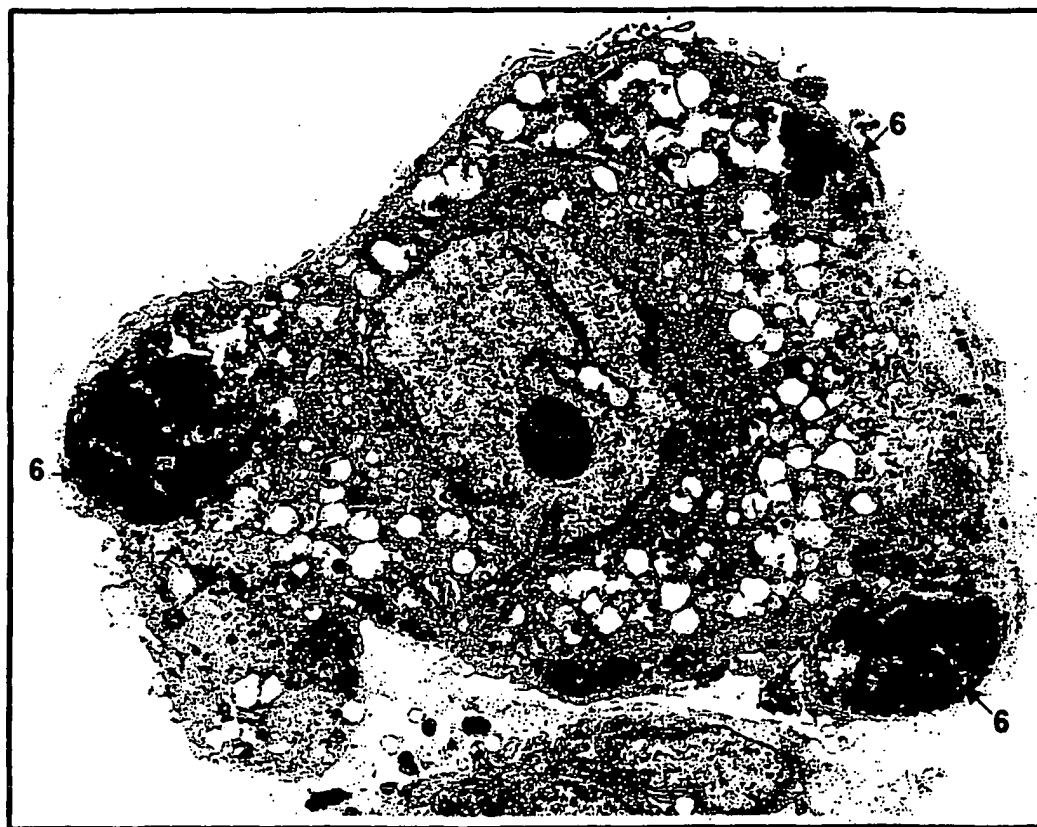


Figure - 5

Figure - 6A

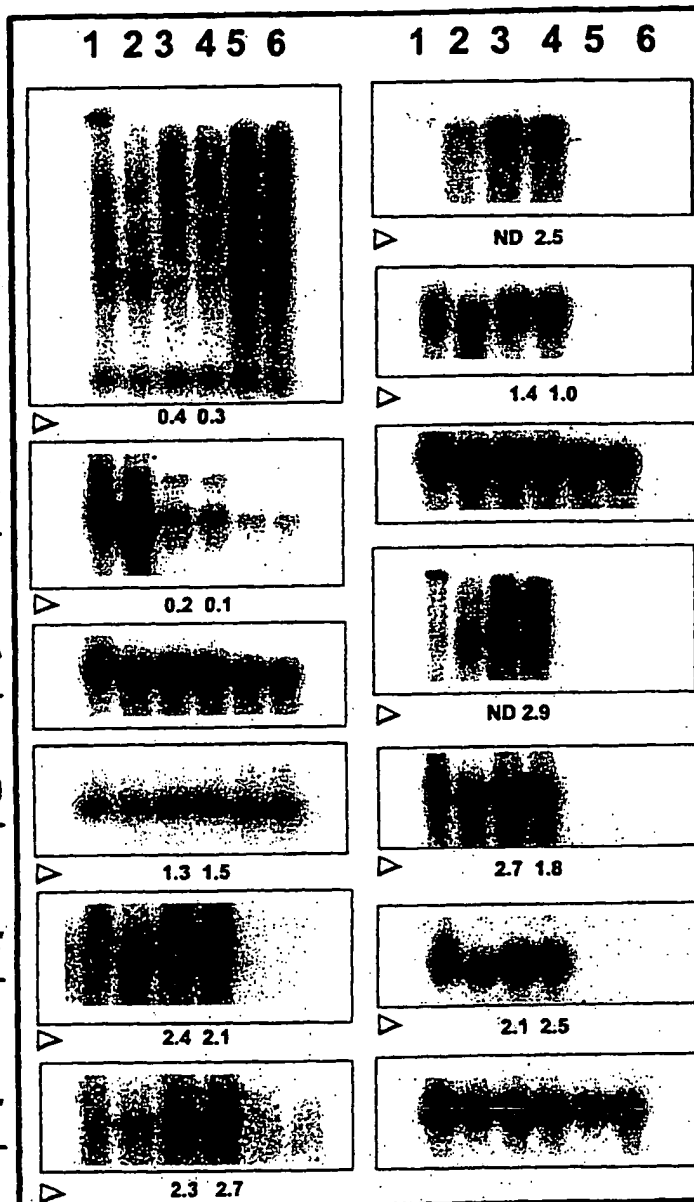


Figure - 6G

Figure - 6H

Figure - 6I

Figure - 6J

Figure - 6K

Figure - 6L

Figure - 6M

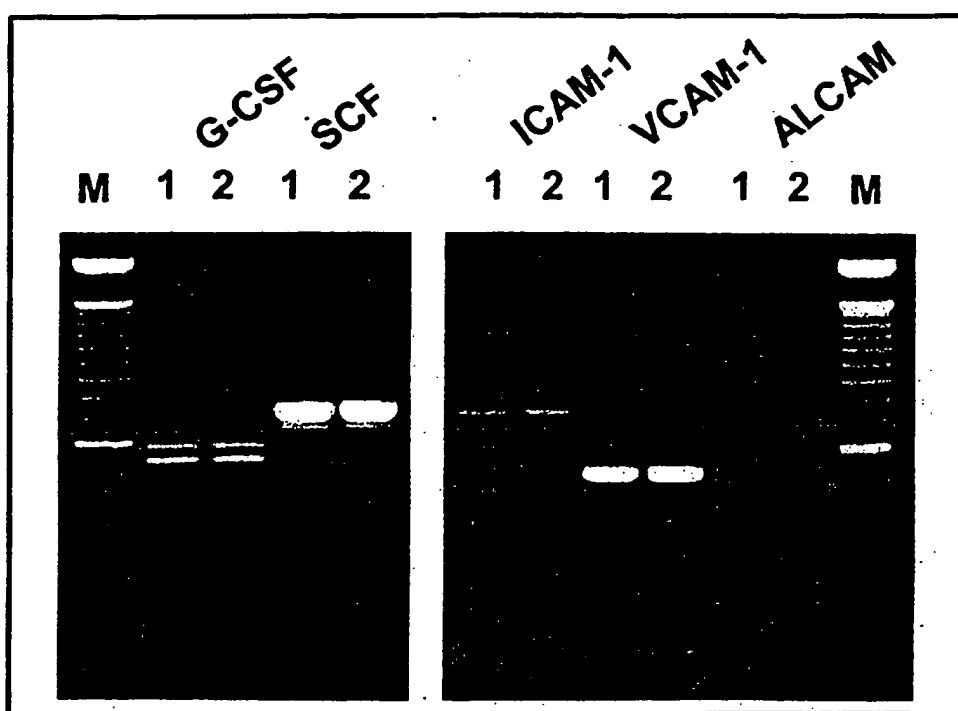


Figure - 7

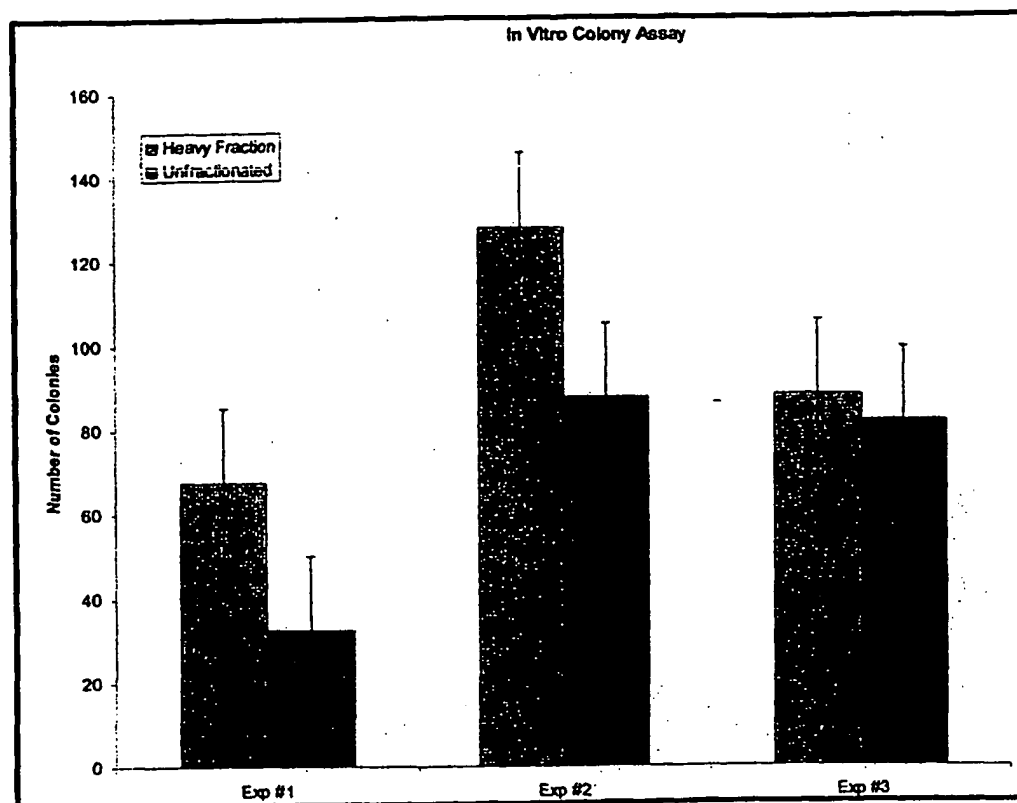


Figure - 8

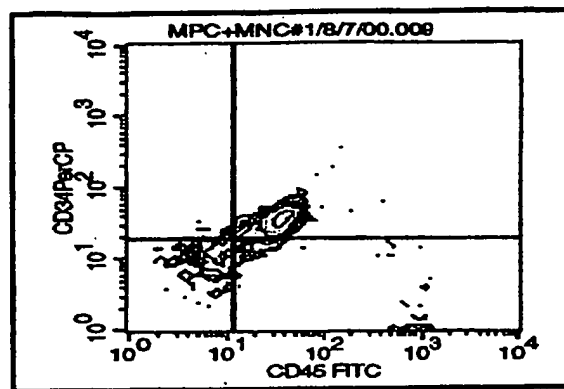
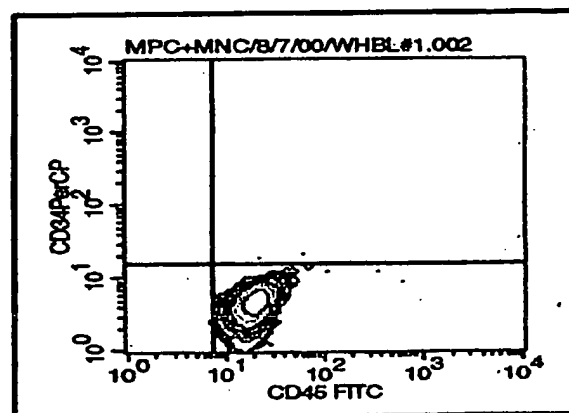
Figure - 9AFigure - 9B

Figure - 10G

Figure - 10E

Figure - 10C

Figure - 10A

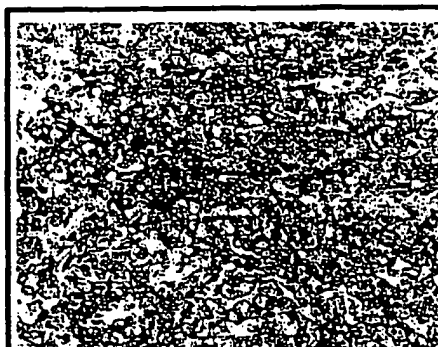


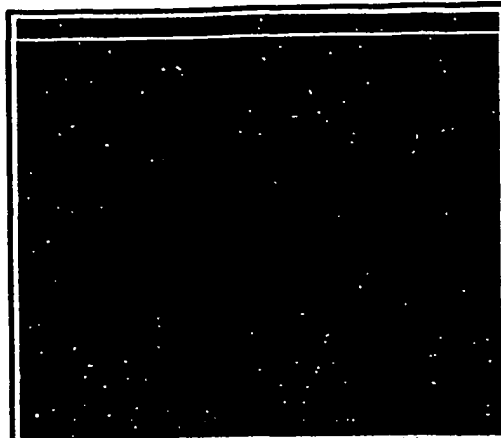
Figure - 10H

Figure - 10F

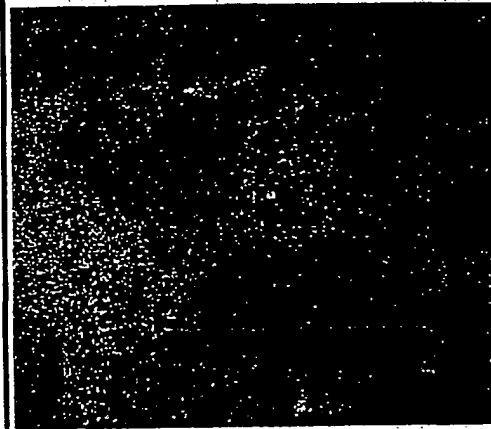
Figure - 10D

Figure - 10B

**Figure - 11A**



**Figure - 11B**



**Figure - 11C**





Figure - 12A

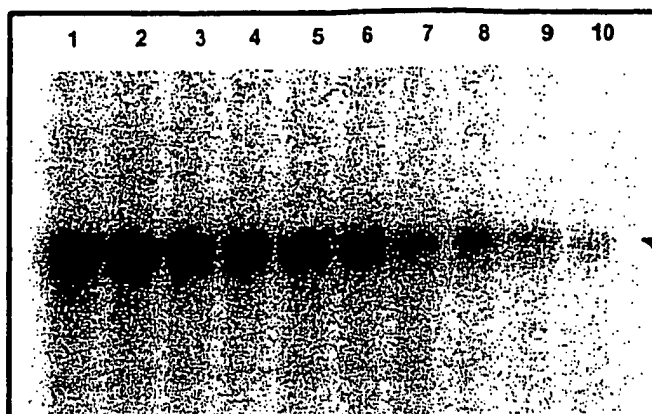


Figure - 12B

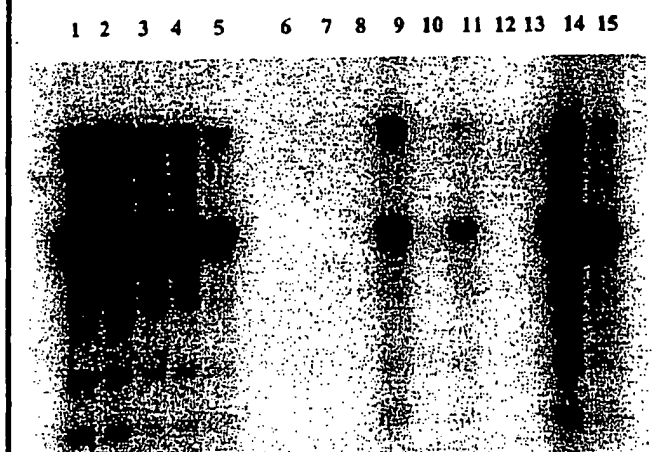
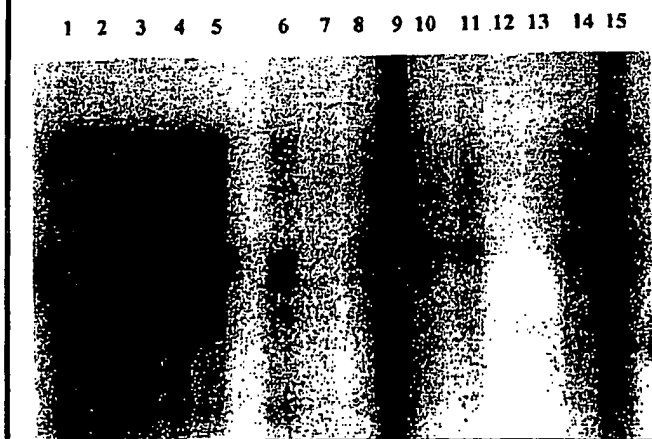
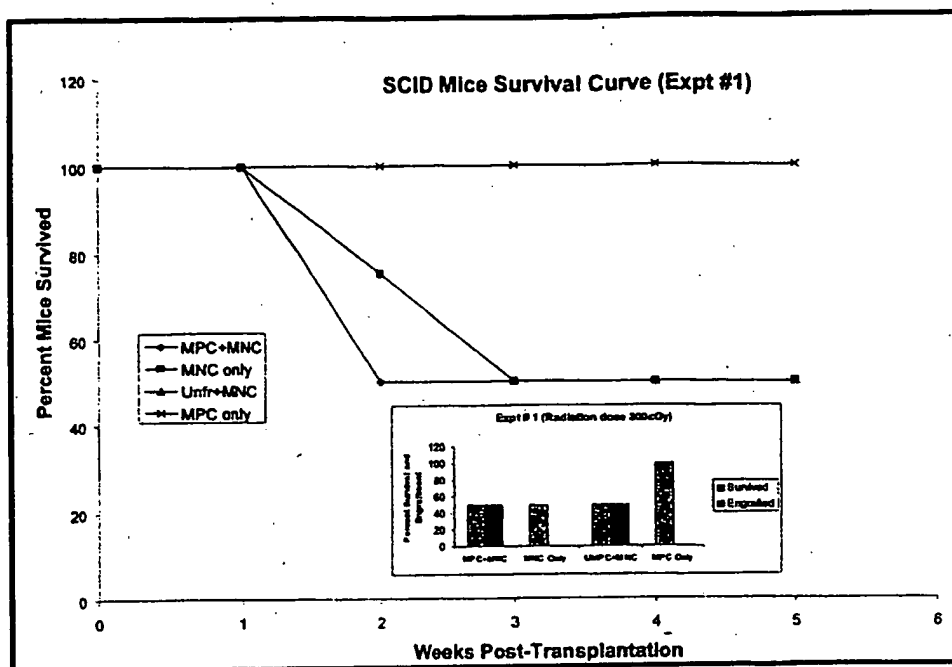
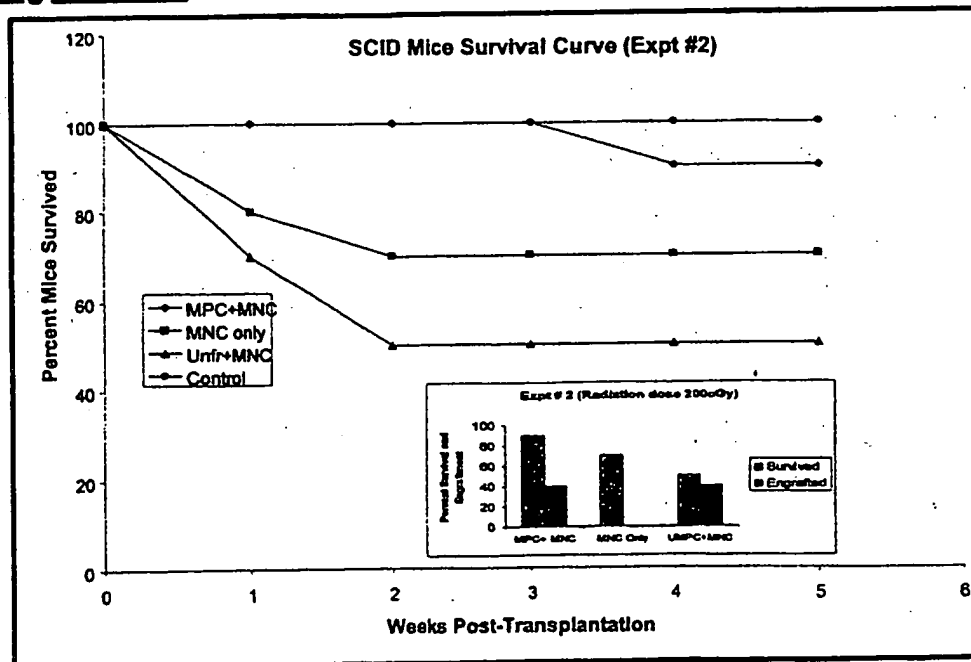


Figure - 12C



**Figure - 13A****Figure - 13B**

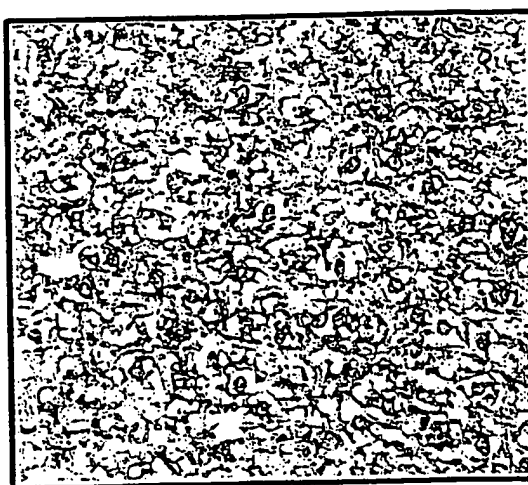


Figure - 14A

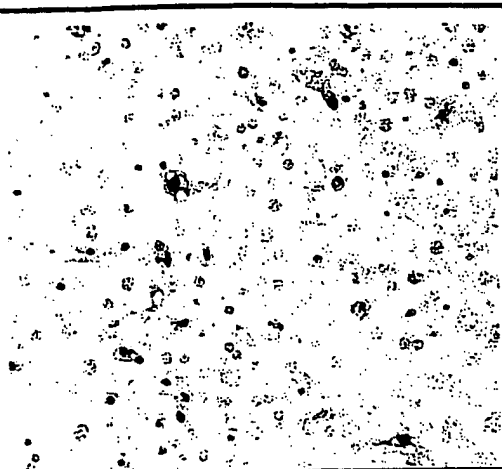


Figure - 14B



Figure - 14C

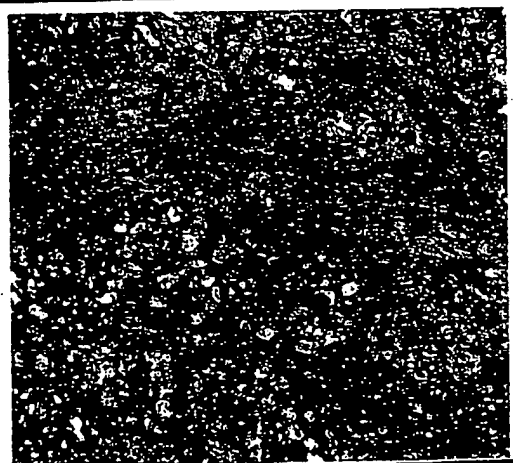
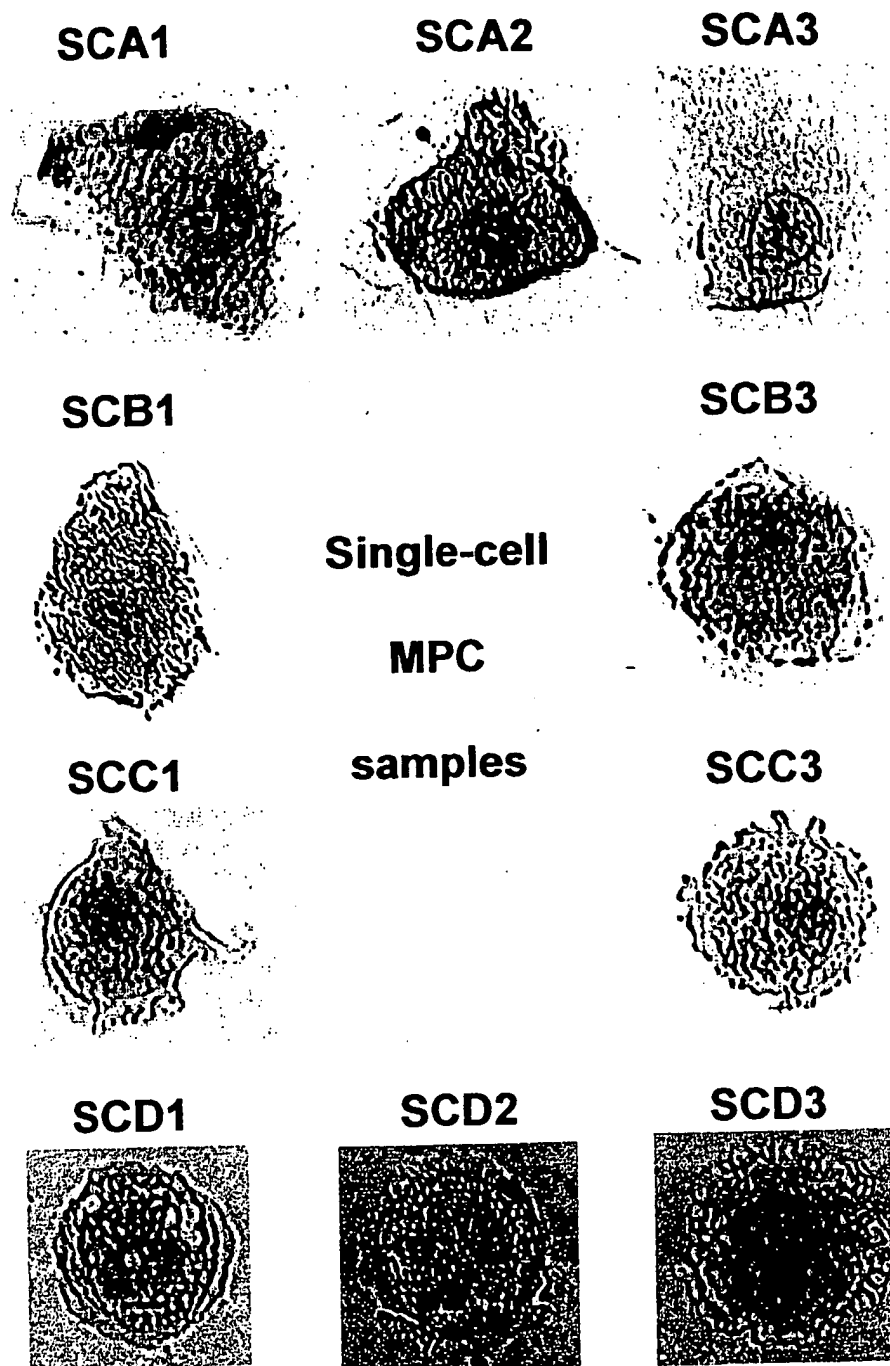


Figure - 14D



**Figure - 15**

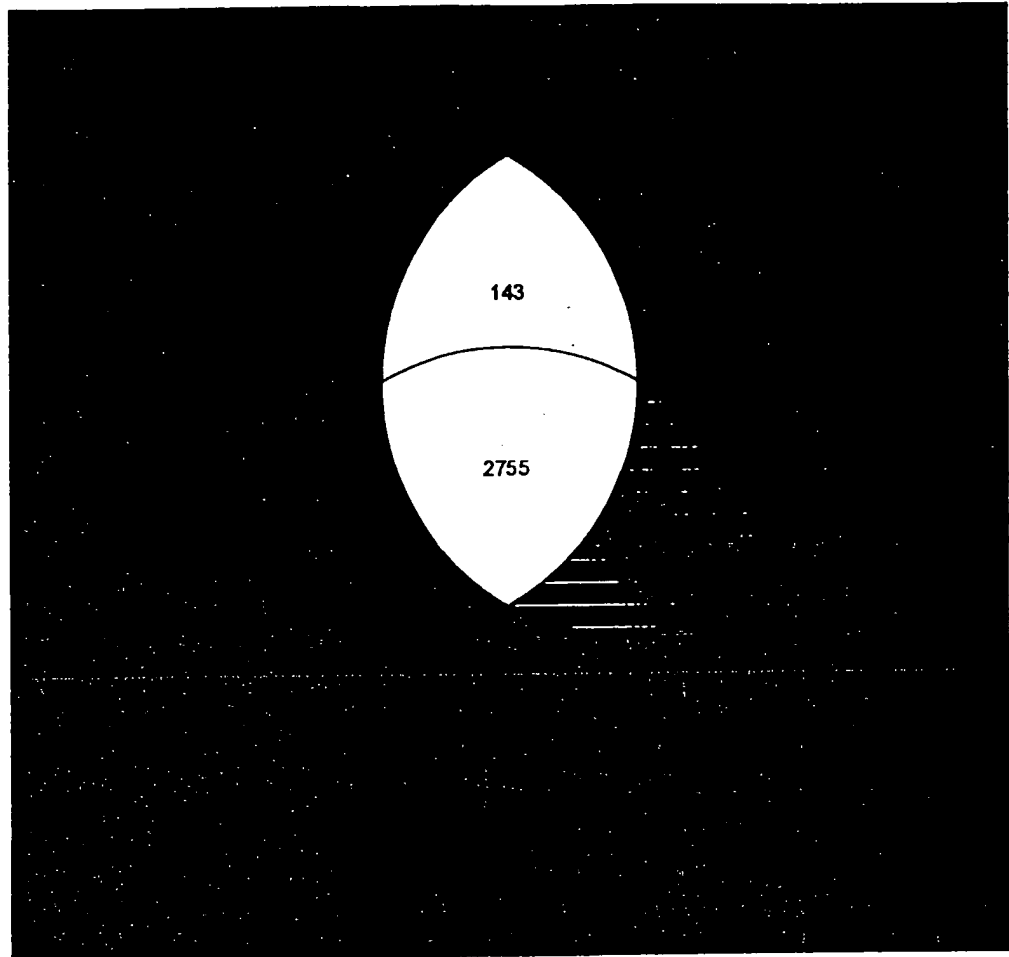


Figure - 16

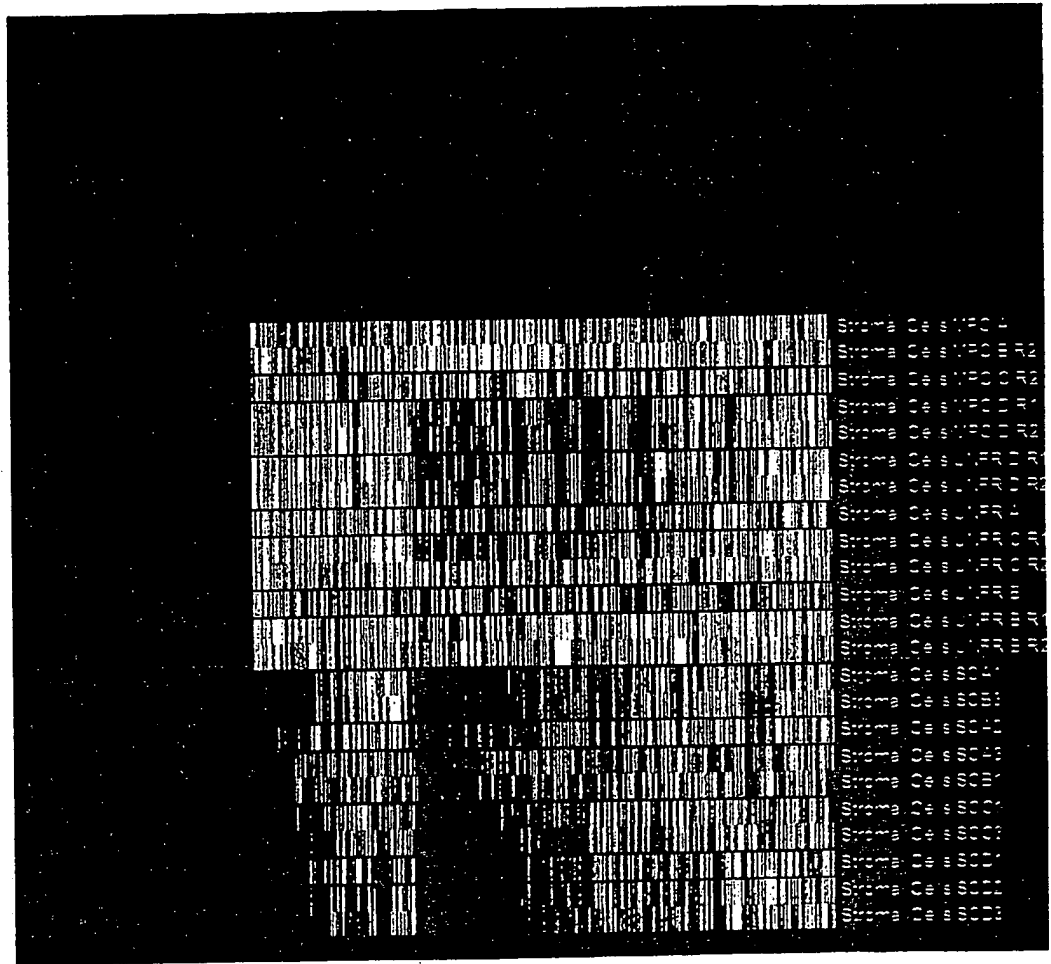


Figure - 17

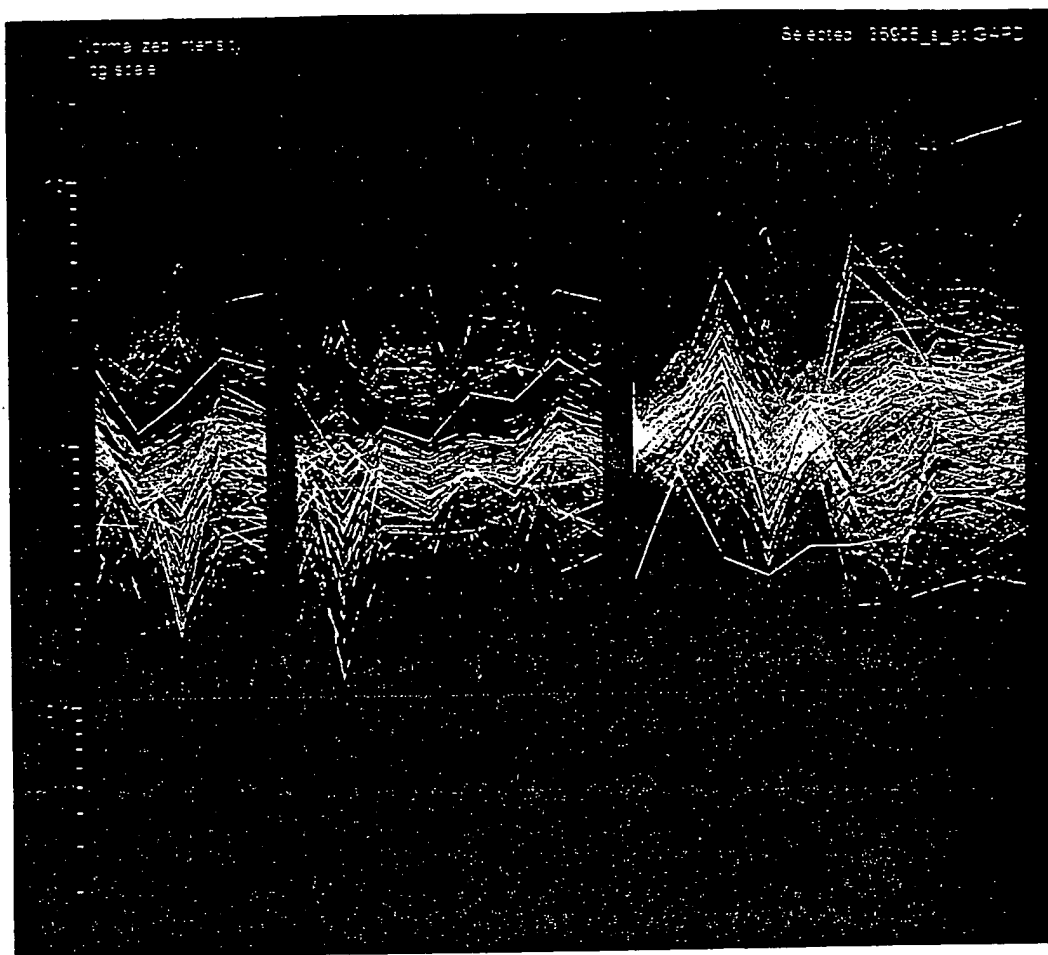
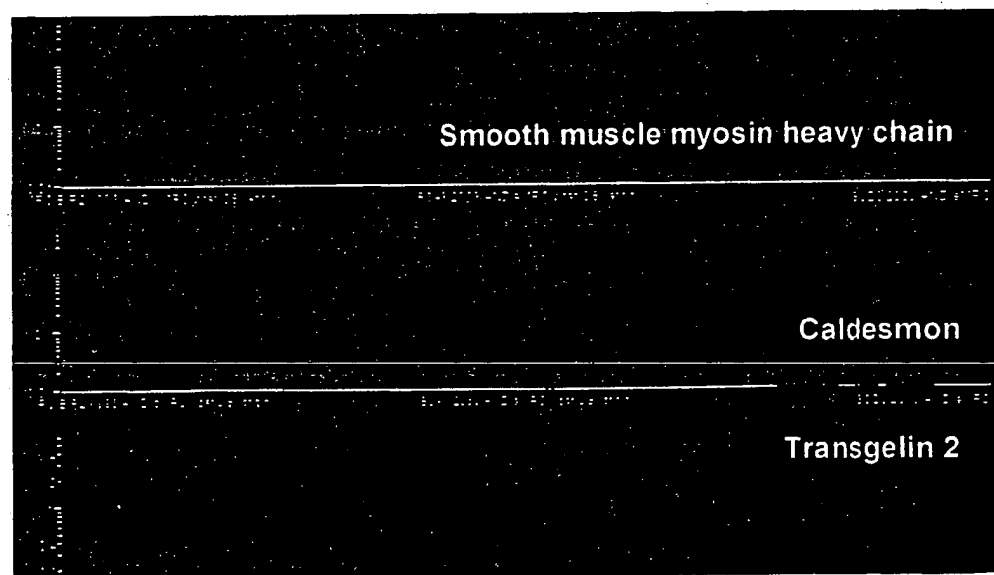
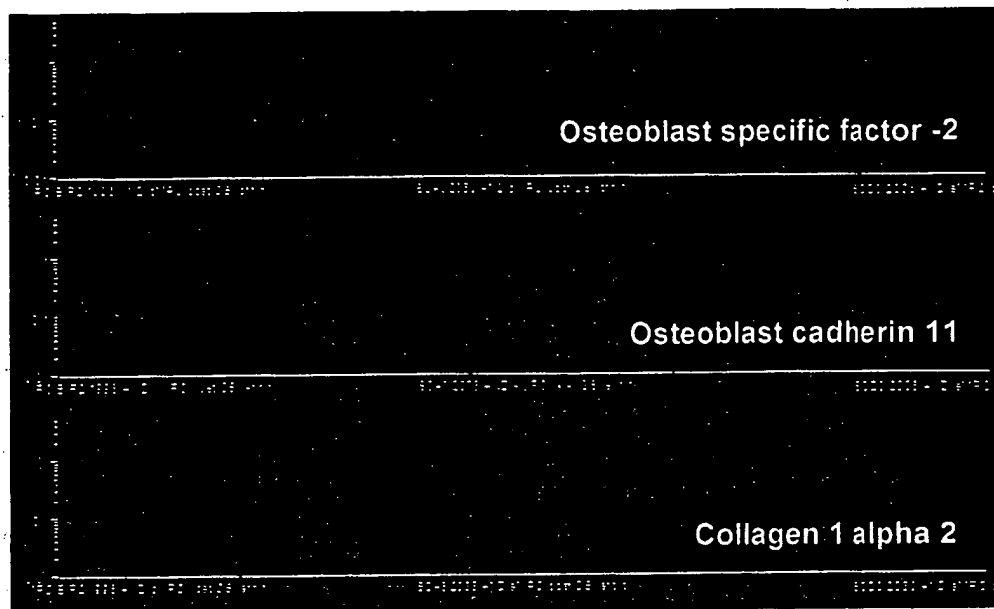


Figure - 18

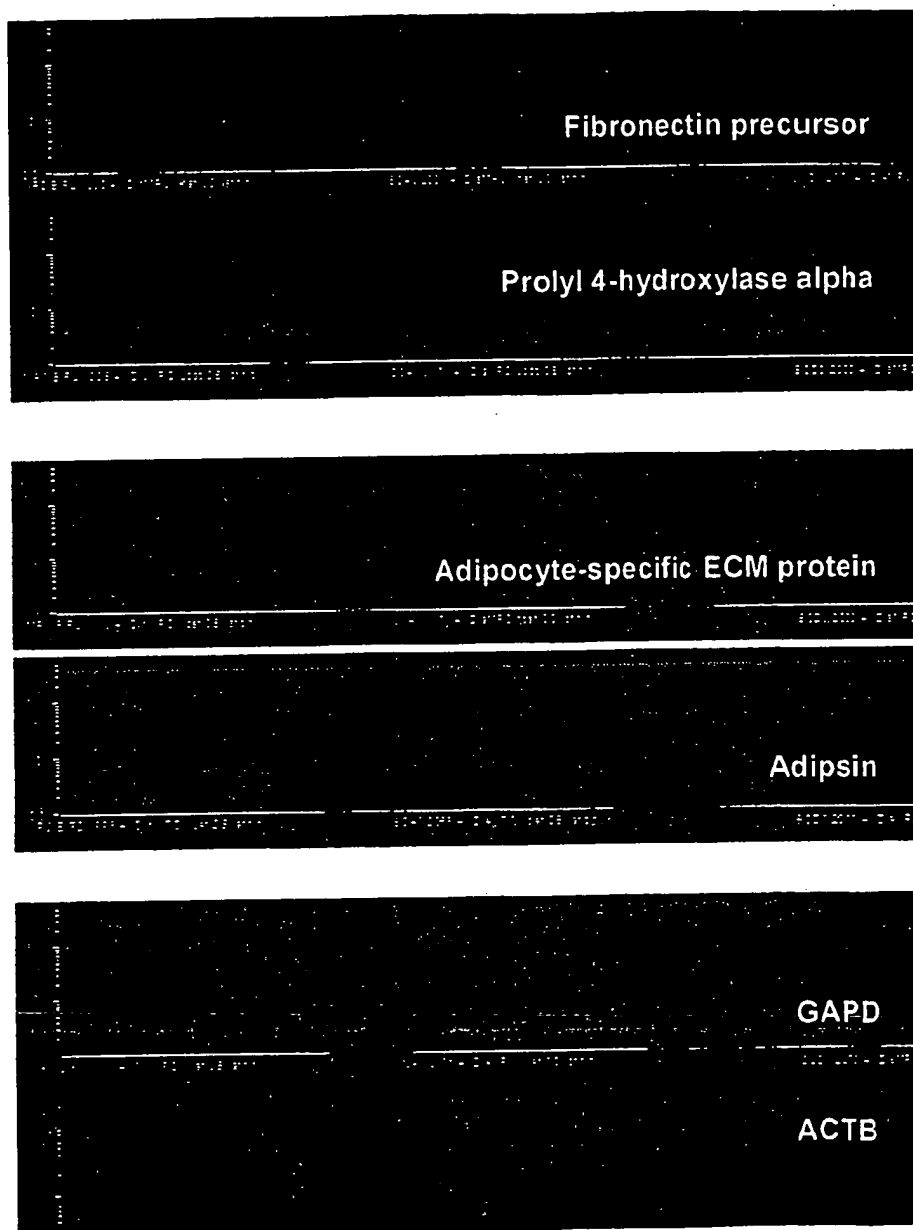
**Collective MPCs  
(Samples 1-5)****Single cell MPCs  
(Samples 6-15)**

**Figure - 19**

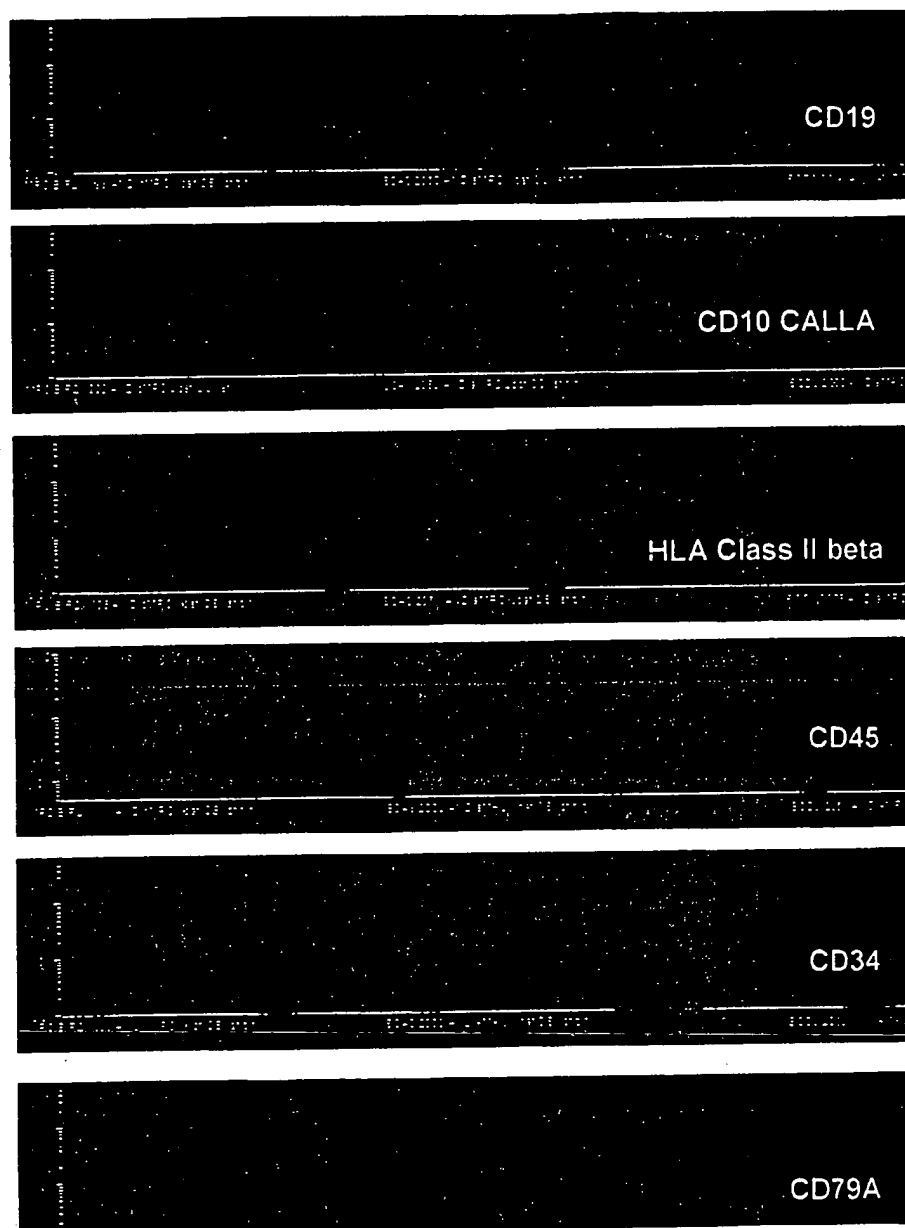


**C illective MPCs  
(Samples 1-5)**

**Single c il MPCs  
(Samples 6-15)**



**Figure - 20**

**Collective MPCs  
(Samples 1-5)****Single cell MPC  
(Samples 6-15)****Figure - 21**

	A		B		C		D		E	
	Systematic	Common	Genbank	Description	Product					
1	Systematic	Common	Genbank	Description	Product					
2	AFFX-hum_alu_at		U14573	***ALU WARNING: Human Alu-Sq subfamily consensus sequence.						
3	38820_at	15-Sep	AF051894	15 kDa selenoprotein	15 kDa selenoprotein					
4	33247_at	POH1	U86782	26S proteasome-associated pad1 homolog	26S proteasome-associated pad1 homolog					
5	32165_at	SFRS7	L41887	35 kDa protein; Homo sapiens splicing factor, arginine/serine-rich 7 (SFRS7) gene, complete cds.	splicing factor, arginine/serine-rich 7					
6	36851_g_at	N33	U42360	39 kDa protein; Human N33 protein form 2 (N33) gene, exon 11 and complete cds.	N33 protein form 2					
7	39328_at	HMGCR	M11058	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	3-hydroxy-3-methylglutaryl-Coenzyme A reductase					
8	41142_at	OXCT	U62961	3-oxoacid CoA transferase	succinyl CoA:3-oxoacid CoA transferase precursor					
9	34411_at	PAPSS1	Y10387	3'-phosphoadenosine 5'-phosphosulfate synthase 1	PAPS synthetase					
10	738_at	NT5C2	D38524	5'-nucleotidase, cytosolic II	5'-nucleotidase					
11	31794_at	NT5C2	D38524	5'-nucleotidase, cytosolic II	5'-nucleotidase					
12	38811_at	ATIC	D82348	5-aminimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	5-aminimidazole-4-carboxamide-1-beta-D-ribo nucleotide transformylase/inosinase					
13	38383_at	MTR	U73398	5-methyltetrahydrofolate-homocysteine methyltransferase	methionine synthase					
14	39025_at	LOC54543	A1557912	6.2 kd protein						

Fig 21

A	B	C	D	E
			60S Ribosomal Protein L35A LIKE pseudogene match: proteins P04646 P02434 P18077 P05744 P41056 CE04362 match: cDNAs Y16430 X52966 X03475 V01440 X55030 J00995 match: ESTs AA554649 AA747384 AA572868 AA329139 AA745138 AA330809 AA483371 AA507788 AA483213 D55111 N90267 N91909 AA662153 AA720551 AA836920 AA501529 AA526745 AA608598 AA649846 AA654164 match: genomic DNAs Z32550 X05705 X05706 X05704 I23465 I45758	
15 40446_at	cICK0721Q.1	AL021366		divalent cation tolerant protein CUTA
16 39059_at	DHCR7	AF034544	7-dehydrocholesterol reductase	delta7-sterol reductase
17 40797_at	ADAM10	AF009615	a disintegrin and metalloproteinase domain 10	ADAM10
18 41601_at	ADAM17	AA142964	a disintegrin and metalloproteinase domain 17 (tumor necrosis factor, alpha, converting enzyme)	
19 34761_r_at	ADAM9	U41766	a disintegrin and metalloproteinase domain 9 (meltrin gamma)	metalloproteinase/disintegrin/cysteine-rich protein precursor
20 37680_at	AKAP12	U81607	A kinase (PRKA) anchor protein (gravin) 12	gravin
21 36633_at	AKAP10	AA114830	A kinase (PRKA) anchor protein 10	
22 34657_at	AKAP11	AB014529	A kinase (PRKA) anchor protein 11	KIAA0629 protein
23 35985_at	AKAP2	AB023137	A kinase (PRKA) anchor protein 2	KIAA0920 protein

Fig 21

	A	B	C	D	E
24	1636_g_at	ABL	U07563	<p>ABL is the cellular homolog proto-oncogene of Abelson's murine leukemia virus and is associated with the 19:22 chromosomal translocation with the BCR gene in chronic myelogenous and acute lymphoblastic leukemia; alternative splicing using alternative first exon 1b; ABL is the cellular homolog proto-oncogene of Abelson's murine leukemia virus and is associated with the 19:22 chromosomal translocation with the BCR gene in chronic myelogenous and acute lymphoblastic leukemia; alternative splicing using exon 1a; Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds.</p>	proto-oncogene tyrosine-protein kinase accessory proteins BAP31/BAP29
25	41724_at	DXS1357E	X81817		
26	41530_at	ACAA2	D16294		
27	34668_at	ACATN	D88152	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	mitochondrial 3-oxoacyl-CoA thiolase
28	36553_at	ASMTL	AA669799	acetyl-Coenzyme A transporter	acetyl-coenzyme A transporter
29	37034_at	ANP32A	U73477	acetylserotonin O-methyltransferase-like acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	acidic nuclear phosphoprotein pp32
30	38479_at	ANP32B	Y07969	acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	APRIL
31	34397_at	OA48-18	AF069250	acid-inducible phosphoprotein	okadaic acid-inducible phosphoprotein
32	39168_at	ALTE	AB018328	Ac-like transposable element	KIAA0785 protein
33	40077_at	ACO1	Z11559	aconitase 1, soluble	iron regulatory factor
34	37578_at	AFAP	D25248	actin filament associated protein	actin filament associated protein
35	1718_at	ARPC2	U50523	actin related protein 2/3 complex, subunit 2 (34 kD)	actin related protein 2/3 complex, subunit 2 (34 kD)

F. 521

	A	B	C	D	E
36	34692_r_at	ARPC4	AF006087	actin related protein 2/3 complex, subunit 4 (20 kD)	p20-Arc
37	38392_at	ARPC5	AF006088	actin related protein 2/3 complex, subunit 5 (16 kD)	p16-Arc
38	32755_at	ACTA2	X13839	actin, alpha 2, smooth muscle, aorta	alpha 2 actin
39	AFHX-HSAC07/ACTB	ACTB	X00351	actin, beta	beta actin
40	AFHX-HSAC07/ACTB	ACTB	X00351	actin, beta	beta actin
41	32318_s_at	ACTB	X63432	actin, beta	mutant beta-actin (beta-actin)
42	34160_at	ACTG1	X04098	actin, gamma 1	gamma-actin
43	39329_at	ACTN1	X15804	actinin, alpha 1	actinin, alpha 1
44	41753_at	ACTN4	U48734	actinin, alpha 4	alpha actinin
45	38642_at	ALCAM	Y10183	activated leucocyte cell adhesion molecule	MEMD protein
46	36171_at	PC4	AI521453	activated RNA polymerase II transcription cofactor 4	
47	39764_at	ACVR1	Z22534	activin A receptor, type I	ALK-2
48	35162_s_at	ACVR2	D31770	activin A receptor, type II	activin type II A receptor precursor
49	34394_at	ADNP	AB018327	activity-dependent neuroprotector	KIAA0784 protein
50	40673_at	ACADSB	U12778	acyl-Coenzyme A dehydrogenase, short/branched chain	acyl-CoA dehydrogenase
51	40459_at	ACOX1	S69189	acyl-Coenzyme A oxidase 1, palmitoyl	peroxisomal acyl-coenzyme A oxidase
52	40745_at	AP1B1	L13939	adaptor-related protein complex 1, beta 1 subunit	beta-prime-adaptin
53	35275_at	AP1G1	AL050025	adaptor-related protein complex 1, gamma 1 subunit	hypothetical protein
54	39795_at	AP2M1	D63475	adaptor-related protein complex 2, mu 1 subunit	adaptor-related protein complex 2, mu 1 subunit
55	39347_at	AP2S1	X97074	adaptor-related protein complex 2, sigma 1 subunit	clathrin-associated protein
56	32039_at	AP3B1	U81504	adaptor-related protein complex 3, beta 1 subunit	beta-3A-adaptin subunit of the AP-3 complex
57	36172_s_at	AP3D1	AF002163	adaptor-related protein complex 3, delta 1 subunit	delta-adaptin
58	38074_at	AP3S1	U91932	adaptor-related protein complex 3, sigma 1 subunit	AP-3 complex sigma3A subunit
59	33102_at	ADD3	D67031	adducin 3 (gamma)	adducin-like protein

Fig 21

	A	B	C	D	E
60	38014_at	ADAR	X79448	adenosine deaminase, RNA-specific	adenosine deaminase, RNA-specific, isoform ADAR-a; adenosine deaminase, RNA-specific, isoform ADAR-b; adenosine deaminase, RNA-specific, isoform ADAR-c
61	38748_at	ADARB1	U76421	adenosine deaminase, RNA-specific, B1 (RED 1 homolog rat)	dsRNA adenosine deaminase DRADA2b
62	168_at	ADK	U50196	adenosine kinase	adenosine kinase
63	33865_at	BS69	AA127624	adenovirus 5 E1A binding protein	
64	33134_at	ADCY3	AB011083	adenylate cyclase 3	KIAA0511 protein
65	40585_at	ADCY7	D25538	adenylate cyclase 7	adenylate cyclase 7
66	33800_at	ADCY9	AF036927	adenylate cyclase 9	adenylate cyclase type IX
67	40788_at	AK2	U84371	adenylate kinase 2	adenylate kinase 2A
68	36639_at	ADSL	AF067853	adenylosuccinate lyase	adenylosuccinate lyase
69	935_at	CAP	L12168	adenylyl cyclase-associated protein	adenylyl cyclase-associated protein
70	33405_at	CAP2	N90755	adenylyl cyclase-associated protein 2	
71	34378_at	ADFP	X97324	adipose differentiation-related protein	adipophilin
72	36861_at	DKFZp5641922	AL049946	adipican	hypothetical protein
73	33987_at	ARF1	M36340	ADP-ribosylation factor 1	ADP-ribosylation factor 1
74	39336_at	ARF3	M74491	ADP-ribosylation factor 3	ADP-ribosylation factor 3
75	36585_at	ARF4	M36341	ADP-ribosylation factor 4	ADP-ribosylation factor 4
76	37537_at	ARFD1	L04510	ADP-ribosylation factor domain protein 1, 64kD	nucleotide binding protein
77	39905_i_at	ARFGAP1	AA402332	ADP-ribosylation factor GTPase activating protein 1	
78	37296_at	ARL1	L28997	ADP-ribosylation factor-like 1	ADP-ribosylation factor-like 1
79	36572_r_at	ARL6IP	D31885	ADP-ribosylation factor-like 6 interacting protein	
80	41146_at	ADPRT	J03473	ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)	poly(ADP-ribose)transferase
81	1287_at	ADPRT	J03473	ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)	poly(ADP-ribose)transferase
82	34777_at	ADM	D14874	adrenomedullin	adrenomedullin precursor
83	32218_at		AF034176	AF034176 Human mRNA (Tripodis and Ragpusis) Homo sapiens cDNA clone ntcon5 contig.	

Fig 21

	A	B	C	D	E
84	34315_at	AFG3L2	Y18314	AFG3 ATPase family gene 3-like 2 (yeast)	paraplegin-like protein
85	33454_at	AGRN	AF016903	agnin	agnin precursor
86	37027_at	AHNAK	M80899	AHNAK nucleoprotein (desmoyokin)	
87	36185_at	AARS	D32050	alanyl-tRNA synthetase	alanyl-tRNA synthetase
88	36686_at	ALDH1A3	U07919	aldehyde dehydrogenase 1 family, member A3	aldehyde dehydrogenase 6
89	32747_at	ALDH2	X05409	aldehyde dehydrogenase 2 family (mitochondrial)	aldehyde dehydrogenase 2 family (mitochondrial)
90	40409_at	ALDH3A2	U46689	aldehyde dehydrogenase 3 family, member A2	aldehyde dehydrogenase
91	37331_g_at	ALDH4A1	U24266	aldehyde dehydrogenase 4 family, member A1	pyrroline-5-carboxylate dehydrogenase
92	36132_at	ALDH7A1	S74728	aldehyde dehydrogenase 7 family, member A1	antiquitin
93	33899_at	ALDH9A1	U34252	aldehyde dehydrogenase 9 family, member A1	gamma-aminobutyraldehyde dehydrogenase
94	38780_at	AKR1A1	J04794	aldo-keto reductase family 1, member A1 (aldehyde reductase)	aldo-keto reductase family 1, member A1 (aldehyde reductase)
95	36589_at	AKR1B1	X15414	aldo-keto reductase family 1, member B1 (aldose reductase)	aldo-keto reductase family 1, member B1 (aldose reductase)
96	37399_at	AKR1C3	D17793	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)
97	32510_at	AKR7A2	AF026947	aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase)	aflatoxin aldehyde reductase AFAR
98	39225_at	AGPS	Y09443	alkylglycerone phosphate synthase	alkyl-dihydroxyacetonephosphate synthase precursor
99	36941_at	AF1Q	U16954	ALL1-fused gene from chromosome 1q	AF1Q protein
100	37040_at	G2AN	D42041	alpha glucosidase II alpha subunit	alpha glucosidase II alpha subunit
101	35223_at	KIAA1017	AB023234	alpha integrin binding protein 63	KIAA1017 protein
102	39147_g_at	ATRX	U72936	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)	putative DNA dependent ATPase and helicase

Fig 21



	A	B	C	D	E
103	818_s_at	ATRX	U72936	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)	putative DNA dependent ATPase and helicase
104	34327_at	HLTF	Z46606	alternative translation initiation; H.sapiens HLTF gene for helicase-like transcription factor.	helicase-like transcription factor
105	35761_at	AASDHPPT	AL050073	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	hypothetical protein
106	39431_at	NPEPPS	AJ132583	aminopeptidase puromycin sensitive	puromycin sensitive aminopeptidase
107	41338_at	AES	A1951946	amino-terminal enhancer of split	
108	36996_at	OS-9	U41635	amplified in osteosarcoma	OS-9 precursor
109	38253_at	AGL	U84011	amylase, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)	glycogen debranching enzyme isoform 6
110	41136_s_at	APP	Y00264	amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease)	amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease)
111	40148_at	APBB2	U62325	amyloid beta (A4) precursor protein-binding, family B, member 2 (F-e65-like)	FE65-like protein
112	38471_r_at	APPBP2	D86981	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	KIAA0228 protein
113	38470_i_at	APPBP2	D86981	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	KIAA0228 protein
114	35364_at	APPBP1	U50939	amyloid beta precursor protein binding protein 1, 59kD	amyloid precursor protein-binding protein 1
115	40064_at	ALS2CR3	AB011121	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3	KIAA0549 protein
116	1577_at	AR	M23263	androgen receptor (cilioretostosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease)	androgen receptor
117	38842_at	AMOTL2	AB023206	angiomin like 2	angiomin like 2
118	39315_at	ANGPT1	D13628	angiotensinogen 1	angiotensin 1
119	1929_at	ANGPT1	U83508	angiotensin 1	angiotensin-1

Fig 21

	A	B	C	D	E
120	36965_at	ANK3	U13616	ankyrin 3, node of Ranvier (ankyrin G)	ankyrin G
121	37403_at	ANXA1	X05908	annexin A1	annexin I
122	36637_at	ANXA11	L19605	annexin A11	56K autoantigen
123	789_s_at	ANXA2	D00017	annexin A2	lipocortin II
124	31684_at	ANXA2P1	M62896	annexin A2 pseudogene 1	
125	31444_s_at	ANXA2P3	M62895	annexin A2 pseudogene 3	
126	37374_at	ANXA4	M82809	annexin A4	annexin IV (placental anticoagulant protein II)
127	37670_at	ANXA7	J04543	annexin A7	annexin VII isoform 1; annexin VII isoform 2
128	41138_at	MIC2	M16279	antigen identified by monoclonal antibodies 12E7, F21 and O13	antigen
129	40506_s_at	PABPC4; APP1; AU75686		APP-1; Homo sapiens polyadenylate binding protein mRNA, complete cds.	polyadenylate binding protein
130	34370_at	ARCN1	X81198	archain 1	archain
131	32253_at	RERE	AB007927	arginine-glutamic acid dipeptide (RE) repeats	KIAA0458 protein
132	549_at	RAIRS	S80343	arginyl-tRNA synthetase	arginyl-tRNA synthetase
133	39164_at	ARIH2	AF099149	ariadne homolog 2 (Drosophila)	TRIAD1 type I
134	41729_at	ARIH1	AJ009771	ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila)	putative RING finger protein
135	36057_at	ALEX2	AB011084	armadillo repeat protein ALEX2	KIAA0512 protein
136	40052_at	ACTR1A	X82206	ARP1 actin-related protein 1 homolog A, centractin alpha (yeast)	alpha-centractin
137	35734_at	ACTR2	A1935551	ARP2 actin-related protein 2 homolog (yeast)	
138	35733_at	ACTR2	AF006082	ARP2 actin-related protein 2 homolog (yeast)	Arp2
139	35271_at	ACTR3	AF006083	ARP3 actin-related protein 3 homolog (yeast)	Arp3
140	40516_at	AHR	L19872	aryl hydrocarbon receptor	AH-receptor
141	36671_at	ASNS	M27396	asparagine synthetase	asparagine synthetase
142	41241_at	NARS	D84273	asparaginyl-tRNA synthetase	Asparaginyl tRNA Synthetase
143	38703_at	DNPEP	AF005050	aspartyl aminopeptidase	aspartyl aminopeptidase
144	34181_at	AGA	X55330	aspartylglucosaminidase	aspartylglucosaminidase

Fig 21

	A	B	C	D	E
145	37229_at	ATR	U49844	ataxia telangiectasia and Rad3 related	FRAP-related protein
146	34817_s_at	A2LP	U70671	ataxin 2 related protein	ataxin-2 related protein
147	379_at	APACD	AB006679	ATP binding protein associated with cell differentiation	ATP binding protein
148	40881_at	ACLY	X64330	ATP citrate lyase	ATP-citrate (pro-S)-lyase
149	41228_r_at	ATP5F1	X60221	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	H+-ATP synthase subunit b
150	34811_at	ATP5G3	U09813	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3	mitochondrial ATP synthase subunit 9 precursor
151	35760_at	ATP5H	AF087135	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d	F1FO-type ATPase subunit d
152	38751_i_at	ATP5I	AA426364	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e	
153	36107_at	ATP5J	AA845575	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6	
154	38693_at	ATP5L	AA917672	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g	
155	40115_at	ATP5C1	D16562	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	ATP synthase gamma-subunit
156	39791_at	ATP2A2	M23114	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2
157	39790_at	ATP2A2	M23115	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2
158	38684_at	ATP2C1	AJ010953	ATPase, Ca++ transporting, type 2C, member 1	
159	35831_at	ATP9A	AB014511	ATPase, Class II, type 9A	putative Ca2+-transporting ATPase
160	40853_at	ATP10D	AI478147	ATPase, Class V, type 10D	KIAA0611 protein
161	36635_at	ATP11B	AB023173	ATPase, Class VI, type 11B	KIAA0956 protein
162	36523_at	ATP7A	L06133	ATPase, Cu++ transporting, alpha polypeptide (Menkes syndrome)	Cu++-transporting P-type ATPase
163	33854_at	ATP6M	AA877795	ATPase, H+ transporting, lysosomal (vacuolar proton pump)	

Fig 21

	A	B	C	D	E
164	37395_at	ATP6S14	D49400	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 14kD	vacuolar ATPase
165	36994_at	ATP6L	M62762	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD	vacuolar H+ ATPase proton channel subunit
166	36167_at	ATP6F	D89052	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 21kD	proton-ATPase-like protein
167	37367_at	ATP6E	X76228	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD	vacuolar H+ ATPase E subunit
168	37948_at	ATP6C	J05682	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 42kD	H+ -ATPase C subunit
169	33875_at	ATP6H	A1547262	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 9kD	
170	40903_at	ATP6M8-9	AL049929	ATPase, H+ transporting, lysosomal (vacuolar proton pump) membrane sector associated protein M8-9	hypothetical protein
171	34889_at	ATP6A1	AA056747	ATPase, H+ transporting, lysosomal (vacuolar proton pump), alpha polypeptide, 70kD, isoform 1	
172	40568_at	ATP6B2	L35249	ATPase, H+ transporting, lysosomal (vacuolar proton pump), beta polypeptide, 56/58kD, isoform 2	vacuolar H+-ATPase 56,000 subunit
173	35770_at	ATP6S1	D16469	ATPase, H+ transporting, lysosomal (vacuolar proton pump), subunit 1	ORF
174	37669_s_at	ATP1B1	U16799	ATPase, Na+/K+ transporting, beta 1 polypeptide	Na,K-ATPase beta subunit
175	32563_at	ATP1B3	U51478	ATPase, Na+/K+ transporting, beta 3 polypeptide	sodium/potassium-transporting ATPase beta-3 subunit
176	35717_at	ABCA8	AB020629	ATP-binding cassette, sub-family A (ABC1), member 8	KIAA0822 protein
177	38261_at	ABCC3	AF085692	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	multidrug resistance-associated protein 3B
178	35648_at	KIAA0442	AB007902	autism-related protein 1	autism-related protein 1
179	38068_at	AMFR	M63175	autocrine motility factor receptor	autocrine motility factor receptor
180	38433_at	AXL	M76125	AXL receptor tyrosine kinase	tyrosine kinase receptor
181	35268_at	AXOT	AL050171	axotrophin	hypothetical protein DKFZp586F1122 similar to axotrophin

Fig 21

	A	B	C	D	E
182	35350_at	GALNAC4S-6ST	AB011170	B cell RAG associated protein	KIAA0598 protein
183	41562_at	BMI1	L13689	B lymphoma Mo-MLV insertion region (mouse)	murine leukemia viral (bmi-1) oncogene homolog
184	1728_at	BMI1	L13689	B lymphoma Mo-MLV insertion region (mouse)	murine leukemia viral (bmi-1) oncogene homolog
185	36578_at	BIRC2	U37547	baculoviral IAP repeat-containing 2	MIHB
186	41278_at	BAF53A	AF041474	BAF53	BAF53a
187	33175_at	BBS4	AA156237	Bardet-Biedl syndrome 4	
188	40790_at	BHLHB2	AB004066	basic helix-loop-helix domain containing, class B, 2	
189	40108_at	BZAP45	D13630	basic leucine-zipper protein BZAP45	basic leucine-zipper protein BZAP45
190	40202_at	BTEB1	D31716	basic transcription element binding protein 1	GC box binding protein
191	35055_at	BTF3	X53281	basic transcription factor 3	general transcription factor
192	38364_at	BCE-1	AF068197	BCE-1 protein	BCE-1
193	40091_at	BCL6	U00115	B-cell CLL/lymphoma 6 (zinc finger protein 51)	zinc-finger protein
194	37294_at	BTG1	X61123	B-cell translocation gene 1, anti-proliferative	B-cell translocation protein 1
195	32060_at	BNIP2	U15173	BCL2/adenovirus E1B 19kD interacting protein 2	BCL2/adenovirus E1B 19kD-interacting protein 2
196	38010_at	BNIP3	AF002697	BCL2/adenovirus E1B 19kD interacting protein 3	E1B 19K/Bcl-2-binding protein Nip3
197	39436_at	BNIP3L	AF079221	BCL2/adenovirus E1B 19kD interacting protein 3-like	BCL2/adenovirus E1B 19kDa-interacting protein 3a
198	34798_at	BAG1	Z35491	BCL2-associated a1hanogene	glucocorticoid receptor-associated protein RAP46
199	35291_at	BAG2	AL050287	BCL2-associated a1hanogene 2	hypothetical protein
200	36463_at	BAG5	AB020680	BCL2-associated a1hanogene 5	KIAA0873 protein
201	38050_at	BTF	D79986	Bcl-2-associated transcription factor	KIAA0164 gene product
202	38101_at	BDG-29	AB011151	BDG-29 protein	KIAA0579 protein
203	39378_at	BECN1	U17999	beclin 1 (coiled-coil, myosin-like BCL2 interacting protein)	
204	39160_at	PDHB	D90086	beta subunit; Human pyruvate dehydrogenase (EC 1.2.4.1) beta subunit gene, exons 1-10.	pyruvate dehydrogenase (lipoamide) beta

Fig 21

	A	B	C	D	E
205	34644_at	B2M	AB021288	beta-2-microglobulin	beta 2-microglobulin
206	40601_at	BBP	AI057115	beta-amyloid binding protein precursor	
				beta-hexosaminidase alpha chain; Human	
207	39340_at	HEXA	M16424	beta-hexosaminidase alpha chain (HEXA)	hexosaminidase A preproprotein
208	38126_at	BGN	J04599	gene, exon 14.	biglycan preproprotein
209	33198_at	BART1	AA206524	biglycan	
				binder of Arl Two	
210	37274_at	Btd	AF018631	biotin-amide amidohydrolase; Homo sapiens biotinidase (BTD) gene, exons 2, 3, and 4 and complete cds.	biotinidase
				biphenyl hydrolase-like (serine hydrolase; breast epithelial mucin-associated antigen)	
211	40912_s_at	BPHL	X81372	bladder cancer associated protein	biphenyl hydrolase-related protein
212	35267_g_at	BLCAP	AL049288	bladder cancer associated protein	bladder cancer associated protein
213	35266_at	BLCAP	AL049288	bladder cancer associated protein	bladder cancer associated protein
214	37700_at	BLMH	X92106	bleomycin hydrolase	bleomycin hydrolase
				bone morphogenetic protein receptor, type 1A	ALK-3
215	39565_at	BMPR1A	Z22535	BRAF35/HDAC2 complex (80 kDa)	
216	39551_at	BHC80	N98667	brain abundant, membrane attached signal protein 1	neuronal tissue-enriched acidic protein
217	32607_at	BASP1	AF039656	brain abundant, membrane attached signal protein 1	
218	32606_at	BASP1	AA135683	brain acyl-CoA hydrolase	acyl-CoA thioester hydrolase
219	37945_at	BACH	U91316	brain cell membrane protein 1	brain cell membrane protein 1
220	37958_at	BCMP1	AL049257	brain cell membrane protein 1	brain-derived neurotrophic factor
221	40023_at	BDNF	X60201	brain-derived neurotrophic factor	
				branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease)	branched chain alpha-ketoacid dehydrogenase E1 beta subunit
222	41683_i_at	BCKDHB	U50708		breast cancer antiestrogen resistance 3 protein
223	36812_at	BCAR3	U92715	breast cancer anti-estrogen resistance 3	
				brefeldin A-inhibited guanine nucleotide-exchange protein 1	
224	38306_at	BIG1	AA477576	bromodomain containing 3	bromodomain containing protein 3
225	37947_at	BRD3	D26362	BTB and CNC homology 1, basic leucine zipper transcription factor 1	BTB and CNC homology 1, basic leucine zipper transcription factor 1
226	31895_at	BACH1	AB002803	zipper transcription factor 1	

Fig 21

	A	B	C	D	E
227	36634_at	BTG2	U72649	BTG family, member 2	BTG2
228	37218_at	BTG3	D64110	BTG family, member 3	ANA
229	41547_at	BUB3	AF047472	BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast)	spleen mitotic checkpoint BUB3
230	34783_s_at	BUB3	AF047473	BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast)	testis mitotic checkpoint BUB3
231	32781_f_at	BPAG1	AA058762	bullous pemphigoid antigen 1 (230/240kD)	
232	32780_at	BPAG1	AB018271	bullous pemphigoid antigen 1 (230/240kD)	KIAA0728 protein
233	32629_f_at	BTN3A1	U90552	butyrophilin, subfamily 3, member A1	butyrophilin
234	39357_at	C2F	U72514	C2f protein	C2f
235	40709_at	LOC58502	W27601	C2H2 (Kruppel-type) zinc finger protein	
236	37031_at	C9orf10	D80005	C9orf10 protein	C9orf10 protein
237	33856_at	CXX1	Y13374	CAAX box 1	putative prenylated protein
238	36976_at	CDH11	D21255	cadherin 11, type 2, OB-cadherin (osteoblast)	OB-cadherin-2
239	2087_s_at	CDH11	D21254	cadherin 11, type 2, OB-cadherin (osteoblast)	OB-cadherin-1
240	2053_at	CDH2	M34064	cadherin 2, type 1, N-cadherin (neuronal)	cadherin 2, type 1 preproprotein
241	31670_s_at	CAMK2G	U81554	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	CaM kinase II isoform
242	38716_at	CAMKK2	AB018330	calcium/calmodulin-dependent protein kinase kinase 2, beta	KIAA0787 protein
243	31854_at	CASK	AF035582	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	CASK
244	41738_at	CALD1	M64110	caldesmon 1	caldesmon
245	41739_s_at	CALD1	M83216	caldesmon 1	caldesmon
246	41288_at	CALM1	AL036744	calmodulin 1 (phosphorylase kinase, delta)	
247	911_s_at	CALM2	M19311	calmodulin 2 (phosphorylase kinase, delta)	calmodulin 2 (phosphorylase kinase, delta)
248	40125_at	CANX	L10284	calnexin	calnexin
249	37001_at	CAPN2	M23254	calpain 2, (m/l) large subunit	neutral protease large subunit
250	36138_at	CAPNS1	X04106	calpain, small subunit 1	calpain, small subunit 1

Fig 21

	A	B	C	D	E
251	41257_at	CAST	D16217	calpastatin	calpastatin
252	33385_g_at	CAST	U31346	calpastatin	calpastatin
253	40953_at	CNN3	S80562	calponin 3, acidic	acidic calponin
254	37345_at	CALU	AF013759	calumenin	calumenin
255	37535_at	CREB1	M27691	cAMP responsive element binding protein 1	cAMP responsive element binding protein 1, isoform A; cAMP responsive element binding protein 1, isoform B
256	40849_s_at	CREB3	U88528	cAMP responsive element binding protein 3 (human)	transcription factor LZIP
257	39438_at	CREBL2	AF039081	cAMP responsive element binding protein-like 2	Cre binding protein-like 2
258	32065_at	CREM	S68134	cAMP responsive element modulator	cyclic AMP-responsive element modulator beta isoform
259	32067_at	CREM	S68271	cAMP responsive element modulator	cyclic AMP-responsive element modulator cyclic AMP-responsive element modulator beta isoform
260	32066_g_at	CREM	S68134	cAMP responsive element modulator	cyclic AMP-responsive element modulator beta isoform
261	40910_at	CAPZA1	U56637	capping protein (actin filament) muscle Z-line, alpha 1	capping protein alpha subunit isoform 1
262	36641_at	CAPZA2	U03851	capping protein (actin filament) muscle Z-line, alpha 2	capping protein alpha
263	37012_at	CAPZB	U03271	capping protein (actin filament) muscle Z-line, beta	F-actin capping protein beta subunit
264	32094_at	CHST3	AB017915	carbohydrate (chondroitin 6)	chondroitin 6-sulfotransferase
265	41447_at	CHSY1	AB023207	sulfotransferase 3	KIAA0990 protein
266	41395_at	CHST1	AB003791	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	keratan sulfate Gal-6-sulfotransferase
267	37960_at	CHST2	AB014679	carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2	N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST)
268	36454_at	CA12	AF037335	carbonic anhydrase XII	carbonic anhydrase precursor
269	34876_at	CPD	U65090	carboxypeptidase D	carboxypeptidase D
270	36606_at	CPE	X51405	carboxypeptidase E	carboxypeptidase E precursor
271	35632_at	CBLB	U26710	Cas-Br-M (murine) ectropic retroviral transforming sequence b	cbl-b
272	40184_at	CSNK1A1	L37042	casein kinase 1, alpha 1	casein kinase I-alpha
273	36949_at	CSNK1D	U29171	casein kinase 1, delta	casein kinase I delta

Fig 21



	A	B	C	D	E
274	38019_at	CSNK1E	L37043	casein kinase 1, epsilon	casein kinase I-epsilon
275	1211_s_at	CRADD	U84388	CASP2 and RIPK1 domain containing adaptor with death domain	death domain containing protein CRADD
276	1867_at	CFLAR	AF005775	CASP8 and FADD-like apoptosis regulator	caspase-like apoptosis regulatory protein 2
277	195_s_at	CASP4	U28014	caspase 4, apoptosis-related cysteine protease	cysteine protease
278	33774_at	CASP8	X98172	caspase 8, apoptosis-related cysteine protease	MACH-alpha-1
279	41156_g_at	CTNNA1	U03100	catenin (cadherin-associated protein), alpha 1 (102kD)	alpha2(E)-catenin
280	41155_at	CTNNA1	U03100	catenin (cadherin-associated protein), alpha 1 (102kD)	alpha2(E)-catenin
281	2085_s_at	CTNNA1	D14705	catenin (cadherin-associated protein), alpha 1 (102kD)	'human alpha-catenin'
282	2069_s_at	CTNNA1	L23805	catenin (cadherin-associated protein), alpha 1 (102kD)	alpha1(E)-catenin
283	35331_at	CTNNAL1	U97067	catenin (cadherin-associated protein), alpha-like 1	alpha-catenin-like protein
284	40777_at	CTNNB1	X87838	catenin (cadherin-associated protein), beta 1 (88kD)	beta-catenin
285	40444_s_at	CTNND1	AB002382	catenin (cadherin-associated protein), delta 1	
286	38466_at	CTSK	X82153	cathepsin K (pseudosynthesis)	Cathepsin O
287	37391_at	CTSL	X12451	cathepsin L	pro-(cathepsin L)
288	36915_at	CTSO	AI810485	cathepsin O	
289	36119_at	CAV1	AF070648	caveolin 1, caveolae protein, 22kD	
290	339_at	CAV2	AF035752	caveolin 2	caveolin-2
291	33113_at	CITED2	U65093	Chp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	msg-related gene 1
292	1052_s_at	CEBPD	M83667	CCAAT/enhancer binding protein (C/EBP), delta	NF-IL6-beta protein
293	39219_at	CEBPG	U20240	CCAAT/enhancer binding protein (C/EBP), gamma	C/EBP gamma

Fig 21

	A	B	C	D	E
294	33861_at	CNOT2	A1123426	CCR4-NOT transcription complex, subunit 2	
295	32820_at	CNOT4	U71267	CCR4-NOT transcription complex, subunit 4	
296	34819_at	CD164	D14043	CD164 antigen, sialomucin	potential transcriptional repressor NOT4Hp
297	34699_at	CD2AP	AL050105	CD2-associated protein	MGC-24 precursor
					hypothetical protein
298	33823_at	CD36L2	D12676	CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2 (lysosomal integral membrane protein II)	85kDa human lysosomal sialoglycoprotein
299	2036_s_at	CD44	M59040	CD44 antigen (homing function and blood group system)	cell adhesion molecule
300	35282_r_at	CD81	M33680	CD81 antigen (target of antiproliferative antibody 1)	CD81 antigen
301	39389_at	CD9	M38690	CD9 antigen (p24)	CD9 antigen
302	32175_at	CDC10	S72008	CDC10 cell division cycle 10 homolog (S. cerevisiae)	cell division cycle 10
303	40404_s_at	CDC16	U18291	CDC16 cell division cycle 16 homolog (S. cerevisiae)	CDC16Hs
304	31877_at	CDC23	AF053977	CDC23 (cell division cycle 23, yeast, homolog)	cell division cycle protein 23
305	40690_at	CKS2	X54942	CDC28 protein kinase 2	Cks1 protein homologue
306	33362_at	CEP3	AF094521	Cdc42 effector protein 3	MSE55-related protein
307	32833_at	CLK1	M59287	CDC-like kinase 1	
308	41535_at	CDK2AP1	AF066484	CDK2-associated protein 1	putative oral tumor suppressor protein
309	41343_at	CDS2	Y16521	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	CDS2 protein
				CDP-diacylglycerol--inositol 3-phosphatidyltransferase	
310	33397_at	CDIPT	AL050383	(phosphatidylinositol synthase)	
311	40591_at	CDC27	S78234	cell division cycle 27	H-NUC
312	450_g_at	CGR19	U66469	cell growth regulatory with ring finger domain	cell growth regulator CGR19
313	36514_at	CGR19	U66469	cell growth regulatory with ring finger domain	cell growth regulator CGR19

Fig 21

	A	B	C	D	E
314	35311_at	CREG	AF084523	cellular repressor of E1A-stimulated genes	cellular repressor of E1A-stimulated genes
315	41333_at	CENTB2	D26069	centaurin, beta 2	centaurin, beta 2
316	34676_at	CENTG2	AB029022	centaurin, gamma 2	KIAA1099 protein
317	38410_at	CETN2	X72964	centrin, EF-hand protein, 2	caltractin
318	35232_f_at	CETN3	A1056696	centrin, EF-hand protein, 3 (CDC31)	
319	31894_at	CENPC1	M95724	homolog, yeast	centromere autoantigen C
320	33805_at	CAP350	AB007949	centromere protein C 1	KIAA0480 protein
321	36190_at	CDR2	M63256	centrosome-associated protein 350	
322	32262_at	CGI-01	AL049669	cerebellar degeneration-related protein (62kD)	major Yo paraneoplastic antigen
323	40931_at	LOC50999	AL080084	CGI-01 protein	hypothetical protein
324	38500_at	LOC51014	AB002450	CGI-100 protein	
325	34359_at	LOC51020	AA524058	CGI-109 protein	
326	38667_at	LOC51031	AA189161	CGI-130 protein	
327	41824_at	LOC51096	AI140114	CGI-150 protein	
328	34862_at	LOC51097	AA005018	CGI-48 protein	
329	37199_at	LOC51626	AI760932	CGI-49 protein	
330	41411_at	LOC51103	AI568877	CGI-60 protein	
331	39814_s_at	LOC51635	AI052724	CGI-65 protein	
332	35759_at	CCT2	AF026166	CGI-86 protein	chaperonin-containing TCP-1 beta subunit homolog
333	40774_at	CCT3	X74801	chaperonin containing TCP1, subunit 2 (beta)	gamma subunit of CCT chaperonin
334	32594_at	CCT4	AF026291	chaperonin containing TCP1, subunit 3 (gamma)	chaperonin containing t-complex polypeptide 1, delta subunit
335	38416_at	CCT6A	L27706	chaperonin containing TCP1, subunit 4 (delta)	chaperonin-like protein
336	38720_at	CCT7	AF026292	chaperonin containing TCP1, subunit 6A (zeta 1)	chaperonin containing t-complex polypeptide 1, eta subunit
337	39767_at	CCT8	D13627	chaperonin containing TCP1, subunit 7 (eta)	chaperonin containing TCP1, subunit 8 (theta)
338	41000_at	CHES1	U68723	chaperonin containing TCP1, subunit 8 (theta)	checkpoint suppressor 1
339	37855_at	CTBS	M95767	chitobiase, di-N-acetyl-	di-N-acetylchitinase

Fig 21

A	B	C	D	E
340 38732_at	CLNS1A	X91788	chloride channel, nucleotide-sensitive, 1A	IcIn protein
341 33891_at	CLIC4	AL080061	chloride intracellular channel 4	
342 32363_at	CH25H	AF059214	cholesterol 25-hydroxylase	cholesterol 25-hydroxylase
343 38112_g_at	CSPG2	X15998	chondroitin sulfate proteoglycan 2 (versican)	chondroitin sulfate proteoglycan 2 (versican)
344 38111_at	CSPG2	X15998	chondroitin sulfate proteoglycan 2 (versican)	chondroitin sulfate proteoglycan 2 (versican)
345 34763_at	CSPG6	AF020043	chondroitin sulfate proteoglycan 6 (barnacan)	chromosome-associated polypeptide
346 37304_at	CBX1	U35451	chromobox homolog 1 (HP1 beta homolog Drosophila)	heterochromatin protein p25
347 38085_at	CBX3	AI740522	chromobox homolog 3 (HP1 gamma homolog, Drosophila)	
348 38084_at	CBX3	AA648295	chromobox homolog 3 (HP1 gamma homolog, Drosophila)	
349 36137_at	CHD4	X86691	chromodomain helicase DNA binding protein 4	Mi-2 protein
350 32111_at	CDYL	AL050164	chromodomain protein, Y chromosome-like	hypothetical protein
351 39550_at	C1orf17	AB011156	chromosome 1 open reading frame 17	KIAA0584 protein
352 39033_at	C1orf8	Z78368	chromosome 1 open reading frame 8	
353 32217_at	C12orf22	AF052105	chromosome 12 open reading frame 22	TGF-beta induced apoptosis protein 12
354 40979_at	C14orf3	AJ243310	chromosome 14 open reading frame 3	C14orf3 protein
355 40045_g_at	C18orf1	AF009425	chromosome 18 open reading frame 1	clone 22
356 36860_at	C19orf7	AB028987	chromosome 19 open reading frame 7	KIAA1064 protein
357 34287_at	C21orf80	AB023175	chromosome 21 open reading frame 80	KIAA0958 protein
358 33406_at	C22orf2	AL050345	chromosome 22 open reading frame 2	hypothetical protein
359 33778_at	C22orf4	AL096779	chromosome 22 open reading frame 4	hypothetical protein
360 41758_at	C22orf5	AL096879	chromosome 22 open reading frame 5	hypothetical protein
361 38690_at	C3orf4	AL080097	chromosome 3 open reading frame 4	hypothetical protein
362 36013_at	C4orf1	AF006621	chromosome 4 open reading frame 1	embryonic lung protein
363 36955_at	C5orf8	U10362	chromosome 5 open reading frame 8	GP36b glycoprotein
364 41375_at	C6orf28	AJ245416	chromosome 6 open reading frame 28	G7b protein
365 41454_at	C6orf34	W27949	chromosome 6 open reading frame 34	
366 36139_at	C6orf5	AL050289	chromosome 6 open reading frame 5	hypothetical protein

Fig 21

	A	B	C	D	E
367	35193_at	CHC1L	AF060219	chromosome condensation 1-like	RCC1-like G exchanging factor RLG
368	34292_at	CXorf12	X92475	chromosome X open reading frame 12	chromosome X open reading frame 12
369	41314_at	CS	AF047042	citrate synthase	citrate synthase
370	41159_at	CLTC	D21260	clathrin, heavy polypeptide (Hc)	clathrin heavy chain
371	38657_s_at	CLTA	M20471	clathrin, light polypeptide (Lca)	clathrin, light polypeptide A, isoform a;
372	35743_at	CPSF4	U79569	cleavage and polyadenylation specific factor 4, 30kD subunit	clathrin, light polypeptide A, isoform b
373	32723_at	CSTF1	L02547	cleavage stimulation factor, 3' pre-RNA, subunit 1, 50kD	no arches
374	41183_at	CSTF3	U15782	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD	cleavage stimulation factor
375	38711_at	CLASP2	AB014527	CLIP-associating protein 2	cleavage stimulation factor 77kDa subunit
376	36017_at	LOC57213	AF055016	CLLL6 protein	KIAA0627 protein
377	36780_at	CLU	M25915	clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J)	CLLL6 protein
378	35180_at	LOC113251	AL050205	c-Mpl binding protein	clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J)
379	40811_at	COASTER	AB011148	coactivator for steroid receptors	apolipoprotein J
380	38052_at	F13A1	M14539	coagulation factor XIII, A1 polypeptide	KIAA0576 protein
381	36972_at	RNP24	X92098	coated vesicle membrane protein	coagulation factor XIII A1 subunit precursor
382	34326_at	COPB	X82103	coatamer protein complex, subunit beta	transmembrane protein
383	36677_at	COPB2	X70476	coatamer protein complex, subunit beta 2 (beta prime)	beta-Coat protein
384	35205_at	COBRA1	AL050280	cofactor of BRCA1	subunit of coatamer complex
385	36648_at	CRSP9	AF031383	cofactor required for Sp1 transcriptional activation, subunit 9 (33kD)	hypothetical protein
386	33659_at	CFL1	X95404	cofilin 1 (non-muscle)	hMed7
387	40879_at	BICD2	AB014599	coiled-coil protein BICD2	cofilin
388	39864_at	CIRBP	D78134	cold inducible RNA binding protein	KIAA0699 protein
389	39839_at	CSDA	M24069	cold shock domain protein A	CIRP
390	32307_s_at	COL1A2	V00503	collagen, type I, alpha 2	cold shock domain protein A
391	32306_g_at	COL1A2	J03464	collagen, type I, alpha 2	alpha 2 type I collagen preproprotein
392	32305_at	COL1A2	J03464	collagen, type I, alpha 2	alpha 2 type I collagen preproprotein

Fig 21

	A	B	C	D	E
393	32488_at	COL3A1	X14420	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)	prepro-alpha-1 type 3 collagen
394	36659_at	COL4A2	X05610	collagen, type IV, alpha 2	alpha (2) chain
395	38420_at	COL5A2	Y14690	collagen, type V, alpha 2	procollagen alpha 2(V)
396	38722_at	COL6A1	X15880	collagen, type VI, alpha 1	alpha-1 collagen VI (AA 574-1009)
397	38077_at	COL6A3	X52022	collagen, type VI, alpha 3	collagen type VI, alpha 3 chain
398	37459_at	COL8A1	X57527	collagen, type VIII, alpha 1	alpha 1(VIII) collagen
399	37892_at	COL11A1	J04177	collagen1, type XI, alpha 1	alpha 1 type XI collagen, isoform A
400	35168_f_at	COL16A1	M92642	collagen, type XVI, alpha 1	preproprotein; alpha 1 type XI collagen, isoform B preproprotein; alpha 1 type XI collagen, isoform C preproprotein
401	37668_at	C1QBP	M69039	complement component 1, q subcomponent binding protein	alpha-1 type XVI collagen complement component 1, q subcomponent binding protein precursor
402	39409_at	C1R	M14058	complement component 1, r subcomponent	complement component 1, r subcomponent
403	40496_at	C1S	J04080	complement component 1, s subcomponent	complement component 1, s subcomponent
404	36638_at	CTGF	X78947	connective tissue growth factor	connective tissue growth factor
405	41202_s_at	OS4	AF000152	conserved gene amplified in osteosarcoma	OS-4 protein
406	33770_at	CHUK	AF009225	conserved helix-loop-helix ubiquitous kinase	IkB kinase alpha subunit
407	1789_at	COPS5	U65928	COP9 constitutive photomorphogenic homolog subunit 5 (Arabidopsis)	Jun activation domain binding protein
408	32539_at	COP9	U51205	COP9 homolog	COP9 signalosome subunit 1 CSN1
409	40138_at	MOV34-34KD	U70735	COP9 subunit 6 (MOV34 homolog, 34 kD)	34 kDa Mov34 homolog
410	40452_at	CPNE1	U83246	copine I	copine I
411	39706_at	CPNE3	AB014536	copine III	KIAA0636 protein
412	37999_at	CPO	D16611	coproporphyrinogen oxidase (coproporphyrin, harderoporphyria)	coproporphyrinogen oxidase
413	37026_at	COPEB	AF001461	core promoter element binding protein	Kruppel-like zinc finger protein Zf9
414	41175_at	CBFB	L20298	core-binding factor, beta subunit	transcription factor
415	32803_at	CN1L	AF104398	cornichon-like	cornichon

Fig 21

A	B	C	D	E
416 34723_at	COX11	U79270	COX11 homolog, cytochrome c oxidase assembly protein (yeast)	COX11 homolog
417 37907_at	F8A; DXS522E	M34677	CpG island protein; Human nested gene protein gene, complete cds.	coagulation factor VIII-associated protein
418 38664_at	CFDP1	AB009285	craniofacial development protein 1	craniofacial development protein 1
419 33831_at	CREBBP	U47741	CREB binding protein (Rubinstein-Taybi syndrome)	CREB-binding protein
420 36948_at	CRH1	AL109701	CREBBP/EP300 inhibitory protein 1	C15orf3
421 38148_at	CRY1	D83702	cryptochrome 1 (photolyase-like)	photolyase
422 37902_at	CRYZ	L13278	crystallin, zeta (quinone reductase)	zeta-crystallin
423 40167_s_at	LOC55884	AF038187	CS box-containing WD protein	
424 38804_at	CSE1L	AF053641	CSE1 chromosome segregation 1-like (yeast)	cellular apoptosis susceptibility protein
425 1768_s_at	CSK	X59932	c-src tyrosine kinase	c-src-kinase
426 41309_g_at	CTBP1	U37408	C-terminal binding protein 1	phosphoprotein CBP
427 40780_at	CTBP2	AF016507	C-terminal binding protein 2	C-terminal binding protein 2
428 39723_at	CUL1	AF062536	cullin 1	cullin 1
429 40141_at	CUL4B	AB014595	cullin 4B	KIAA0695 protein
430 31823_at	CUTL1	M74099	cut-like 1, CCAAT displacement protein (Drosophila)	cut-like 1, CCAAT displacement protein
431 36872_at	ARPP-19	AL120559	cyclic AMP phosphoprotein, 19 kD	
432 41808_at	DMTF1	AF052102	cyclin D binding myb-like transcription factor 1	cyclin D binding myb-like transcription factor 1
433 38418_at	CCND1	X59798	cyclin D1 (PRAD1: parathyroid adenomatosis 1)	cyclin
434 2020_at	CCND1	M73554	cyclin D1 (PRAD1: parathyroid adenomatosis 1)	bcl-1
435 36650_at	CCND2	D13639	cyclin D2	cyclin D2
436 40225_at	GAK	D88435	cyclin G associated kinase	HsGAK
437 37723_at	CCNG2	U47414	cyclin G2	cyclin G2
438 1913_at	CCNG2	U47414	cyclin G2	cyclin G2
439 1924_at	CCNH	U11791	cyclin H	cyclin H
440 1836_at	CCNI	D50310	cyclin I	cyclin I
441 1792_g_at	CDK2	M68520	cyclin-dependent kinase 2	cdc2-related protein kinase

Fig 21

	A	B	C	D	E
442	33317_at	CDK7	L20320	cyclin-dependent kinase 7 (MO15 homolog, <i>Xenopus laevis</i> , cdk-activating kinase)	protein serine/threonine kinase
443	1969_s_at	CDK7	X77743	cyclin-dependent kinase 7 (MO15 homolog, <i>Xenopus laevis</i> , cdk-activating kinase)	CDK activating kinase
444	35140_at	CDK8	R59697	cyclin-dependent kinase 8	
445	2031_s_at	CDKN1A	U03106	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	cyclin-dependent kinase inhibitor 1A
446	33847_s_at	CDKN1B	AI304854	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	
447	36053_at	CDKN2C	AF041248	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	cyclin-dependent kinase inhibitor
448	38700_at	CSRP1	M33146	cysteine and glycine-rich protein 1	cysteine and glycine-rich protein 1
449	41401_at	CSRP2	U57646	cysteine and glycine-rich protein 2	cysteine and glycine-rich protein 2
450	40936_at	CRIM1	AI651806	cysteine-rich motor neuron 1	
451	38772_at	CYR61	Y11307	cysteine-rich, angiogenic inducer, 61	CYR61 protein
452	40408_at	CARS	LO6845	cysteinyI-tRNA synthetase	cysteinyI-tRNA synthetase
453	39317_at	CMAH	D86324	cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminic acid hydroxylase)	CMP-N-acetylneuraminic acid hydroxylase
454	34340_at	CYB5-M	AA173896	cytochrome b5 outer mitochondrial membrane precursor	
455	35818_at	HCS	D00265	cytochrome c	cytochrome c
456	39921_at	COX5B	AI526089	cytochrome c oxidase subunit Vb	
457	41206_r_at	COX6A1	AI540925	cytochrome c oxidase subunit Vla	
458	36165_at	COX6C	W51774	polypeptide 1	
459	39031_at	COX7A1	AA152406	cytochrome c oxidase subunit Vlc	
460	41760_at	COX7A2	AA978033	polypeptide 1 (muscle)	
461	34330_at	COX7A2L	AB007618	cytochrome c oxidase subunit Vlla	
462	34381_at	COX7C	AI708889	polypeptide 2 (liver)	COX7RP
				cytochrome c oxidase subunit Vlla	
				polypeptide 2 like	
				cytochrome c oxidase subunit Vllc	

Fig 21



	A	B	C	D	E
463	38080_at	COX8	AI525665	cytochrome c oxidase subunit VIII	
464	35819_at	CYC1	X06994	cytochrome c-1	cytochrome c-1
465	33389_at	CYP51	U23942	cytochrome P450, 51 (lanosterol 14-alpha-demethylase)	lanosterol 14-demethylase cytochrome P450
466	859_at	CYP1B1	U03688	cytochrome P450, subfamily 1 (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile)	cytochrome P450
467	40071_at	CYP1B1	U03688	cytochrome P450, subfamily 1 (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile)	cytochrome P450
468	37509_at	CRLF3	AF046059	cytokine receptor-like factor 3	cytokine receptor related protein 4
469	37306_at	KIAA0068	D38549	cytoplasmic FMRP interacting protein 1	
470	1706_at	A-RAF-1	U01337	cytoplasmic; Human Ser/Thr protein kinase (A-RAF-1) gene, complete cds.	Ser/Thr protein kinase
471	34338_at	CKAP1	D49738	cytoskeleton-associated protein 1	cytoskeleton associated protein
472	32529_at	CKAP4	X69910	cytoskeleton-associated protein 4	P63 protein
473	40282_s_at	DF	M84526	D component of complement (adipsin)	adipsin/complement factor D
474	40877_s_at	MIN7	AF041080	D15F37 (pseudogene)	
475	1243_at	DDB2	U18300	damage-specific DNA binding protein 2 (48kD)	DDBb p48
476	36616_at	DAZAP2	D31767	DAZ associated protein 2	DAZ associated protein 2
477	37663_at	DDX1	X70649	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1	member of DEAD box protein family
478	35306_at	DDX15	AB001636	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 15	ATP-dependent RNA helicase #46
479	40490_at	DDX21	U41387	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 21	Gu protein
480	39744_at	DDX3	AF000982	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3	dead box, X isoform
481	34647_at	DDX5	X52104	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase, 68kD)	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5
482	36153_at	DDX9	L13848	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 9 (RNA helicase A, nuclear DNA helicase II; leukophysin)	RNA helicase A
483	41872_at	DFNA5	AF073308	deafness, autosomal dominant 5	nonsyndromic hearing impairment protein

Fig 21

A	B	C	D	E
484 1356_at	DAP3	U18321	death associated protein 3	ionizing radiation resistance conferring protein
485 39114_at	DEPP	AB022718	decidual protein induced by progesterone	DEPP
486 37638_at	DOCK1	D50857	dedicator of cyto-kinesis 1	DOCK180 protein
487 38413_at	DAD1	D15057	defender against cell death 1	DAD-1
488 32824_at	CLN2	AF039704	deficient in late-infantile neuronal ceroid lipofuscinosis; Homo sapiens lysosomal pepstatin insensitive protease (CLN2) gene, complete cds.	lysosomal pepstatin insensitive protease
489 33337_at	DEGS	AF002668	degenerative spermatocyte homolog, lipid desaturase (Drosophila)	MLD
490 38992_at	DEK	X64229	DEK oncogene (DNA binding)	putative oncogene
491 37951_at	DLC1	AF035119	deleted in liver cancer 1	deleted in liver cancer-1
492 33791_at	DLEU1	Y15227	deleted in lymphocytic leukemia, 1	deleted in lymphocytic leukemia, 1
493 38744_at	DSS1	N95406	Deleted in split-hand/split-foot 1 region	
494 36629_at	DSIP1	AI635895	delta sleep inducing peptide, immunoreactor	
495 35814_at	GA17	AF064603	dendritic cell protein	GA17 protein
496 38385_at	DSTN	S65738	destin (actin depolymerizing factor)	actin depolymerizing factor
497 39410_at	DDEF2	AB007860	development and differentiation enhancing factor 2	development- and differentiation-enhancing factor 2
498 39044_s_at	DGKD	D73409	diacylglycerol kinase, delta (130kD)	diacylglycerol kinase delta
499 38003_s_at	DGKZ	U94905	diacylglycerol kinase, zeta (104kD)	diacylglycerol kinase zeta
500 33920_at	DIAPH1	AF051782	diaphanous homolog 1 (Drosophila)	diaphanous 1
501 37692_at	DBI	AI557240	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein)	
502 39041_at	DLAT	Y00978	dihydrolipoamide S-acetyltransferase (E2 complex)	PDC-E2 precursor (AA -54 to 561)
503 40607_at	DPYSL2	U97105	dihydropyrimidinase-like 2	N2A3
504 36149_at	DPYSL3	D78014	dihydropyrimidinase-like 3	dihydropyrimidinase related protein-3
505 39503_s_at	DPYSL4	AB006713	dihydropyrimidinase-like 4	dihydropyrimidinase related protein 4
506 38220_at	DPYD	U20938	dihydropyrimidine dehydrogenase	dihydropyrimidine dehydrogenase
507 40485_at	HSA249128	AA176780	DIPB protein	

Fig 21

	A	B	C	D	E
508	479_at	DAB2	U53446	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	DOC-2
509	36643_at	DDR1	L20817	discoidin domain receptor family, member 1	tyrosine protein kinase
510	40575_at	DLG5	AB011155	discs, large (Drosophila) homolog 5	KIAA0583 protein
511	33753_at	DAAM1	AB014566	dishevelled associated activator of morphogenesis 1	KIAA0666 protein
512	33150_at	SAS10	AI126004	disruptor of silencing 10	
513	40916_at	dJ635G19.1	AL035494	dJ635G19.1 (LAMR1 (Laminin Receptor 1 (67kD) (RPSA, 40S Ribosomal Protein SA, P40)) pseudogene); match: cDNAs: Em:X15005 Em:J03799 Em:X61156 Em:M64923 Em:X06406 Em:AF140348 Em:J02870 Em:L16589 Em:Z22749 Em:D25224 Em:M14199 Em:M27798; match: ESTs: Em:AA642	dJ635G19.2.1 (novel protein (isoform 1))
514	38456_s_at	dJ734P14.1	AL049650	dJ734P14.1 (KRAB box and C2H2 Zinc finger domain protein pseudogene) match: cDNAs: Em:M27878 Em:M29580 Em:U27186 Em:D31763 Em:AB007872 Em:U09366 Em:U09413 Em:X17617 Em:AF011573 Em:AF020591 Em:X78925 match: proteins: Sw:P52736 Sw:Q06730 Sw:P51523 Tr:Q14585 Sw:P15620 Sw:Q02386 Sw:P51786 Sw:Q99676 Tr:O60792 Sw:Q03923 Sw:O75820 Tr:Q61116 Tr:Q64247	dJ734P14.2.1 (snRNP (small nuclear ribonucleoprotein particle) protein B)

Fig 21

	A	B	C	D	E
515	38455_at	dJ734P14.1	AL049650	dJ734P14.1 (KRAB box and C2H2 Zinc finger domain protein pseudogene) match: cDNAs: Em:M27878 Em:M29580 Em:U27186 Em:D31763 Em:AB007872 Em:U09366 Em:U09413 Em:X17617 Em:AF011573 Em:AF020591 Em:X78925 match: proteins: Sw:P52736 Sw:Q06730 Sw:P51523 Tr:Q14585 Sw:P15620 Sw:Q02386 Sw:P51786 Sw:Q99676 Tr:O60792 Sw:Q03923 Sw:O75820 Tr:Q61116 Tr:Q64247	dJ734P14.2.1 (snRNP (small nuclear ribonucleoprotein particle) protein B)
516	35809_g_at	dJ862K6.4	AL031681	dJ862K6.4 (pseudogene similar to part of NBP (Nucleotide Binding Protein)) match: proteins: Sw:P53384 Sw:P52920 Sw:P21590 Sw:Q57731 Sw:P40558	dJ862K6.2.2 (splicing factor, arginine/serine-rich 6 (SRP55-2)(isoform 2))
517	35808_at	dJ862K6.4	AL031681	dJ862K6.4 (pseudogene similar to part of NBP (Nucleotide Binding Protein)) match: proteins: Sw:P53384 Sw:P52920 Sw:P21590 Sw:Q57731 Sw:P40558	dJ862K6.2.2 (splicing factor, arginine/serine-rich 6 (SRP55-2)(isoform 2))
518	32433_at	dJ90L6.1	Z97353	dJ90L6.1 (RPL15 (60S Ribosomal Protein L15) pseudogene); match: proteins: Sw:O74895 Sw:P51417 Sw:P39030 Sw:O17445 Sw:P54780 Sw:O23515 Sw:O65050 Wp:CE12148 Sw:P30736 Sw:P41051 Sw:P54060 Sw:O65082 Sw:P52818 Sw:P79324 Sw:O82712 Sw:O13418 Sw:O82528 Sw:P05748; Human DNA sequence from clone RP1-90L6 on chromosome 22q11.21-11.23 Contains an RPL15 (60S Ribosomal Protein L15) pseudogene, ESTs, STSs and GSSs, complete sequence.	

Fig 21

	A	B	C	D	E
519	34183_at	DKFZP434C171	AL080169	DKFZP434C171 protein	hypothetical protein
520	40801_at	DKFZP434C212	AA643063	DKFZP434C212 protein	
521	38400_at	DKFZP434D1335	AI920820	DKFZP434D1335 protein	
522	33392_at	DKFZP434J154	AL080155	DKFZP434J154 protein	hypothetical protein
523	39411_at	DKFZP434J214	AL080156	DKFZP434J214 protein	hypothetical protein
524	40564_at	DKFZP564A043	N42007	DKFZP564A043 protein	
525	37000_at	DKFZP564B167	AL035304	DKFZP564B167 protein	hypothetical protein
526	33433_at	DKFZP564F0522	AL049943	DKFZP564F0522 protein	hypothetical protein
527	41437_at	DKFZP564F1123	AL080178	DKFZP564F1123 protein	hypothetical protein
528	39442_at	DKFZP564G0222	AL080115	DKFZP564G0222 protein	hypothetical protein
529	40437_at	DKFZP564G2022	AL049944	DKFZP564G2022 protein	hypothetical protein
530	36456_at	DKFZP564I052	AL080063	DKFZP564I052 protein	hypothetical protein
531	38033_at	DKFZP564M1416	AL049934	DKFZP564M1416 protein	hypothetical protein
532	36078_at	DKFZP564O0423	AL080120	DKFZP564O0423 protein	hypothetical protein
533	38256_s_at	DKFZP564O092	W21827	DKFZP564O092 protein	
534	39034_at	DKFZP564O123	AL080122	DKFZP564O123 protein	hypothetical protein
535	41662_at	DKFZP566B183	AL050272	DKFZP566B183 protein	hypothetical protein
536	32807_at	DKFZP566C134	AF004292	DKFZP566C134 protein	
537	38687_at	DKFZP566D193	AL050051	DKFZP566D193 protein	hypothetical protein
538	33776_at	DKFZP566K023	AL050062	DKFZP566K023 protein	hypothetical protein
539	41335_at	DC8	AL050084	DKFZP566O1646 protein	hypothetical protein
540	36961_at	DKFZP586A011	AL050286	DKFZP586A011 protein	hypothetical protein
541	38717_at	DKFZP586A0522	AL050159	DKFZP586A0522 protein	hypothetical protein
542	40831_at	DKFZP586B0923	AL050190	DKFZP586B0923 protein	hypothetical protein
543	34821_at	DKFZP586D0623	AL050197	DKFZP586D0623 protein	hypothetical protein
544	39986_at	DKFZP586D0919	AL050100	DKFZP586D0919 protein	hypothetical protein
545	34269_at	DKFZP586F1019	AL050102	DKFZP586F1019 protein	hypothetical protein
546	35736_at	DKFZP586F1918	AL050091	DKFZP586F1918 protein	hypothetical protein
547	40832_s_at	DKFZP586G011	AL050126	DKFZP586G011 protein	hypothetical protein
548	36007_at	DKFZP586L151	AL050137	DKFZP586L151 protein	hypothetical protein
549	34833_at	DKFZP586O0120	AL050157	DKFZP586O0120 protein	hypothetical protein
550	37333_at	DNMT1	X63692	DNA (cytosine-5)-methyltransferase 1 DNA segment on chromosome X (unique) 9879 expressed sequence	DNA (cytosine-5)-methyltransferase ITBA2 protein DNA segment on chromosome X and Y (unique) 155 expressed sequence
551	40891_f_at	DXS9879E	X92896	DNA segment on chromosome X (unique) DNA segment on chromosome X and Y (unique) 155 expressed sequence	
552	34215_at	DXYS155E	L03426		

Fig 21

	A	B	C	D	E
553	1252_at	D5S346	M73547	DNA segment, single copy probe LNS-CAV/LNS-CAII (deleted in polyposis)	polyposis locus-encoded protein
554	37162_at	D10S170	S72869	DNA segment, single copy, probe pH4 (transforming sequence, thyroid-1,	DNA segment, single copy, probe pH4 (transforming sequence, thyroid-1,
555	39118_at	DNAJA1	L08069	DnaJ (Hsp40) homolog, subfamily A, member 1	DNAJ homologue-2
556	276_at	DNAJA1	L08069	DnaJ (Hsp40) homolog, subfamily A, member 1	DNAJ homologue-2
557	41233_at	DNAJB6	AB014888	DnaJ (Hsp40) homolog, subfamily B, member 6	MRJ
558	35799_at	DNAJB9	AL080081	DnaJ (Hsp40) homolog, subfamily B, member 9	hypothetical protein
559	36166_at	DNAJC8	AF083190	DnaJ (Hsp40) homolog, subfamily C, member 8	SPF31
560	816_g_at	DOK1	U70987	docking protein 1, 62kD (downstream of tyrosine kinase 1)	GAP binding protein p62dok
561	34433_at	DOK1	AF035299	docking protein 1, 62kD (downstream of tyrosine kinase 1)	docking protein 1
562	34879_at	DPM1	AF007875	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit	dolichol monophosphate mannosase synthase
563	38957_at	DCAMKL1	AB002367	doublecortin and CaM kinase-like 1	doublecortin and CaM kinase-like 1
564	32168_s_at	DSCR1	U85267	Down syndrome critical region gene 1	Down syndrome critical region protein 1
565	36088_at	DSCR2	AJ006291	Down syndrome critical region gene 2	leucine rich protein
566	35166_at	DSCR3	D87343	Down syndrome critical region gene 3	DCRA
567	32621_at	DR1	M97388	down-regulator of transcription 1, TBP-binding (negative cofactor 2)	TATA binding protein-associated phosphoprotein
568	37981_at	DBN1	D17530	drebrin 1	drebrin E
569	40920_at	cdc14B	AF023158	dual specific protein; Homo sapiens tyrosine phosphatase (cdc14B) mRNA, complete cds.	tyrosine phosphatase
570	39727_at	DUSP11	AF023917	dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	PIR1
571	38272_at	DUSP14	AF038844	dual specificity phosphatase 14	MKP-1 like protein tyrosine phosphatase
572	41225_at	DUSP3	AL049417	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	

Fig 21

	A	B	C	D	E
573	41193_at	DUSP6	AB013382	dual specificity phosphatase 6	DUSP6
574	36946_at	DYRK1A	D86550	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A	serine/threonine protein kinase
575	1512_at	DYRK1A	D86550	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A	serine/threonine protein kinase
576	760_at	DYRK2	Y09216	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 isoform 1
577	39931_at	DYRK3	Y12735	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	Dyrk3 protein
578	38368_at	DUT	U31930	dUTP pyrophosphatase	deoxyuridine nucleotidohydrolase
579	38475_at	DCTN2	U50733	dynactin 2 (p50)	dynamitin
580	34891_at	PIN	AI540958	dynein, cytoplasmic, light polypeptide	
581	34829_at	DKC1	U59151	dyskeratosis congenita 1, dyskerin	Cbf5p homolog
582	32234_at	DYT1	AF007871	dystonia 1, torsion (autosomal dominant; torsin A)	torsinA
583	36989_at	DAG1	L19711	dystroglycan 1 (dystrophin-associated glycoprotein 1)	dystroglycan
584	40488_at	DMD	M18533	dystrophin (muscular dystrophy, Duchenne and Becker types)	dystrophin
585	40106_at	E1B-AP5	AJ007509	E1B-55kDa-associated protein 5	E1B-55kDa-associated protein
586	33354_at	SMURF2	AA630312	E3 ubiquitin ligase SMURF2	
587	40375_at	EGR3	X63741	early growth response 3	transcription factor
588	36135_at	EBNA1BP2	U86602	EBNA1 binding protein 2	nucleolar protein p40
589	37730_at	p100	U22055	EBNA-2 co-activator (100kD)	100 kDa coactivator
590	33254_at	EVI5	AF008915	ecotropic viral integration site 5	EVI-5 homolog
591	39542_at	ENC1	AF059611	ectodermal-neural cortex (with BTB-like domain)	nuclear matrix protein NRP/B
592	41124_r_at	ENPP2	L35594	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	autotaxin
593	41123_s_at	ENPP2	L35594	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	autotaxin
594	32551_at	EFEMP1	U03877	EGF-containing fibulin-like extracellular matrix protein 1	extracellular protein

Fig 21

A	B	C	D	E
595 36488_at	EGFL5	AB011542	EGF-like-domain, multiple 5	MEGF9
596 40509_at	ETFA	J04058	electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II)	electron transfer flavoprotein, alpha polypeptide
597 36881_at	ETFB	X71129	electron-transfer-flavoprotein, beta polypeptide	electron transfer flavoprotein beta subunit
598 1288_s_at	EEF1A	J04617	elongation factor EF-1-alpha; Human	eukaryotic translation elongation factor 1 alpha 1
599 31853_at	EED	AF080227	complete cds.	embryonic ectoderm development protein
600 39861_at	EMS1	M98343	ems1 sequence (mammary tumor and squamous cell carcinoma-associated (p80/85 src substrate)	amplixin
601 41478_at	dJ477H23.1	AL033538	end of last exon based on GENSCAN prediction presumably this gene and dJ477H23.2 are part of the same gene match: ESTs: Em:AA354647	dJ477H23.1 (novel protein)
602 37408_at	ENDO180	AB014609	endocytic receptor (macrophage mannose receptor family)	KIAA0709 protein
603 37914_at	ENDOFIN	AB002303	endosome-associated FYVE-domain protein	endosome-associated FYVE-domain protein
604 39010_at	ENSA	A1658639	endosulfine alpha	
605 40387_at	EDG2	U80811	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2	lysophosphatidic acid receptor homolog
606 40874_at	EDF1	AJ005259	endothelial differentiation-related factor 1	endothelial differentiation-related factor 1
607 39079_at	ERH	D85758	enhancer of rudimentary homolog (Drosophila)	human protein homologous to DROER protein
608 2035_s_at	ENO1	M55914	enolase 1, (alpha)	c-myc binding protein
609 34335_at	EFNB2	A1765533	ephrin-B2	
610 37731_at	EPS15	Z29064	epidermal growth factor receptor pathway substrate 15	epidermal growth factor receptor pathway substrate 15
611 1467_at	EPS8	U12535	epidermal growth factor receptor pathway substrate 8	epidermal growth factor receptor kinase substrate
612 37762_at	EMP1	Y07909	epithelial membrane protein 1	progression associated protein
613 39631_at	EMP2	U52100	epithelial membrane protein 2	XMP

Fig 21



	A	B	C	D	E
614	35816_at	cystatin B	U46692	EPM1 disease gene; cysteine protease inhibitor; Human cystatin B gene, complete cds.	cystatin B
615	32585_at	EPB41L2	AF027299	erythrocyte membrane protein band 4.1-like 2	protein 4.1-G
616	38375_at	ESD	AF112219	esterase D/formylglutathione hydrolase	esterase D
617	38283_at	EBAG9	AB007619	estrogen receptor binding site associated, antigen, 9	EBAG9
618	37161_at		W28948	ESTs	
619	40885_s_at		N30151	ESTs	
620	33328_at	C1S	W28612	ESTs	
621	33453_at	ATP6S1	AI400326	ESTs	
622	31801_at		AI808712	ESTs	
623	41598_at		AA890010	ESTs	
624	32744_at	RPS21	AI526078	ESTs, Highly similar to RS21_HUMAN 40S RIBOSOMAL PROTEIN S21 [H.sapiens]	
625	39750_at		W61005	ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]	
626	34906_g_at		AA977136	ESTs, Moderately similar to GLK5_HUMAN GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 5 PRECURSOR [H.sapiens]	
627	35787_at		AI986201	ESTs, Moderately similar to T46365 hypothetical protein DKFZp434A1518.1 [H.sapiens]	
628	41463_at		AL042729	ESTs, Weakly similar to 0903209A peptide PD, basic Pro rich [H.sapiens]	
629	41273_at		AL046940	ESTs, Weakly similar to N-WASP [H.sapiens]	
630	38097_at	PIG8	AF010313	eloposide-induced mRNA	Pig8
631	40888_f_at	EEF1A1	W28170	eukaryotic translation elongation factor 1 alpha 1	

fig 21

	A	B	C	D	E
632	35175_f_at	EEF1A2	X70940	eukaryotic translation elongation factor 1 alpha 2	elongation factor 1 alpha-2
633	35748_at	EEF1B2	X60489	eukaryotic translation elongation factor 1 beta 2	elongation factor-1-beta
634	41256_at	EEF1D	Z21507	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	human elongation factor-1-delta
635	1676_s_at	EEF1G	M55409	eukaryotic translation elongation factor 1 gamma	pancreatic tumor-related protein
636	36587_at	EEF2	Z11692	eukaryotic translation elongation factor 2	human elongation factor 2
637	663_at	EIF1A	L18960	eukaryotic translation initiation factor 1A	protein synthesis factor
638	34278_at	EIF1A	L18960	eukaryotic translation initiation factor 1A	protein synthesis factor
639	1154_at	EIF2S1	J02645	eukaryotic translation initiation factor 2, subunit 1 (alpha, 35kD)	eukaryotic translation initiation factor 2, subunit 1 (alpha, 35kD)
640	40515_at	EIF2B2	AF035280	eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD)	eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD)
641	1644_at	EIF3S2	U36764	eukaryotic translation initiation factor 3, subunit 2 (beta, 36kD)	TGF-beta receptor interacting protein 1
642	35327_at	EIF3S3	U54559	eukaryotic translation initiation factor 3, subunit 3 (gamma, 40kD)	translation initiation factor eIF3 p40 subunit
643	32576_at	EIF3S5	U94855	eukaryotic translation initiation factor 3, subunit 5 (epsilon, 47kD)	translation initiation factor 3 47 kDa subunit
644	38681_at	EIF3S6	U62962	eukaryotic translation initiation factor 3, subunit 6 (48kD)	murine mammary tumor integration site 6 (oncogene homolog)
645	35298_at	EIF3S7	U54558	eukaryotic translation initiation factor 3, subunit 7 (zeta, 66/67kD)	translation initiation factor eIF3 p66 subunit
646	35323_at	EIF3S9	U78525	eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD)	eukaryotic translation initiation factor
647	41785_at	EIF4G2	U73824	eukaryotic translation initiation factor 4 gamma, 2	p97
648	33907_at	EIF4G3	AF012072	eukaryotic translation initiation factor 4 gamma, 3	eIF4GII

Fig 21

	A	B	C	D	E
649	1420_s_at	EIF4A2	D30655	eukaryotic translation initiation factor 4A, isoform 2	eukaryotic initiation factor 4AII
650	37752_at	EIF4E	M15353	eukaryotic translation initiation factor 4E	cap-binding protein
651	35263_at	EIF4EBP2	N73769	eukaryotic translation initiation factor 4E binding protein 2	
652	167_at	EIF5	U49436	eukaryotic translation initiation factor 5	translation initiation factor 5
653	37318_at	ETF1	X81625	eukaryotic translation termination factor 1	C11 protein
				excision repair cross-complementing rodent repair deficiency, complementation group 3 (xeroderma pigmentosum group B complementing)	excision repair cross-complementing rodent repair deficiency, complementation group 3 (xeroderma pigmentosum group B complementing)
654	1885_at	ERCC3	M31899	excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group G (Cockayne syndrome))	
655	2063_at	ERCC5	L20046		excision repair protein
656	33734_at	HSD11B1	AL022398	exons 1-4 beyond this clone; match: proteins P28845 P50172 P51975 Q29608	dJ434O14.1 (Hydroxysteroid (11-beta) Dehydrogenase 1 (EC 1.1.1.146))
657	222_at	EXT1	S79639	exostos (multiple) 1	exostos (multiple) 1
658	36526_at	EXTL2	AF000416	exostos (multiple)-like 2	EXT-like protein 2
659	38809_s_at	EXTL3	AB011091	exostos (multiple)-like 3	KIAA0519 protein
660	37729_at	XPO1	Y08614	exportin 1 (CRM1 homolog, yeast)	exportin 1
661	38753_at	XPOT	AF039022	exportin, tRNA (nuclear export receptor for tRNAs)	exportin t
662	39673_i_at	ECM2	AB011792	extracellular matrix protein 2, female organ and adipocyte specific	extracellular matrix protein
663	39674_r_at	ECM2	AB011792	extracellular matrix protein 2, female organ and adipocyte specific	extracellular matrix protein
664	35226_at	EYA2	U71207	eyes absent homolog 2 (Drosophila)	Eab1
665	38318_at	FAM8A1	AL050128	family with sequence similarity 8, member A1	
666	31879_at	FUBP3	U69127	far upstream element (FUSE) binding protein 3	FUSE binding protein 3

Fig 21

	A	B	C	D	E
				farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase)	farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase)
667	37325_at	FDP5	D14697	farnesyl-diphosphate farnesyltransferase 1	farnesyl-diphosphate farnesyltransferase
668	34848_at	FDFT1	X69141	farnesyltransferase, CAAX box, alpha	farnesyl-protein transferase alpha-subunit
669	1499_at	FNTA	L10413	Fas (TNFRSF6)-associated via death domain	mediator of receptor induced toxicity
670	38755_at	FADD	X84709	fasciculation and elongation protein zeta 1 (zyglin I)	FEZ1
671	37743_at	FEZ1	U60060	fasciculation and elongation protein zeta 2 (zyglin II)	FEZ2
672	38651_at	FEZ2	U60061	FAT tumor suppressor homolog 1 (Drosophila)	homologue of Drosophila Fat protein
673	40454_at	FAT	X87241	fatty-acid-Coenzyme A ligase, long-chain 2	long-chain acyl-CoA synthetase
674	40082_at	FACL2	D10040	fatty-acid-Coenzyme A ligase, long-chain 3	Acyl-CoA synthetase 3
675	33880_at	FACL3	D89053	fatty-acid-Coenzyme A ligase, long-chain 3	
676	33881_at	FACL3	AA977580	F-box and leucine-rich repeat protein 11	KIAA1004 protein
677	33360_at	FBXL11	AB023221	F-box and leucine-rich repeat protein 7	KIAA0840 protein
678	37205_at	FBXL7	AB020647	F-box and WD-40 domain protein 1B	KIAA0696 protein
679	32854_at	FBXW1B	AB014596	F-box only protein 21	KIAA0875 protein
680	32169_at	FBXO21	AB020682	F-box only protein 7	hypothetical protein
681	35337_at	FBXO7	AL050254		
682	33817_at	D10S102	S63912	FBRNP; heterogeneous ribonucleoprotein homolog; This sequence comes from Fig. 3; D10S102=FBRNP (human, fetal brain, mRNA, 3043 nt).	FBRNP
683	1877_g_at	nifH	HG1103-HT1103	Fe protein	dinitrogenase reductase
684	34678_at	FER1L3	AL096713	fer-1-like 3, myoferlin (C. elegans)	hypothetical protein
685	32148_at	FARP1	AI701049	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	

Fig 2)

	A	B	C	D	E
686	33943_at	FTH1	L20941	ferritin, heavy polypeptide 1	ferritin heavy chain
687	41091_at	FALZ	U05237	fetal Alzheimer antigen	fetal Alzheimer antigen
688	32535_at	FBN1	X63556	fibrillin 1 (Marfan syndrome)	fibrillin
689	39945_at	FAP	U09278	fibroblast activation protein, alpha	fibroblast activation protein
690	1380_at	FGF7	M60828	fibroblast growth factor 7 (keratinocyte growth factor)	keratinocyte growth factor
691	2057_g_at	FGFR1	M34641	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)	fibroblast growth factor receptor 1, isoform 1 precursor; fibroblast growth factor receptor 1, isoform 2 precursor; fibroblast growth factor receptor 1, isoform 3 precursor; fibroblast growth factor receptor 1, isoform 4 precursor; fibroblast growth factor receptor 1, isoform 5 precursor; fibroblast growth factor receptor 1, isoform 6 precursor; fibroblast growth factor receptor 1, isoform 7 precursor; fibroblast growth factor receptor 1, isoform 8 precursor; fibroblast growth factor receptor 1, isoform 9 precursor
692	31720_s_at	FN1	M10905	fibronectin 1	fibronectin 1, isoform 1 preproprotein;
693	31719_at	FN1	X02761	fibronectin 1	fibronectin 1, isoform 2 preproprotein
694	34853_at	FLRT2	AB007865	fibronectin leucine rich transmembrane protein 2	fibronectin precursor
695	38026_at	FBLN1	U01244	fibulin 1	fibronectin leucine rich transmembrane protein 2
696	39038_at	FBLN5	AF093118	fibulin 5	fibulin-1D
697	38078_at	FLNB	AF042166	filamin B, beta (actin binding protein 278)	UP50
698	38761_s_at	FKBP9	AA487755	FK506 binding protein 9 (63 kD)	beta-filamin
699	40665_at	FMO3	M83772	flavin containing monooxygenase 3	flavoprotein
700	35254_at	FLN29	AB007447	FLN29 gene product	Fln29
701	38356_at	FST	M19481	follicle stimulating hormone precursor; Human follistatin gene, exon 6.	follicle stimulating hormone precursor; FST317 precursor; follistatin isoform FST344 precursor

Fig 21

	A	B	C	D	E
702	41027_at	FKHL7		forkhead (Drosophila)-like 7; FREAC3; Homo sapiens forkhead/winged helix-like transcription factor 7 (FKHL7) gene, complete cds.	forkhead/winged helix-like transcription factor 7
703	36319_at	FOXF2	AF078096 U13220	forkhead box F2	forkhead protein FREAC-2
704	40570_at	FOXO1A	AF032885	forkhead box O1A (rhabdomyosarcoma)	forkhead protein
705	34740_at	FOXO3A	AF032886	forkhead box O3A	forkhead protein
706	32542_at	FHL1	AF063002	four and a half LIM domains 1	LIM protein SLIMMER
707	38422_s_at	FHL2	U29332	four and a half LIM domains 2	heart protein
708	41649_at	FHX	AF038177	FOXJ2 forkhead factor	
709	34997_r_at	FZD5	U43318	frizzled homolog 5 (Drosophila)	transmembrane receptor
710	34472_at	FZD6	AB012911	frizzled homolog 6 (Drosophila)	Frizzled-6
711	33222_at	FZD7	AB017365	frizzled homolog 7 (Drosophila)	frizzled-7
712	38923_at	FRG1	L76159	FSHD region gene 1	FSHD region gene 1
713	38139_at	FPGT	AF017445	fructose-1-phosphate guanylyltransferase	GDP-L-fructose pyrophosphorylase
714	41814_at	FUCA1	M29877	fructosidase, alpha-L-1, tissue	fructosidase, alpha-L-1, tissue
715	40022_at	FCMD	AB008226	Fukuyama type congenital muscular dystrophy (fukutin)	fukutin
716	32546_at	FH	U59309	fumarate hydratase	fumarase precursor
717	36145_at	SIAHBP1	U51586	fuse-binding protein-interacting repressor	siah binding protein 1
718	40480_s_at	FYN	M14333	FYN oncogene related to SRC, FGR, YES	FYN oncogene related to SRC, FGR, YES
719	2039_s_at	FYN	M14333	FYN oncogene related to SRC, FGR, YES	FYN oncogene related to SRC, FGR, YES
720	34288_at	RDC1	U67784	G protein-coupled receptor	orphan G protein-coupled receptor
721	37308_at	GPR107	AI88084	G protein-coupled receptor 107	
722	37298_at	GABARAP	AF044671	GABA(A) receptor-associated protein	MM46
723	35785_at	GABARAPL1	W28281	GABA(A) receptor-associated protein like 1	
724	35767_at	GABARAPL2	AI565760	GABA(A) receptor-associated protein-like 2	
725	37825_at	GALK2	M84443	galactokinase 2	galactokinase
726	37742_at	GLB1	M34423	galactosidase, beta 1	galactosidase, beta 1

Fig 21

	A	B	C	D	E
727	37263_at	GGH	U55206	gamma-glutamyl hydrolase (conjugase, folic polygamma glutamyl hydrolase)	human gamma-glutamyl hydrolase
728	32531_at	GJA1	X52947	gap junction protein, alpha 1, 43kD (connexin 43)	connexin 43
729	36603_at	GCN1L1	D86973	GCN1 general control of amino-acid synthesis 1-like 1 (yeast)	
730	35307_at	GDI2	Y13286	GDP dissociation inhibitor 2	GDP dissociation inhibitor beta
731	39386_at	KIAA0110	D14811	gene predicted from cDNA with a complete coding sequence	gene predicted from cDNA with a complete coding sequence
732	32180_s_at	RES4-22	AB000461	gene with multiple splice variants near HD locus on 4p16.3	gene with multiple splice variants near HD locus on 4p16.3
733	466_at	GTF2I	U77948	general transcription factor II, i	Bruton's tyrosine kinase-associated protein-135
734	35450_s_at	GTF2I	AF015553	general transcription factor II, i	TFII-I protein
735	37010_at	GTF2A2	A1203737	general transcription factor IIA, 2 (12kD subunit)	
736	869_at	GTF2A2	U14193	general transcription factor IIA, 2 (12kD subunit)	transcription factor IIA small 12 kDa subunit
737	37882_at	GTF2E1	X63468	general transcription factor IIE, polypeptide 1 (alpha subunit, 56kD)	TFII-E-alpha
738	37295_at	GTF2E2	X63469	general transcription factor IIE, polypeptide 2 (beta subunit, 34kD)	TFII-E-beta
739	38782_at	GTF2H1	M95809	general transcription factor IIH, polypeptide 1 (62kD subunit)	basic transcription factor 62kD subunit
740	40754_at	GTF2H3	Z30093	general transcription factor IIH, polypeptide 3 (34kD subunit)	basic transcription factor 2, 35 kD subunit
741	36188_at	GTF3A	D32257	general transcription factor IIIA	Xenopus transcription factor IIIA homologue
742	35296_at	GGPS1	AB019036	geranylgeranyl diphosphate synthase 1	geranylgeranyl pyrophosphate synthase
743	763_at	GMFB	AB001106	glia maturation factor, beta	glia maturation factor
744	39793_at	GBAS	AF029786	glioblastoma amplified sequence	GBAS
				glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV)	
745	32643_at	GBE1	L07956		1,4-alpha-glucan branching enzyme
746	34332_at	GNPI	D31766	glucosamine-6-phosphate isomerase	glucosamine-6-phosphate isomerase

Fig 21

	A	B	C	D	E
747	38218_at	GCNT1	M97347	glucosaminyl (N-acetyl) transferase 1, core 2 (beta-1,6-N-acetylglucosaminyltransferase)	beta-1,6-N-acetylglucosaminyltransferase
748	39122_at	GPI	K03515	glucose phosphate isomerase	neuroleukin
749	38986_at	GRP58	Z49835	glucose regulated protein, 58kD	protein disulfide isomerase
750	38042_at	G6PD	X03674	glucose-6-phosphate dehydrogenase	glucose-6-phosphate dehydrogenase
751	33308_at	GUSB	M15182	glucuronidase, beta	glucuronidase, beta
752	37341_at	GLUD1	M20867	glutamate dehydrogenase 1	glutamate dehydrogenase 1
753	35485_at	GRM4	X80818	glutamate receptor, metabotropic 4	metabotropic glutamate receptor type 4
754	40522_at	GLUL	X59834	glutamate-ammonia ligase (glutamine synthase)	glutamate--ammonia ligase
755	31850_at	GCLC	M90656	glutamate-cysteine ligase, catalytic subunit	gamma-glutamylcysteine synthetase
756	33163_r_at	GCLM	L35546	glutamate-cysteine ligase, modifier subunit	gamma-glutamylcysteine synthetase light subunit
757	35343_at	GOT1	M37400	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)	aspartate aminotransferase 1
758	40764_at	GOT2	M22632	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)	aspartate aminotransferase 2 precursor
759	34719_at	GLS	AB020645	glutaminase	KIAA0838 protein
760	32626_at	GFPT1	M90516	glutamine-fructose-6-phosphate transaminase 1	glutamine:fructose-6-phosphate amidotransferase
761	39640_at	GFPT2	AB016789	glutamine-fructose-6-phosphate transaminase 2	Glutamine:fructose-6-phosphate amidotransferase
762	35300_at	EPRS	X54326	glutamyl-prolyl-tRNA synthetase	glutamyl-tRNA synthetase
763	34311_at	GLRX	X76648	glutaredoxin (thioltransferase)	glutaredoxin
764	37033_s_at	GPX1	X13710	glutathione peroxidase 1	glutathione S-transferase A4-4
765	40508_at	GSTA4	AF025887	glutathione S-transferase A4	glutathione synthetase
766	38386_r_at	GSS	U34683	glutathione synthetase	glutathione synthetase
767	824_at	GSTTLp28	U90313	glutathione S-transferase like; glutathione transferase omega	glutathione S-transferase homolog
768	AFFX-HUMGAP1	GAPD	M33197	glyceraldehyde-3-phosphate dehydrogenase	glyceraldehyde-3-phosphate dehydrogenase
769	35905_s_at	GAPD	U34995	glyceraldehyde-3-phosphate dehydrogenase	

Fig 21



	A	B	C	D	E
770	AFFX-HUMGAP1	GAPD	M33197	glyceraldehyde-3-phosphate dehydrogenase	glyceraldehyde-3-phosphate dehydrogenase
771	39392_at	GNPAT	AJ002190	glyceronephosphate O-acyltransferase	dihydroxyacetone phosphate acyltransferase
772	37357_at	GCSH	D00723	glycine cleavage system protein H (aminomethyl carrier)	glycine cleavage system protein H (aminomethyl carrier)
773	39665_at	GLRB	U33267	glycine receptor, beta	glycine receptor beta subunit
774	40645_at	GSK3B	L33801	glycogen synthase kinase 3 beta	protein kinase
775	40876_at	GYG	U31525	glycogenin	glycogenin
776	35334_at	GYG2	U94362	glycogenin 2	glycogenin-2 alpha
777	38379_at	GNMB	X76534	glycoprotein (transmembrane) nmb	glycoprotein (transmembrane) nmb
778	37251_s_at	GPM6B	AF016004	glycoprotein M6B	
779	33126_at	AD-017	L13435	glycosyltransferase AD-017	
780	36582_g_at	GARS	U09510	glycyl-tRNA synthetase	glycyl-tRNA synthetase
781	36581_at	GARS	U09510	glycyl-tRNA synthetase	glycyl-tRNA synthetase
782	36201_at	GLO1	D13315	glyoxalase I	lactoyl glutathione lyase
783	40133_s_at	GRHPR	W28944	glyoxylate reductase/hydroxypyruvate reductase	
784	37449_i_at	GNAS	X04409		guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1, isoform alpha-s-2; neuroendocrine secretory protein 55; guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1, isoform XL-alpha-s; guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1, isoform alpha-s-1
785	37448_s_at	GNAS	X56009	GNAS complex locus GNAS complex locus	alpha subunit of GsGTP binding protein

Fig 21

A	B	C	D	E
786 37450_r_at	GNAS	X04409	GNAS complex locus	guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1, isoform alpha-s-2; neuroendocrine secretory protein 55; guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1, isoform XL-alpha-s; guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1, isoform alpha-s-1
787 37959_at	GGA3		golgi associated, gamma adaptin ear containing, ARF binding protein 3	ADP-ribosylation factor binding protein 3, isoform short; ADP-ribosylation factor binding protein 3, isoform long
788 32713_at	GOLGA1	D63876		Golgi complex autoantigen golgin-97
789 32150_at	GOLGA4	U51587	golgi autoantigen, golgin subfamily a, 1	256 kD golgin
790 36827_at	GOLPH1	X82834	golgi autoantigen, golgin subfamily a, 4	unknown protein
		AF020762	golgi phosphoprotein 1	
791 38620_at	GOSR2	AA905543	golgi SNAP receptor complex member 2	
792 34737_at	GOLTC1	AF058718	golgi transport complex 1 (90 kD subunit)	putative 13 S Golgi transport complex 90kD subunit brain-specific isoform
793 41767_r_at	KIAA0855	AB020662	golgin-67	KIAA0855 protein
794 36950_at	HSGP25L2G	X90872	gp25L2 protein	
795 36035_at	GPAA1	AB002135	GPAA1P anchor attachment protein 1 homolog (yeast)	glycosylphosphatidylinositol anchor attachment 1 (GPAA1)
796 32595_at	GRSF1	U07231	G-rich RNA sequence binding factor 1	G-rich sequence factor-1
797 39822_s_at	GADD45B	AF078077	growth arrest and DNA-damage-inducible, beta	growth arrest and DNA-damage-inducible protein GADD45beta
798 39821_s_at	GADD45B	N95168	growth arrest and DNA-damage-inducible, beta	
799 661_at	GAS1	L13698	growth arrest-specific 1	growth arrest-specific 1
800 41839_at	GAS1	L13698	growth arrest-specific 1	growth arrest-specific 1
801 37658_at	GAS6	L13720	growth arrest-specific 6	growth-arrest-specific protein
802 1598_g_at	GAS6	L13720	growth arrest-specific 6	growth-arrest-specific protein
803 37615_at	GRB10	D86962	growth factor receptor-bound protein 10	growth factor receptor-bound protein 10
804 41752_at	GHITM	W28190	growth hormone inducible transmembrane protein	

Fig 21

	A	B	C	D	E
805	160030_at	GHR	X06562	growth hormone receptor	growth hormone receptor
806	40113_at	GS3955	D87119	GS3955 protein	GS3955
807	37279_at	GEM	U10550	GTP binding protein overexpressed in skeletal muscle	Gem
808	33809_at	GNAI1	AL049933	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1	hypothetical protein
809	37307_at	GNAI2	X04828	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2
810	34608_at	GNB2L1	M24194	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	MHC B complex protein 12.3
811	35272_at	GNG5	AI541042	guanine nucleotide binding protein (G protein), gamma 5	
812	37735_at	GNG10	UJ31383	guanine nucleotide binding protein 10	G protein gamma-10 subunit
813	35735_at	GBP1	M55542	guanylate binding protein 1, interferon-inducible, 67kD	guanylate binding protein isoform I
814	905_at	GUK1	L76200	guanylate kinase 1	guanylate kinase
815	32249_at	HFL1	M65292	H factor (complement)-like 1	factor H homologue
816	32250_at	HF1	X07523	H factor 1 (complement)	complement factor H
817	420_at	ACTH-R	X65633	H.sapiens ACTH-R gene for adrenocorticotrophic hormone receptor	candidate adrenocorticotrophic hormone receptor
818	31673_s_at	cell adhesion regu	X65784	H.sapiens CAR gene.	cell matrix adhesion regulator
819	37003_at	CD63; MLA1; ME4	X62654	H.sapiens gene for Me491/CD63 antigen.	ME491 /CD63 antigen
820	38076_at	P1 gene for c subu	X69907	H.sapiens gene for mitochondrial ATP synthase c subunit (P1 form).	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1
821	35125_at	hrp S6	X67309	H.sapiens gene for ribosomal protein S6.	ribosomal protein S6
822	34646_at	rpS7	Z25749	H.sapiens gene for ribosomal protein S7.	ribosomal protein S7
823	31510_s_at	hH3.3B	Z48950	H.sapiens hH3.3B gene for histone H3.3.	histone H3.3

Fig 21

	A	B	C	D	E
824	33820_g_at	ldhB	X13794	H.sapiens lactate dehydrogenase B gene exon 1 and 2 (EC 1.1.1.27) (and joined CDS).	lactate dehydrogenase B
825	33819_at	ldhB	X13794	H.sapiens lactate dehydrogenase B gene exon 1 and 2 (EC 1.1.1.27) (and joined CDS).	lactate dehydrogenase B
826	34787_at	ORF1	X93209	H.sapiens mRNA for NRD1 convertase.	NRD1 convertase
827	36012_at	PIBF1	Y09631	H.sapiens mRNA for PIBF1 protein, complete.	PIBF1 protein
828	31526_f_at	tre	X63547	H.sapiens mRNA for tre oncogene (clone 213).	oncogene
829	40471_at	PxF	Y09048	H.sapiens PxF gene.	PxF protein
830	37038_at	PXMP1	X83467	H.sapiens PXMP1 gene, exon 1 (and joined CDS).	70kD peroxisomal integral membrane protein
831	31583_at	rpS8	X67247	H.sapiens rpS8 gene for ribosomal protein S8.	ribosomal protein S8
832	1685_at	SPHAR	X82554	H.sapiens SPHAR gene for cyclin-related protein.	S-phase response (cyclin-related)
833	38127_at	syndecan-1	Z48199	H.sapiens syndecan-1 gene (exons 2-5).	syndecan 1
834	37310_at	uPA	X02419	H.sapiens uPA gene.	urokinase-plasminogen activator
835	34308_at	H2AFL	U90551	H2A histone family, member L	histone 2A-like protein
836	39337_at	H2AFZ	M37583	H2A histone family, member Z	H2A histone family, member Z
837	33458_r_at	H2BFL	AI688098	H2B histone family, member L	
838	40818_at	LOC51580	D14041	H-2K binding factor-2	H-2K binding factor-2
839	254_at	H3F3A	M11353	H3 histone, family 3A	H3 histone, family 3A
840	39969_at	H4FG	AA255502	H4 histone family, member G	
841	32591_at	HCDI	AI494623	HCDI protein	
842	35215_at	HDCMA18P	AL049996	HDCMA18P protein	hypothetical protein
843	39353_at	HSPE1	AI912041	heat shock 10kD protein 1 (chaperonin 10)	
844	37720_at	HSPD1	M22382	heat shock 60kD protein 1 (chaperonin)	mitochondrial matrix protein
845	36614_at	HSPA5	X87949	heat shock 70kD protein 5 (glucose-regulated protein, 78kD)	heat shock 70kD protein 5 (glucose-regulated protein, 78kD)
846	41510_s_at	HSPA9B	L15189	heat shock 70kD protein 9B (mortalin-2)	MTHSP75

Fig 21

	A	B	C	D	E
847	32316_s_at	HSPCA	X15183	heat shock 90kD protein 1, alpha	heat shock 90kD protein 1, alpha
848	33984_at	HSPCB	M16660	heat shock 90kD protein 1, beta	heat shock 90kD protein 1, beta
849	31906_at	HSBP1	AF068754	heat shock factor binding protein 1	heat shock factor binding protein 1 HSBP1
850	1468_at	TRAP1	U12595	heat shock protein 75	tumor necrosis factor type 1 receptor associated protein
851	38054_at	HBXIP	AF029890	hepatitis B virus x interacting protein	hepatitis B virus X interacting protein
852	38779_r_at	HDGF	D16431	hepatoma-derived growth factor (high-mobility group protein 1-like)	hepatoma-derived GF
853	35644_at	HEPH	AB014598	hephaestin	KIAA0698 protein
854	38094_at	HNRPA	M65028	heterogeneous nuclear ribonucleoprotein A/B	hnRNP type A/B protein
855	37334_at	HNRPA0	U23803	heterogeneous nuclear ribonucleoprotein A0	heterogeneous ribonucleoprotein A0
856	34987_s_at	HNRPA1	X79536	heterogeneous nuclear ribonucleoprotein A1	hnRNP core protein A1
857	36654_s_at	HNRPA2B1	M29065	heterogeneous nuclear ribonucleoprotein A2/B1	heterogeneous nuclear ribonucleoprotein A2/B1, isoform A2; heterogeneous nuclear ribonucleoprotein A2/B1, isoform B1
858	33666_at	HNRPC	M16342	heterogeneous nuclear ribonucleoprotein C (C1/C2)	heterogeneous nuclear ribonucleoprotein C, isoform b; heterogeneous nuclear ribonucleoprotein C, isoform a
859	38016_at	HNRPD	M94630	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kD)	DNA-binding protein
860	33845_at	HNRPH1	W28483	heterogeneous nuclear ribonucleoprotein H1 (H)	
861	41132_r_at	HNRPH2	U01923	heterogeneous nuclear ribonucleoprotein H2 (H')	heterogeneous nuclear ribonucleoprotein H2
862	41283_at	HNRPH3	AF052131	heterogeneous nuclear ribonucleoprotein H3 (2H9)	heterogeneous nuclear ribonucleoprotein H3, isoform a; heterogeneous nuclear ribonucleoprotein H3, isoform b
863	40836_s_at	HNRPH3	W26677	heterogeneous nuclear ribonucleoprotein H3 (2H9)	

Fig 21

	A	B	C	D	E
864	39415_at	HNRPK	X72727	heterogeneous nuclear ribonucleoprotein K	transformation upregulated nuclear protein
865	35201_at	HNRPL	X16135	heterogeneous nuclear ribonucleoprotein L	heterogeneous nuclear ribonucleoprotein L
866	37717_at	HNRPM	L03532	heterogeneous nuclear ribonucleoprotein M	M4 protein
867	39792_at	HNRPR	AF000364	heterogeneous nuclear ribonucleoprotein R	heterogeneous nuclear ribonucleoprotein R
868	38654_at	HNRPU	X65488	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	hnRNP U protein
869	32818_at	HXB	X78565	hexabrachion (tenascin C, cytactin)	human tenascin-C
870	39827_at	RTP801	AA522530	HIF-1 responsive RTP801	
871	31504_at	HDLBP	M64098	high density lipoprotein binding protein (vigilin)	high density lipoprotein binding protein
872	32220_at	HMG1	D63874	high-mobility group (nonhistone chromosomal) protein 1	HMG-1
873	306_s_at	HMG14	J02621	high-mobility group (nonhistone chromosomal) protein 14	high-mobility group (nonhistone chromosomal) protein 14
874	35738_at	HMG17L3	A1347088	high-mobility group (nonhistone chromosomal) protein 17-like 3	
875	38065_at	HMG2	X62534	high-mobility group (nonhistone chromosomal) protein 2	high-mobility group (nonhistone chromosomal) protein 2
876	38843_at	HMG2L1	AL079310	high-mobility group protein 2-like 1	hypothetical protein
877	35693_at	HPCAL1	AF070616	hippocalcin-like 1	BDP-1 protein
878	1009_at	HINT1	U51004	histidine triad nucleotide binding protein 1	protein kinase C inhibitor
879	34231_at	HBOA	AF074606	histone acetyltransferase	histone acetyltransferase
880	41855_at	HAT1	AF030424	histone acetyltransferase 1	histone acetyltransferase 1
881	38771_at	HDAC1	D50405	histone deacetylase 1	RPD3 protein
882	34368_at	HDAC2	U31814	histone deacetylase 2	transcriptional regulator homolog RPD3
883	38271_at	HDAC4	AB006626	histone deacetylase 4	KIAA0288 protein
884	39046_at	H2AV	AL049324	histone H2A.F/Z variant	
885	39092_at	H2AV	AW007731	histone H2A.F/Z variant	
886	38824_at	HTATIP2	AF039103	HIV-1 Tat interactive protein 2, 30 kD	Tat-interacting protein TIP30
887	40220_at	HIS1	AB021179	HMBA-inducible	HEXIM1 protein

Fig 21

	A	B	C	D	E
888	39809_at	HBP1	AF019214	HMG-box containing protein 1	HMG box containing protein 1
				HMG-domain containing protein which is the 57 kd subunit within SWI/SNF-related BAF complexes; contains a proline-rich N-terminus, a kinesin-like coiled-coil region, and a highly acidic c-terminus; Homo sapiens BAF57 (BAF57) gene, complete cds.	
889	33828_at	BAF57	AF035262	HMT1 hnRNP methyltransferase-like 1 (S. cerevisiae)	BAF57
890	39348_at	HRMT1L1	X99209	HMT1 hnRNP methyltransferase-like 2 (S. cerevisiae)	arginine methyltransferase
891	32825_at	HRMT1L2	Y10805	HNRNP Core Protein A1 LIKE pseudogene; match: proteins P04256 Q28521 P49312 P09651 P51991 P51992 P51968 P17130 P22626	arginine methyltransferase
892	31463_s_at	dJ256G22.1	AL022097	holocytochrome c synthase (cytochrome c heme-lyase)	holocytochrome c-type synthetase
893	38943_at	HCCS	U36787	homeo box B2	homeo box B2
894	39610_at	HOXB2	X16665	homeo box C6	homeo box C6
895	40674_s_at	HOXC6	S82986	Homer, neuronal immediate early gene, 3	homer-3
896	38233_at	HOMER-3	AF093265	Homo sapiens (clone t17252) ubiquinol cytochrome c reductase Rieske iron-sulphur protein (UQCRCF1) gene, exon 2.	Rieske Fe-S protein
897	34401_at	UQCRCF1	L32977	Homo sapiens (clone FFE-7) type II inosine monophosphate dehydrogenase (IMPDH2) gene, exons 1-13, complete cds.	inosine monophosphate dehydrogenase type II
898	36624_at	IMPDH2	L33842	Homo sapiens aldehyde oxidase (AOX1) gene, exon 35 and complete cds.	aldehyde oxidase
899	37599_at	AOX1	AF017060	Homo sapiens alpha NAC mRNA, complete cds.	alpha NAC
900	39740_g_at	NACA	AF054187		

fig 21

A	B	C	D	E
901 39739_at	NACA	AF054187	Homo sapiens alpha NAC mRNA, complete cds.	alpha NAC
902 41154_r_at	CTNNA1	AF102803	Homo sapiens alphaE-catenin (CTNNA1) gene, exon 18 and complete cds.	alphaE-catenin
903 41153_f_at	CTNNA1	AF102803	Homo sapiens alphaE-catenin (CTNNA1) gene, exon 18 and complete cds.	alphaE-catenin
904 39324_at		AL050078	Homo sapiens cDNA FLJ10784 f1s, clone NT2RP4000448, highly similar to Homo sapiens mRNA; cDNA DKFZp566G0746	
905 35310_at		D45288	Homo sapiens cDNA FLJ13267 f1s, clone OVARC1000964	
906 35754_at		L40391	Homo sapiens cDNA FLJ13553 f1s, clone PLACE1007454	
907 33325_at		W26667	Homo sapiens cDNA FLJ14821 f1s, clone OVARC1000556, highly similar to RIBOSOMAL PROTEIN S6 KINASE II ALPHA 2 (EC 2.7.1.-)	
908 38102_at		W28575	Homo sapiens cDNA FLJ25016 f1s, clone CBL01574	
909 41253_s_at		AI983043	Homo sapiens cDNA FLJ30436 f1s, clone BRACE2009037	
910 39162_at		AA156987	Homo sapiens cDNA FLJ30544 f1s, clone BRAWH2001412	
911 41807_at		AL040137	Homo sapiens cDNA FLJ31959 f1s, clone NT2RP7007422	
912 38643_at		W87466	Homo sapiens cDNA FLJ33151 f1s, clone UTERU2000263	
913 34246_at		AA418437	Homo sapiens cDNA: FLJ21175 f1s, clone CAS11071	
914 40813_at		A1768188	Homo sapiens cDNA: FLJ21243 f1s, clone COL01164	

fig 21



	A	B	C	D	E
915	40923_at		AA290994	Homo sapiens cDNA: FLJ21449 fis, clone COL04483, highly similar to AF010235 Homo sapiens mRNA from chromosome 5q31-33 region	
916	38993_r_at		W27522	Homo sapiens cDNA: FLJ21904 fis, clone HEP03585	
917	38093_at		U90909	Homo sapiens cDNA: FLJ21927 fis, clone HEP04178, highly similar to HSU90909 Human clone 23722 mRNA sequence	
918	34840_at		AI700633	Homo sapiens cDNA: FLJ22642 fis, clone HSI06970	
919	32838_at	smooth muscle m	S67247	Homo sapiens cDNA: FLJ23324 fis, clone HEP12482, highly similar to HUMMYOHC Human nonmuscle myosin heavy chain-B (MYH10) mRNA	smooth muscle myosin heavy chain isoform SMemb
920	33737_f_at		AI871359	Homo sapiens cervical cancer suppressor-1 mRNA, complete cds	
921	41663_at		AF038202	Homo sapiens clone 23570 mRNA sequence	
922	36815_at		AF038185	Homo sapiens clone 23700 mRNA sequence	
923	41841_at		AF052138	Homo sapiens clone 23718 mRNA sequence	
924	37794_at		AF035281	Homo sapiens clone 23903 mRNA sequence	
925	38764_at		AF007142	Homo sapiens clone 23938 mRNA sequence	
926	35342_at		AF052159	Homo sapiens clone 24416 mRNA sequence	
927	31867_at		AF052174	Homo sapiens clone 24630 mRNA sequence	
928	36758_at		AF070578	Homo sapiens clone 24674 mRNA sequence	
929	41864_at		AF052181	Homo sapiens clone 24790 mRNA sequence	

Fig 21

	A	B	C	D	E
930	38070_at		AL080234	Homo sapiens clone FBD3 Cri-du-chat critical region mRNA	
931	34773_at	TBCA	AF038952	Homo sapiens cofactor A protein mRNA, complete cds.	cofactor A protein
932	39027_at	COX4	AF017115	Homo sapiens cytochrome c oxidase subunit IV precursor (COX4) gene, nuclear gene encoding mitochondrial protein, complete cds.	cytochrome c oxidase subunit IV precursor
933	40878_f_at	D15F37	AF041081	Homo sapiens D15F37 pseudogene, S4 allele, mRNA sequence.	
934	631_g_at	DCTD	L39874	Homo sapiens deoxycytidylate deaminase gene, complete cds.	deoxycytidylate deaminase
935	630_at	DCTD	L39874	Homo sapiens deoxycytidylate deaminase gene, complete cds.	deoxycytidylate deaminase
936	33936_at	GALC	D86181	Homo sapiens DNA for galactocerebrosidase, exon 17 and complete cds.	galactocerebrosidase
937	40134_at	ATP5J2; ATP5JL	AF047436	Homo sapiens F1Fo-ATPase synthase f subunit mRNA, complete cds.	F1Fo-ATPase synthase f subunit
938	36103_at	SCYA3; LD78ALP	D90144	Homo sapiens gene for LD78 alpha precursor, complete cds.	LD78 alpha precursor
939	40725_at	GOSR1; P28; GS2	AF047438	Homo sapiens GOS28/P28 protein mRNA, complete cds.	GOS28/P28 protein
940	38708_at	RAN; TC4; ARA24	AF054183	Homo sapiens GTP binding protein mRNA, complete cds.	GTP binding protein
941	35790_at	VPS26; HB58; HB	AF054179	Homo sapiens H beta 58 homolog mRNA, complete cds.	H beta 58 homolog
942	36576_at	H2AFY; H2A.y; H2	AF054174	Homo sapiens histone macroH2A1.2 mRNA, complete cds.	histone macroH2A1.2
943	35303_at	INSIG1	U96876	Homo sapiens insulin induced protein 1 (INSIG1) gene, complete cds.	insulin induced protein 1
944	1038_s_at	interferon-gamma	U19247	Homo sapiens interferon-gamma receptor alpha chain gene, exon 7 and complete cds.	interferon-gamma receptor alpha chain

Fig 21

	A	B	C	D	E
945	895_at	MIF	L19686	Homo sapiens macrophage migration inhibitory factor (MIF) gene, complete cds.	macrophage migration inhibitory factor
946	38967_at	C14orf2; MP68; P	AF054175	Homo sapiens mitochondrial proteolipid 68MP homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds.	mitochondrial proteolipid 68MP homolog
947	31881_at		Y14155	Homo sapiens mRNA for Hmrb33 protein, 3' untranslated region	
948	34677_f_at	tl132	AJ012755	Homo sapiens mRNA for TL132	TL132 protein
949	38786_at		AL079279	Homo sapiens mRNA full length insert cDNA clone EUROMAGE 248114	
950	33418_at		AL096752	Homo sapiens mRNA; cDNA DKFZp434A012 (from clone DKFZp434A012)	
951	38630_at		AL080192	Homo sapiens mRNA; cDNA DKFZp434B102 (from clone DKFZp434B102)	
952	41529_g_at		W72239	Homo sapiens mRNA; cDNA DKFZp434M162 (from clone DKFZp434M162)	
953	36451_at		AI743299	Homo sapiens mRNA; cDNA DKFZp434M245 (from clone DKFZp434M245)	
954	36821_at	DKFZp564A026	AL050367	Homo sapiens mRNA; cDNA DKFZp564A026 (from clone DKFZp564A026)	hypothetical protein
955	37366_at		AL049969	Homo sapiens mRNA; cDNA DKFZp564A072 (from clone DKFZp564A072)	
956	39506_at		AA933984	Homo sapiens mRNA; cDNA DKFZp564B222 (from clone DKFZp564B222)	
957	39748_at		AL050021	Homo sapiens mRNA; cDNA DKFZp564D016 (from clone DKFZp564D016)	

Fig 21

	A	B	C	D	E
958	38357_at		AL049321	Homo sapiens mRNA; cDNA DKFZp564D156 (from clone DKFZp564D156)	
959	33716_at		N95443	Homo sapiens mRNA; cDNA DKFZp564E122 (from clone DKFZp564E122)	
960	35301_at		AL049941	Homo sapiens mRNA; cDNA DKFZp564E2222 (from clone DKFZp564E2222)	
961	35842_at		AL049265	Homo sapiens mRNA; cDNA DKFZp564F053 (from clone DKFZp564F053)	
962	40552_s_at		AL049987	Homo sapiens mRNA; cDNA DKFZp564F112 (from clone DKFZp564F112)	
963	39170_at		AL049957	Homo sapiens mRNA; cDNA DKFZp564J0323 (from clone DKFZp564J0323)	
964	34303_at		AL049949	Homo sapiens mRNA; cDNA DKFZp564L0822 (from clone DKFZp564L0822)	
965	36509_at		AL049998	Homo sapiens mRNA; cDNA DKFZp564L222 (from clone DKFZp564L222)	
966	40353_at		AL049962	Homo sapiens mRNA; cDNA DKFZp564P0823 (from clone DKFZp564P0823)	
967	35290_at		AL050081	Homo sapiens mRNA; cDNA DKFZp566J2146 (from clone DKFZp566J2146)	
968	38079_at		AL049367	Homo sapiens mRNA; cDNA DKFZp586B0918 (from clone DKFZp586B0918)	
969	32195_at		AL049450	Homo sapiens mRNA; cDNA DKFZp586B1922 (from clone DKFZp586B1922)	

Fig 21

	A	B	C	D	E
970	39379_at		AL049397	Homo sapiens mRNA; cDNA DKFZp586C1019 (from clone DKFZp586C1019)	
971	37575_at		AL050192	Homo sapiens mRNA; cDNA DKFZp586C1723 (from clone DKFZp586C1723)	
972	34283_at		AL050125	Homo sapiens mRNA; cDNA DKFZp586F071 (from clone DKFZp586F071)	
973	39600_at		AL080110	Homo sapiens mRNA; cDNA DKFZp586G1922 (from clone DKFZp586G1922)	
974	34752_at		AL080111	Homo sapiens mRNA; cDNA DKFZp586G2222 (from clone DKFZp586G2222)	
975	39103_s_at		H98552	Homo sapiens mRNA; cDNA DKFZp586I0523 (from clone DKFZp586I0523)	
976	36092_at		AL080213	Homo sapiens mRNA; cDNA DKFZp586I1823 (from clone DKFZp586I1823)	
977	35187_at		AL080216	Homo sapiens mRNA; cDNA DKFZp586K1123 (from clone DKFZp586K1123)	
978	35363_at	DDX17	AL080113	Homo sapiens mRNA; cDNA DKFZp586K2322 (from clone DKFZp586K2322)	
979	41013_at		AL080114	Homo sapiens mRNA; cDNA DKFZp586M2022 (from clone DKFZp586M2022)	
980	41690_at		AL049471	Homo sapiens mRNA; cDNA DKFZp586N012 (from clone DKFZp586N012)	
981	40349_at		AL049442	Homo sapiens mRNA; cDNA DKFZp586N1720 (from clone DKFZp586N1720)	

Fig 2.1

	A	B	C	D	E
982	32672_at		AL049387	Homo sapiens mRNA; cDNA DKFZp586N1918 (from clone DKFZp586N1918)	
983	36668_at	DIA1	M28713	Homo sapiens NADH-cytochrome b5 reductase (b5R) gene, exon 9.	NADH-cytochrome b5 reductase
984	38542_at		U89322	Homo sapiens nucleophosmin phosphoprotein (NPM) gene, 3' flanking sequence.	
985	40587_s_at	EEF1E1; P18	AF054186	Homo sapiens p18 protein mRNA, complete cds.	p18 protein
986	41448_at	HOXA4	AC004080	Homo sapiens PAC clone RP1-170O19 from 7p15-p21, complete sequence.	even-skipped homeo box 1 (homolog of Drosophila)
987	36159_s_at	PrP	U29185	Homo sapiens prion protein (PrP) gene, complete cds.	prion protein
988	32756_at	ECH1	AF030249	Homo sapiens putative dienoyl-CoA isomerase (ECH1) gene, exons 7-10, and complete cds.	putative dienoyl-CoA isomerase
989	35824_at	RP58	AJ223321	Homo sapiens RP58 gene, complete CDS.	RP58 protein
990	39169_at	SEC61G	AF054184	Homo sapiens Sec61 gamma mRNA, complete cds.	Sec61 gamma
991	41222_at	STAT6	AF067575	Homo sapiens signal transducer and activator of transcription 6 (STAT6) gene, exons 15 through 23 and complete cds.	signal transducer and activator of transcription 6
992	38817_at	SPAG7; ACRP; F3	AF047437	Homo sapiens sperm acrosomal protein mRNA, complete cds.	sperm acrosomal protein
993	36033_at		AL049309	Homo sapiens splicing factor, arginine/serine-rich 12 (SFRS12) mRNA, complete cds	
994	31481_s_at	TMSB10	M92383	Homo sapiens thymosin beta-10 gene, 3'end.	thymosin beta-10
995	1693_s_at	TIMP	D11139	Homo sapiens TIMP gene for tissue inhibitor of metalloproteinases, partial cds.	tissue inhibitor of metalloproteinases

Fig 21

A	B	C	D	E
996 37311_at	TALDO1; TAL-H;	AF010400	Homo sapiens transaldolase-related protein gene, exons 3-8 and complete cds.	transaldolase-related protein
997 32229_at	EIF4EL3; 4EHP; 4	AF038957	Homo sapiens translation initiation factor 4e mRNA, complete cds.	translation initiation factor 4e
998 1323_at	UBB	X04803	Homo sapiens ubiquitin gene.	ubiquitin
999 32153_s_at	UBB	U49869	Homo sapiens ubiquitin gene.	ubiquitin
1000 38372_at		U66042	Homo sapiens unknown mRNA	
1001 38814_at	ATP6V1G1; ATP6	AF038954	Homo sapiens vacuolar H(+)-ATPase subunit mRNA, complete cds.	vacuolar H(+)-ATPase subunit
1002 41597_s_at	SEC22L1; SEC22	AF047442	Homo sapiens vesicle trafficking protein sec22b mRNA, complete cds.	vesicle trafficking protein sec22b
1003 34957_at	X5L	Y18504	Homo sapiens X5L gene.	XAP-5-like protein
1004 38662_at		AL047596	Homo sapiens, clone IMAGE:3028427, mRNA, partial cds	
1005 38312_at		AL050002	Homo sapiens, clone IMAGE:3140802, mRNA	
1006 33388_at		AL080223	Homo sapiens, clone IMAGE:3855224, mRNA, partial cds	
1007 38676_at		AA059408	Homo sapiens, clone IMAGE:4132509, mRNA	
1008 40238_at		AI674208	Homo sapiens, clone IMAGE:4150198, mRNA, partial cds	
1009 32119_at		AL049423	Homo sapiens, clone IMAGE:4182947, mRNA	
1010 38650_at	IGFBP5	L27560	Homo sapiens, clone IMAGE:4183312, mRNA, partial cds	
1011 1396_at	IGFBP5	L27560	Homo sapiens, clone IMAGE:4183312, mRNA, partial cds	
1012 40432_at		AA522891	Homo sapiens, clone IMAGE:4391536, mRNA	
1013 36130_f_at	MT1E	R92331	Homo sapiens, Similar to RNA helicase-related protein, clone MGC:9246 IMAGE:3892441, mRNA, complete cds	

Fig 21

A	B	C	D	E
1014 41246_at		A1743134	Homo sapiens, Similar to serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2, clone MGC:23129 IMAGE:4578406, mRNA, complete cds	
1015 41533_at		U79298	Homo sapiens, similar to unknown, clone MGC:39325 IMAGE:5440447, mRNA, complete cds	
1016 39733_at	HERPUD1	AF055001	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1
1017 525_g_at	hPMS1	U13695	homolog of yeast mutL gene; Human homolog of yeast mutL (hPMS1) gene, complete cds.	postmeiotic segregation 1
1018 32545_r_at	RSU-1	L12535	homologous to mouse Rsu-1; putative; Human RSU-1/RSP-1 mRNA, complete cds.	ras suppressor protein 1
1019 32544_s_at	RSU-1	L12535	homologous to mouse Rsu-1; putative; Human RSU-1/RSP-1 mRNA, complete cds.	ras suppressor protein 1
1020 39800_s_at	HAX1	U68566	HAX1 binding protein	HAX-1
1021 38104_at	DECR1; NADPH	U78302	Human 2,4-dienoyl-CoA reductase gene, exon 10 and complete cds.	2,4-dienoyl-CoA reductase
1022 37708_r_at	ADH5	M81118	Human alcohol dehydrogenase chi polypeptide (ADH5) gene exons 8-9, complete cds.	alcohol dehydrogenase
1023 37707_i_at	ADH5	M81118	Human alcohol dehydrogenase chi polypeptide (ADH5) gene exons 8-9, complete cds.	alcohol dehydrogenase
1024 39333_at	COL4A1	M26576	Human alpha-1 collagen type IV gene, exon 52.	alpha-1 type IV collagen
1025 38417_at	AMPD2	M91029	Human AMP deaminase (AMPD2) mRNA.	AMP deaminase isoform L splicing variant
1026 37747_at	ANX5	U05770	Human annexin V (ANX5) gene, exon 13.	annexin V

Fig 21



	A	B	C	D	E
1027	41143_at	CALM1	U12022	Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds.	calmodulin
1028	239_at	CTSD	M63138	Human cathepsin D (catD) gene, exons 7, 8, and 9.	cathepsin D
1029	1916_s_at	c-fos	V01512	Human cellular oncogene c-fos (complete sequence).	v-fos FBJ murine osteosarcoma viral oncogene homolog
1030	1915_s_at	c-fos	V01512	Human cellular oncogene c-fos (complete sequence).	v-fos FBJ murine osteosarcoma viral oncogene homolog
1031	32583_at	JUN	J04111	Human c-jun proto oncogene (JUN), complete cds, clone hCJ-1.	v-jun avian sarcoma virus 17 oncogene homolog
1032	1895_at	JUN	J04111	Human c-jun proto oncogene (JUN), complete cds, clone hCJ-1.	v-jun avian sarcoma virus 17 oncogene homolog
1033	41604_at		U79297	Human clone 23589 mRNA sequence	
1034	32185_at		U00946	Human clone A9A2BRB5 (CAC)n/(GTG)n repeat-containing mRNA	
1035	33667_at	PPIA	X52851	Human cyclophilin gene for cyclophilin (EC 5.2.1.8).	peptidylprolyl isomerase
1036	38459_g_at	CYB5	L39945	Human cytochrome b5 (CYB5) gene, exon 6 and complete cds.	cytochrome b5
1037	38458_at	CYB5	L39945	Human cytochrome b5 (CYB5) gene, exon 6 and complete cds.	cytochrome b5
1038	36163_at	DLD; E3; LAD; DL	L13761	Human dihydrolipoamide dehydrogenase gene, exon 14.	dihydrolipoamide dehydrogenase
1039	1424_s_at	YWHAH; YWHA1	D78577	Human DNA for 14-3-3 protein eta chain, exon2 and complete cds.	14-3-3 protein eta chain
1040	31797_at	dJ73H22.1	AL035699	Human DNA sequence from clone 73H22 on chromosome 6q23, complete sequence.	dJ73H22.1 (TBP-like protein)
1041	40193_at	ENO2	X51956	Human ENO2 gene for neuron specific (gamma) enolase.	human gamma enolase
1042	38326_at	G0S2	M69199	Human G0S2 protein gene, complete cds.	G0S2 protein
1043	40567_at	TUBA3; FLJ25113	X01703	Human gene for alpha-tubulin (b alpha 1).	alpha-tubulin

Fig 21

	A	B	C	D	E
1044	39775_at	SERPINC1; C1IN; X54486		Human gene for C1-inhibitor.	C1 inhibitor
1045	40862_i_at	CKB; CKBB	X15334	Human gene for creatine kinase B (EC 2.7.3.2).	creatine kinase B
1046	37641_at	IFI44; p44; MTAP	D28915	Human gene for hepatitis C-associated microtubular aggregate protein p44, exon 9 and complete cds.	hepatitis C-associated microtubular aggregate protein p44
1047	40211_at	HNRPA1; HNRNPX	X12871	Human gene for heterogeneous nuclear ribonucleoprotein (hnRNP) core protein A1.	hnrp a1 protein
1048	408_at	MGSA	X54489	Human gene for melanoma growth stimulatory activity (MGSA).	melanoma growth stimulatory activity preprotein
1049	36203_at	ODC1	X16277	Human gene for ornithine decarboxylase ODC (EC 4.1.1.17).	ornithine decarboxylase (ODC)
1050	36873_at	VLDLR	D16532	Human gene for very low density lipoprotein receptor, exon 19.	very low density lipoprotein receptor
1051	34759_at		U68494	Human hbc647 mRNA sequence	
1052	32805_at	AKR1C1; DD1; D0	U05861	Human hepatic dihydrodiol dehydrogenase gene, exon 9.	hepatic dihydrodiol dehydrogenase
1053	41231_f_at	HMG17; MGC562	X13546	Human HMG-17 gene for non-histone chromosomal protein HMG-17.	put. HMG-17 protein
1054	38294_at	HOXD4; HOX4; H	X17360	Human HOX 5.1 gene for HOX 5.1 protein.	hox 5.1 protein
1055	40637_at	HSP73 HSC70 HS	Y00371	Human hsc70 gene for 71 kd heat shock cognate protein.	71 Kd heat shock cognate protein
1056	232_at	LAMB2	M55210	Human laminin B2 chain gene, exon 28.	laminin B2 chain
1057	40767_at	TFPI	M59499	Human lipoprotein-associated coagulation inhibitor (LACI) gene, exon 9 and complete cds.	lipoprotein-associated coagulation inhibitor
1058	38637_at	LOX	L16895	Human lysyl oxidase (LOX) gene, exon 7.	lysyl oxidase
1059	37532_at	MCAD	M91432	Human medium-chain acyl-CoA dehydrogenase (MCAD) gene, exon 12.	medium-chain acyl-CoA dehydrogenase
1060	870_f_at	MT3; GIF; GIB	M93311	Human metallothionein-III gene, complete cds.	metallothionein-III

Fig 21

A	B	C	D	E
1061 40890_at	MTX	U46920	Human metaxin (MTX) gene, complete cds.	metaxin
1062 32145_at	ADD1	X58141	Human mRNA for erythrocyte adducin alpha subunit.	erythrocyte alpha adducin
1063 37381_g_at	TF2B	X59268	Human mRNA for general transcription factor IIB.	IIB protein
1064 33683_at	TI-227H	D50525	Human mRNA for TI-227H.	
1065 41747_s_at	MEF2A	U49020	Human myocyte-specific enhancer factor 2A (MEF2A) gene, last coding exon, and complete cds.	myocyte-specific enhancer factor 2A, C9 form; myocyte-specific enhancer factor 2A, C4 form
1066 38066_at	NQO1	M81600	Human NAD(P)H:quinone oxidoreductase gene, exon 6.	NAD(P)H:quinone oxidoreductase
1067 39729_at	NKEFB	L19185	Human natural killer cell enhancing factor (NKEFB) mRNA, complete cds.	enhancer protein
1068 33994_g_at	MLC	M22919	Human nonmuscle/smooth muscle alkali myosin light chain gene, complete cds.	non-muscle myosin light chain; smooth muscle myosin light chain
1069 32841_at	ZNF9; DM2; CNB1	U19765	Human nucleic acid binding protein gene, complete cds.	nucleic acid binding protein
1070 32590_at	NCL	M60858	Human nucleolin gene, complete cds.	nucleolin
1071 1782_s_at	Op18	M31303	Human oncoprotein 18 (Op18) gene, complete cds.	oncoprotein 18
1072 216_at	PTGDS	M98539	Human prostaglandin D2 synthase gene, exon 7.	prostaglandin D2 synthase (21kD, brain)
1073 237_s_at	PPP2CA	M60483	Human protein phosphatase 2A catalytic subunit-alpha gene, complete cds.	protein phosphatase-2A catalytic subunit-alpha
1074 812_at	PPP1R2	U68111	Human protein phosphatase inhibitor 2 (PPP1R2) gene, exon 6 and complete cds.	protein phosphatase inhibitor 2
1075 33180_at	PPP1R2	U68111	Human protein phosphatase inhibitor 2 (PPP1R2) gene, exon 6 and complete cds.	protein phosphatase inhibitor 2
1076 35356_at		W21884	Human putative ribosomal protein S1 mRNA	

Fig 21

	A	B	C	D	E
1077	491_at	PTPRG	U46116	Human receptor tyrosine phosphatase gamma (PTPRG) gene, exon 30 and complete cds.	receptor tyrosine phosphatase gamma
1078	492_g_at	PTPRG	U46116	Human receptor tyrosine phosphatase gamma (PTPRG) gene, exon 30 and complete cds.	receptor tyrosine phosphatase gamma
1079	36611_at	ACP1	U25849	Human red cell-type low molecular weight acid phosphatase (ACP1) gene, exon 6 and 7, complete cds.	red cell-type low molecular weight acid phosphatase
1080	174_s_at	SH3P18	U61167	Human SH3 domain-containing protein SH3P18 mRNA, complete cds	SH3 domain-containing protein SH3P18
1081	241_g_at	SRM	M64231	Human spermidine synthase gene, complete cds.	spermidine synthase
1082	36688_at	SCP-X/SCP-2	U11313	Human sterol carrier protein-X/sterol carrier protein-2 (SCP-X/SCP-2) gene, exon 16, and complete cds.	sterol carrier protein-X/sterol carrier protein-2
1083	32587_at	ZFP36L2; BRF2	U07802	Human Tis11d gene, complete cds.	Tis11d
1084	31680_at	TOP1P2	M55630	Human topoisomerase I pseudogene 2. Human transformation-related protein mRNA, 3' end	transformation-related protein
1085	36446_s_at	HMG1L2	L24521	Human transmembrane protein (CD59) gene, exon 4.	CD59 protein
1086	39351_at	CD59	M84349	Human transposon-like element mRNA	
1087	38727_at	THE1	M23161	Human vascular cell adhesion molecule-1 (VCAM1) gene, complete CDS.	vascular cell adhesion molecule-1
1088	41433_at	VCAM1	M73255	huntingtin interacting protein 2	huntingtin interacting protein
1089	40121_at	HIP2	U58522	Huntingtin interacting protein H	KIAA0946 protein
1090	35973_at	HYPH	AB023163	HYA22 protein	HYA22
1091	40196_at	HYA22	D88153	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase alpha-subunit of trifunctional protein
1092	36952_at	HADHA	D16480		

Fig 21

A	B	C	D	E
1093/39741_at	HADHB	D16481	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	3-ketoacyl-CoA thiolase beta-subunit of trifunctional protein
1094/36626_at	HSD17B4	X87176	hydroxysteroid (17-beta) dehydrogenase 4	17beta-hydroxysteroid dehydrogenase
1095/41583_at	FEN1	AC004770	<p>Hypothetical protein of unknown function; Hypothetical 52 kDa protein; Hypothetical protein exhibits similarity to motifs found in (U79010) delta 6 desaturase, a hypothetical cytochrome b5 containing fusion protein, and hypothetical proteins encoded by (Z81122) T13F2.1 [Caenorhabditis elegans] and (Z70271) W08D2.4 [Caenorhabditis elegans]; DNA structure-specific endonuclease FEN1; FLAP ENDONUCLEASE-1; MATURATION FACTOR 1 (MF1); DNase IV; RAD2_HUMAN; Hypothetical human Best's macular dystrophy related protein; Simulated translation extends ORF of previously reported partial coding sequence for Best's macular dystrophy related protein (AF038536); Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.</p>	BC269730_1; BC269730_2; FEN1_HUMAN; BC269730_4

Fig 21

	A	B	C	D	E
				Hypothetical protein of unknown function; Hypothetical 52 kDa protein; Hypothetical protein exhibits similarity to motifs found in (U79010) delta 6 desaturase, a hypothetical cytochrome b5 containing fusion protein, and hypothetical proteins encoded by (Z81122) T13F2.1. [Caenorhabditis elegans] and (Z70271) W08D2.4 [Caenorhabditis elegans]; DNA structure-specific endonuclease FEN1; FLAP ENDONUCLEASE-1; MATURATION FACTOR 1 (MF1); DNase IV; RAD2_HUMAN; Hypothetical human Best's macular dystrophy related protein; Simulated translation extends ORF of previously reported partial coding sequence for Best's macular dystrophy related protein (AF038536); Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.	BC269730_1; BC269730_2; FEN1_HUMAN; BC269730_4
1096	34224_at	FEN1	AC004770		hypothetical protein CG018
1097	1527_s_at	CG018	U50527	hypothetical gene CG018	hypothetical protein AF038182
1098	33466_at	LOC90355	AF038182	AF038182; BC009203	

Fig 21

A	B	C	D	E
			<p>Hypothetical human protein (partial CDS); CDS constructed from combination of BLASTX, EST matches and Xgrail predictions. N-terminus of protein likely encoded in flanking cosmid R29942. Predicted protein exhibits weak similarity to hypothetical protein PID161226191 (AL021106) from <i>Drosophila melanogaster</i>; Hypothetical human protein most similar to Rat ionotropic glutamate receptor (L34938); CDS constructed primarily from XGRail predictions and BLASTX similarity to (L34938) ionotropic glutamate receptor [Rattus norvegicus] and gil2160125 (U29873) NMDAR-L [Rattus norvegicus]. Also exhibits similarity to PID16258718 (Z78413) T01C3.10 [Caenorhabditis elegans]. C-terminus of hypothetical protein is ill-defined at this point; definition will require identification and characterization of appropriate cDNAs; Hypothetical 59.8 kDa human protein; CDS constructed from EST matches and Xgrail predictions. C-terminus of predicted protein not fully confirmed by EST or cDNA coverage. Hypothetical protein exhibits no significant database similarities when queried against</p>	R32184_1; R32184_2; R32184_3
1099 35983_at	MGC2436	AC004528	hypothetical protein	hypothetical protein, similar to (AC007017) putative RNA helicase A [Arabidopsis thaliana]
1100 38440_s_at	FLJ20811	AA015605		
1101 39140_at	LOC54505	AL079292	hypothetical protein	
1102 37819_at	LOC54104	AF007130	hypothetical protein	
1103 39517_at	LOC56007	AF035313	hypothetical protein 23851	
1104 41561_s_at	LOC55977	A1651368	hypothetical protein 24636	

Fig 21

	A	B	C	D	E
1105	41128_at	LOC92703	AF070537	hypothetical protein BC013073	
1106	38972_at	LOC115207	AF052169	hypothetical protein BC013764	
1107	34864_at	CGI-57	AF070538	hypothetical protein CGI-57	hypothetical protein CGI-57
1108	39960_at	CL640	AF091086	hypothetical protein CL640	hypothetical protein CL640
1109	38837_at	DJ971N18.2	W26226	hypothetical protein DJ971N18.2	
1110	35142_at	DKFZP564D172	AF070617	hypothetical protein DKFZp564D172	
1111	34830_at	DKFZP564K0822	W25986	hypothetical protein DKFZp564K0822	
1112	31852_at	DKFZP564O043	AL050390	hypothetical protein DKFZp564O043	
1113	33895_at	DKFZP586F1318	AL050373	hypothetical protein DKFZP586F1318	hypothetical protein
1114	39692_at	DKFZP586F2423	AL080209	hypothetical protein DKFZp586F2423	
1115	35682_at	FLB6421	AI133727	hypothetical protein FLB6421	
1116	36647_at	FLJ10326	AA526812	hypothetical protein FLJ10326	
1117	34804_at	FLJ10618	AL049246	hypothetical protein FLJ10618	
1118	36840_at	FLJ10737	AF052158	hypothetical protein FLJ10737	
1119	35283_at	FLJ10738	H05692	hypothetical protein FLJ10738	
1120	37610_at	FLJ10803	AI765280	hypothetical protein FLJ10803	
1121	33173_g_at	FLJ10849	T75292	hypothetical protein FLJ10849	
1122	39923_at	FLJ10971	AI935420	hypothetical protein FLJ10971	
1123	38105_at	FLJ11021	W26521	hypothetical protein FLJ11021 similar to splicing factor, arginine/serine-rich 4	
1124	33394_at	FLJ11126	AA034074	hypothetical protein FLJ11126	
1125	35709_at	FLJ11149	AF038172	hypothetical protein FLJ11149	
1126	38141_at	FLJ11193	AF038176	hypothetical protein FLJ11193	
1127	40859_at	FLJ11806	AI561196	hypothetical protein FLJ11806	
1128	41177_at	FLJ12443	AW024285	hypothetical protein FLJ12443	
1129	41434_at	FLJ12552	AF070557	hypothetical protein FLJ12552	hypothetical protein FLJ12552
1130	36580_at	FLJ13910	AL050139	hypothetical protein FLJ13910	hypothetical protein FLJ13910
1131	32222_at	FLJ14639	AA152202	hypothetical protein FLJ14639	
1132	38710_at	FLJ20113	AL096714	hypothetical protein FLJ20113	
1133	38652_at	FLJ20154	AF070644	hypothetical protein FLJ20154	
1134	40868_at	FLJ20274	AA442799	hypothetical protein FLJ20274	
1135	34739_at	FLJ20275	W26023	hypothetical protein FLJ20275	
1136	34857_at	FLJ20986	Z24724	hypothetical protein FLJ20986	
1137	32251_at	FLJ21174	AA149307	hypothetical protein FLJ21174	
1138	40615_at	FLJ21439	AA780049	hypothetical protein FLJ21439	
1139	33915_at	FLJ23027	W22655	hypothetical protein FLJ23027	

Fig 21



	A	B	C	D	E
1140	35198_at	LOC57146	AF070596	hypothetical protein from clone 24796	hypothetical protein from clone 24796
1141	38483_at	HSA011916	AJ011916	hypothetical protein HSA011916	hypothetical protein
1142	41236_at	HSU79252	U79252	hypothetical protein HSU79252	hypothetical protein HSU79252
1143	38443_at	MGC14433	U79291	hypothetical protein MGC14433	
1144	39811_at	MGC2749	AA02538	hypothetical protein MGC2749	
1145	32051_at	MGC2840	AJ224875	hypothetical protein MGC2840 similar to a putative glucosyltransferase	glucosyltransferase
1146	35219_at	MGC3047	AL050202	hypothetical protein MGC3047	
1147	41696_at	MGC3077	AI620381	hypothetical protein MGC3077	
1148	41147_at	MGC4276	AF038186	hypothetical protein MGC4276 similar to CG8198	hypothetical protein MGC4276 similar to CG8198
1149	37242_at	MGC5149	U79260	hypothetical protein MGC5149	
1150	36975_at	MGC8721	W26659	hypothetical protein MGC8721	
1151	35677_at	MGC9084	AL035369	hypothetical protein MGC9084	hypothetical protein
1152	32504_at	MY014	AW024812	hypothetical protein My014	
1153	38106_at	YR-29	AJ012409	hypothetical protein YR-29	hypothetical protein
1154	37640_at	HPRT1	M31642	hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)	hypoxanthine phosphoribosyltransferase 1
1155	1039_s_at	HIF1A	U22431	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	hypoxia-inducible factor 1 alpha
1156	39781_at	IGFBP4	U20982	IGF binding protein-4; Human insulin-like growth factor binding protein-4 (IGFBP4) gene, promoter and complete cds.	insulin-like growth factor binding protein-4
1157	38046_at	IK	AJ005579	IK cytokine, down-regulator of HLA II	Prer protein
1158	218_at	IK	S74221	IK cytokine, down-regulator of HLA II	IK factor
1159	37690_at	ILVBL	U61263	ilvB (bacterial acetolactate synthase)-like immediate early protein	acetolactate synthase homolog immediate early protein
1160	36097_at	ETR101	M62831		
1161	1237_at	IER3	S81914	immediate early response 3	immediate early response 3, isoform short; immediate early response 3, isoform long
1162	34391_at	IGBP1	Y08915	immunoglobulin (CD79A) binding protein 1 alpha 4 protein	

Fig 21

A	B	C	D	E
1163 38636_at	ISLR	AB003184	immunoglobulin superfamily containing leucine-rich repeat	ISLR
1164 40695_at	IMPDH1	J05272	IMP (inosine monophosphate)	IMP (inosine monophosphate)
1165 36875_at	IBTK	AL050018	dehydrogenase 1	dehydrogenase 1
1166 36617_at	ID1	X77956	inhibitor of Bruton's tyrosine kinase	hypothetical protein
1167 41215_s_at	ID2	D13891	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein
			inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	
			inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein	Id-2H
1168 34344_at	IKBKAP	AF044195	inner membrane protein, mitochondrial (mitofilin)	IkappaB kinase complex associated protein
1169 37659_at	IMMT	L42572		transmembrane protein
1170 755_at	ITPR1	D26070	inositol 1,4,5-trisphosphate receptor, type 1	human type 1 inositol 1,4,5-trisphosphate receptor
1171 32778_at	ITPR1	D26070	inositol 1,4,5-trisphosphate receptor, type 1	human type 1 inositol 1,4,5-trisphosphate receptor
1172 36154_at	IHPK1	D87452	inositol hexaphosphate kinase 1	KIAA0263 protein
1173 32697_at	IMPA1	AF042729	inositol(myo)-1(or 4)-monophosphatase 1	lithium-sensitive myo-inositol monophosphatase A1
1174 36496_at	IMPA2	AF014398	inositol(myo)-1(or 4)-monophosphatase 2	myo-inositol monophosphatase 2
1175 35833_at	LOC51141	AL080184	insulin induced protein 2	
1176 41049_at	IRS1	S62539	insulin receptor substrate 1	insulin receptor substrate-1
1177 851_s_at	IRS1	S62539	insulin receptor substrate 1	insulin receptor substrate-1
1178 38737_at	IGF1	X57025	insulin-like growth factor 1 (somatomedin C)	insulin-like growth factor I
1179 1501_at	IGF1	X57025	insulin-like growth factor 1 (somatomedin C)	insulin-like growth factor I
1180 160027_s_at	IGF2R	Y00285	insulin-like growth factor 2 receptor	insulin-like growth factor 2 receptor
1181 40422_at	IGFBP2	X16302	insulin-like growth factor binding protein 2 (36kD)	insulin-like growth factor binding protein 2 (36kD)
1182 1737_s_at	IGFBP4	M62403	insulin-like growth factor binding protein 4	insulin-like growth factor binding protein 4

Fig 21

A	B	C	D	E
1183 2062_at	IGFBP7	L19182	insulin-like growth factor binding protein 7	
1184 37991_at	ITM1	L38961	integral membrane protein 1	integral membrane protein 1
1185 37326_at	A4	U93305	integral membrane protein; swiss-prot accession: O04901; may play role in cell differentiation in intestinal epithelium	LIM domain only 6
1186 41163_at	P24B	AL109672	integral type I protein	p24B protein
1187 32808_at	ITGB1; CD29; FN1	X07979	integrin beta 1 subunit precursor; Human mRNA for integrin beta 1 subunit.	integrin beta 1 isoform 1A precursor; integrin beta 1 isoform 1B precursor; integrin beta 1 isoform 1C-1 precursor; integrin beta 1 isoform 1D precursor
1188 1195_s_at	ICAP-1A	AF012024	integrin cytoplasmic domain-associated protein 1	1C-2 precursor
1189 120_at	ITGA1	X68742	integrin, alpha 1	integrin cytoplasmic domain associated protein
1190 37484_at	ITGA1	X68742	integrin, alpha 1	
1191 36892_at	ITGA7	AF032108	integrin, alpha 7	
1192 39071_at	ITGAV	M14648	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)	integrin alpha-7
1193 39754_at	ITGB5	X53002	integrin, beta 5	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)
1194 2058_s_at	ITGB5	M35011	integrin, beta 5	
1195 40681_at	ITGBL1	AB008375	integrin, beta-like 1 (with EGF-like repeat domains)	integrin, beta 5
1196 35365_at	ILK	U40282	integrin-linked kinase	osteoblast specific cysteine-rich protein
1197 41743_i_at	OPTN; NRP; FIP2	AF061034	interacts with adenovirus E3-14.7KDa, a TNF-alpha cytolysis antagonist; leucine zipper protein; alternatively translated; long form; interacts with adenovirus E3-14.7KDa, a TNF-alpha cytolysis antagonist; leucine zipper protein; alternatively translated; short form; Homo sapiens FIP2 alternatively translated mRNA, complete cds.	integrin-linked kinase
				FIP2

Fig 21

A	B	C	D	E
			interacts with adenovirus E3-14.7KDa, a TNF-alpha cytolysis antagonist; leucine zipper protein; alternatively translated; long form; interacts with adenovirus E3-14.7KDa, a TNF-alpha cytolysis antagonist; leucine zipper protein; alternatively translated; short form; Homo sapiens FIP2 alternatively translated mRNA, complete cds.	FIP2
1198 41742_s_at	OPTN; NRP; FIP2AF061034		interferon induced transmembrane protein 1 (9-27)	interferon induced transmembrane protein 1 (9-27)
1199 676_g_at	IFITM1	J04164	interferon induced transmembrane protein 1 (9-27)	interferon induced transmembrane protein 1 (9-27)
1200 675_at	IFITM1	J04164	interferon induced transmembrane protein 3 (1-8U)	interferon-induced protein with tetra-tricopeptide repeats 1
1201 41745_at	IFITM3	X57352	interferon, gamma-inducible protein 16	interferon-gamma induced protein
1202 1456_s_at	IFI16	M63838	interferon, gamma-inducible protein 30	interferon, gamma-inducible protein 30
1203 925_at	IFI30	J03909	interferon, gamma-inducible protein 30	interferon, gamma-inducible protein 30
1204 39728_at	IFI30	J03909	interferon-induced protein with tetra-tricopeptide repeats 1	interferon-induced protein with tetra-tricopeptide repeats 1
1205 32814_at	IFIT1	M24594	interferon-related developmental regulator 1	PC4 protein
1206 37679_at	IFRD1	Y10313	interleukin 1 receptor, type I	interleukin 1 receptor, type I
1207 1368_at	IL1R1	M27492	interleukin 10 receptor, beta	
1208 33228_g_at	IL10RB	A1984234	interleukin 10 receptor, beta	
1209 33227_at	IL10RB	A1984234	interleukin 27	
1210 38969_at	IL27	A1828168	interleukin 6 (interferon, beta 2)	interleukin 6 (interferon, beta 2)
1211 38299_at	IL6	X04430	interleukin 8	interleukin 8
1212 35372_r_at	IL8	M17017	interleukin enhancer binding factor 2, 45kD	NF45 protein
1213 36189_at	ILF2	U10323	intermediate filament-like MGC:2625	hypothetical protein
1214 36030_at	DKFZP586I2223	AL080214	intersectin 1 (SH3 domain protein)	intersectin short form
1215 35776_at	ITSN1	AF064243	intestinal cell kinase	KIAA0936 protein
1216 41431_at	ICK	AB023153	IQ motif containing GTPase activating protein 1	ras GTPase-activating-like protein
1217 1825_at	IQGAP1	L33075		

Fig 21

	A	B	C	D	E
1218	39023_at	IDH1	AF020038	isocitrate dehydrogenase 1 (NADP+), soluble	NADP-dependent isocitrate dehydrogenase
1219	40112_at	IDH3B	AA522698	isocitrate dehydrogenase 3 (NAD+) beta	NAD+-specific isocitrate dehydrogenase
1220	40111_g_at	IDH3B	U49283	isocitrate dehydrogenase 3 (NAD+) beta	beta precursor
1221	40478_at	KIAA1162	AL021396	isoform 1 match: proteins: Tr:Q9UJA1	hypothetical protein
1222	32695_at	dJ196E23.1	Z97832	isoform 2 match: protein Q99991	bombesin-like receptor 3
1223	40827_at	IARS	U04953	isoleucine-tRNA synthetase	isoleucyl-tRNA synthetase
1224	36985_at	IDI1	X17025	isopentenyl-diphosphate delta isomerase	isopentenyl-diphosphate delta isomerase
1225	41775_at	ICMT	AF084084	isoprenylcysteine carboxyl methyltransferase	prenylcysteine carboxyl methyltransferase
1226	34877_at	JAK1	AL039831	Janus kinase 1 (a protein tyrosine kinase)	
1227	34318_at	JM4	AJ005896	JM4 protein	JM4 protein
1228	40957_at	JJAZ1	D63881	joined to JAZF1	joined to JAZF1
1229	41250_at	JTV1	U24169	JTV1 gene	JTV-1
1230	41483_s_at	JUND	X56681	jun D proto-oncogene	junD protein
1231	1612_s_at	JUND	X56681	jun D proto-oncogene	junD protein
1232	40464_g_at	KPNB2	U70322	karyopherin (importin) beta 2	transportin
1233	39028_at	KPNB3	Y08890	karyopherin (importin) beta 3	Ran_GTP binding protein 5
1234	35725_at	KPNA3	D89618	karyopherin alpha 3 (importin alpha 4)	karyopherin alhph 3
1235	32487_s_at	KPNA4	AB002533	karyopherin alpha 4 (importin alpha 3)	Qip1
1236	32708_g_at	KATNA1	AI191768	katanin p60 (ATPase-containing) subunit A 1	
1237	37386_i_at	KDELR1	X55885	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1	KDEL receptor
1238	39080_at	KDELR2	M88458	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	KDEL receptor 2
1239	33402_at	KDELR3	AL035081	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	hypothetical protein
1240	37150_at	AB026190	AB026190	kelch motif containing protein	Kelch motif containing protein
1241	32329_at	KRTHB6	X99142	keratin, hair, basic, 6 (monilethrx)	type II intermediate filament of hair keratin
1242	39346_at	KHDRBS1	M88108	KH domain containing, RNA binding, signal transduction associated 1	p62

Fig 21

A	B	C	D	E
1243 32679_at	KIAA0009	D13634	KIAA0009 gene product	KIAA0009 gene product
1244 34760_at	KIAA0022	D14664	KIAA0022 gene product	KIAA0022 gene product
1245 41129_at	KIAA0033	D26067	KIAA0033 protein	
1246 38797_at	KIAA0062	D31887	KIAA0062 protein	
1247 36978_at	KIAA0077	D38521	KIAA0077 protein	
1248 37718_at	KIAA0096	D43636	KIAA0096 protein	
1249 37293_at	KIAA0097	D43948	KIAA0097 gene product	KIAA0097 protein
			KIAA0098 is a human counterpart of mouse chaperonin containing TCP-1 gene. Start codon is not identified. ha01413 cDNA clone for KIAA0098 has a 2-bp insertion between 736-737 of the sequence of KIAA0098.; Homo sapiens mRNA for KIAA0098 protein, partial cds.	
1250 40417_at	KIAA0098	D43950		KIAA0098 protein
1251 39783_at	KIAA0100	D43947	KIAA0100 gene product	KIAA0100 protein
1252 37359_at	KIAA0102	D14658	KIAA0102 gene product	KIAA0102 gene product
1253 38031_at	KIAA0111	D21853	KIAA0111 gene product	KIAA0111 gene product
1254 40279_at	KIAA0121	D50911	KIAA0121 gene product	KIAA0121 protein
1255 36845_at	KIAA0136	D50926	KIAA0136 protein	
1256 32099_at	KIAA0138	D50928	KIAA0138 gene product	KIAA0138 gene product
1257 38472_at	KIAA0143	D63477	KIAA0143 protein	
1258 41728_at	KIAA0152	D63486	KIAA0152 gene product	KIAA0152 gene product
1259 37642_at	KIAA0157	D63877	KIAA0157 protein	KIAA0157 protein
1260 32661_s_at	KIAA0170	D79992	KIAA0170 gene product	KIAA0170 gene product
1261 37225_at	KIAA0172	D79994	KIAA0172 protein	
1262 36942_at	KIAA0174	D79996	KIAA0174 gene product	KIAA0174 gene product
1263 31863_at	KIAA0179	D80001	KIAA0179 protein	
1264 37734_at	KIAA0184	D80006	KIAA0184 protein	
1265 41669_at	KIAA0191	D83776	KIAA0191 protein	
1266 36192_at	KIAA0193	D83777	KIAA0193 gene product	KIAA0193 gene product
1267 38056_at	KIAA0195	D83779	KIAA0195 gene product	KIAA0195 gene product
1268 38419_at	KIAA0196	D83780	KIAA0196 gene product	KIAA0196 gene product
1269 38067_at	KIAA0202	D86957	KIAA0202 protein	
1270 32586_at	KIAA0217	D86971	KIAA0217 protein	
1271 38728_at	KIAA0225	D86978	KIAA0225 protein	

Fig 21

A	B	C	D	E
1272 40971_at	KIAA0229	D86982	KIAA0229 protein	
1273 37748_at	KIAA0232	D86985	KIAA0232 gene product	KIAA0232 protein
1274 38892_at	KIAA0240	D87077	KIAA0240 protein	
1275 40765_at	KIAA0251	D87438	KIAA0251 protein	
1276 41634_at	KIAA0256	D87445	KIAA0256 gene product	KIAA0256 protein
1277 36971_at	KIAA0257	D87446	KIAA0257 protein	
1278 32237_at	KIAA0265	D87454	KIAA0265 protein	
1279 39405_at	KIAA0266	D87455	KIAA0266 gene product	KIAA0266 gene product
1280 35039_at	KIAA0276	D87466	KIAA0276 protein	
1281 38592_s_at	KIAA0284	A1928210	KIAA0284 protein	
1282 41381_at	KIAA0308	AB002306	KIAA0308 protein	
1283 37943_at	KIAA0321	AB002319	KIAA0321 protein	
1284 32592_at	KIAA0323	AB002321	KIAA0323 protein	
1285 39797_at	KIAA0349	AB002347	KIAA0349 protein	
1286 34661_at	KIAA0350	AB002348	KIAA0350 protein	KIAA0350 protein
1287 32208_at	KIAA0355	AB002353	KIAA0355 gene product	KIAA0355 gene product
1288 32223_at	KIAA0365	AB002363	KIAA0365 gene product	
1289 33442_at	KIAA0367	AB002365	KIAA0367 protein	
1290 35830_at	KIAA0370	AB002368	KIAA0370 protein	
1291 40517_at	KIAA0372	AB002370	KIAA0372 gene product	KIAA0372 gene product
1292 34837_at	KIAA0376	AB002374	KIAA0376 protein	
1293 41457_at	KIAA0423	AB007883	KIAA0423 protein	
1294 35167_at	KIAA0433	AB007893	KIAA0433 protein	KIAA0433 protein
1295 33340_at	KIAA0438	AB007898	KIAA0438 gene product	KIAA0438 gene product
1296 40805_at	KIAA0440	AB007900	KIAA0440 protein	KIAA0440 protein
1297 32091_at	KIAA0446	AB007915	KIAA0446 gene product	KIAA0446 protein
1298 41243_at	KIAA0447	AB007916	KIAA0447 gene product	KIAA0447 protein
1299 32206_at	KIAA0451	AB007920	KIAA0451 gene product	KIAA0451 protein
1300 36069_at	SRGAP2	AB007925	KIAA0456 protein	KIAA0456 protein
1301 37230_at	KIAA0469	AB007938	KIAA0469 gene product	KIAA0469 protein
1302 33893_r_at	KIAA0470	AB007939	KIAA0470 gene product	KIAA0470 protein
1303 34445_at	KIAA0471	AB007940	KIAA0471 gene product	KIAA0471 protein
1304 35318_at	KIAA0475	AB007944	KIAA0475 gene product	KIAA0475 protein
1305 35786_at	KIAA0476	AB007945	KIAA0476 gene product	KIAA0476 protein
1306 35762_at	KIAA0483	AB007952	KIAA0483 protein	KIAA0483 protein
1307 41830_at	KIAA0494	AB007963	KIAA0494 gene product	KIAA0494 protein

Fig 21

	A	B	C	D	E
1308	35534_at	KIAA0514	AB011086	KIAA0514 gene product	KIAA0514 protein
1309	38724_at	KIAA0515	AB011087	KIAA0515 protein	KIAA0515 protein
1310	34192_at	KIAA0532	AB011104	KIAA0532 protein	KIAA0532 protein
1311	33787_at	KIAA0537	AB011109	KIAA0537 gene product	KIAA0537 protein
1312	35184_at	KIAA0546	AB011118	KIAA0546 protein	KIAA0546 protein
1313	31849_at	KIAA0564	AB011136	KIAA0564 protein	KIAA0564 protein
1314	39434_at	KIAA0592	AB011164	KIAA0592 protein	KIAA0592 protein
1315	41379_at	KIAA0594	AB011166	KIAA0594 protein	KIAA0594 protein
1316	32866_at	KIAA0605	AB011177	KIAA0605 gene product	KIAA0605 protein
1317	39852_at	KIAA0610	AB011182	KIAA0610 protein	KIAA0610 protein
1318	40160_at	KIAA0618	AL080109	KIAA0618 gene product	hypothetical protein
1319	40083_at	KIAA0625	AB014525	KIAA0625 protein	KIAA0625 protein
1320	33241_at	KIAA0626	AB014526	KIAA0626 gene product	KIAA0626 protein
1321	39376_at	KIAA0630	AB014530	KIAA0630 protein	KIAA0630 protein
1322	34353_at	KIAA0648	AB014548	KIAA0648 protein	KIAA0648 protein
1323	38082_at	KIAA0650	AB014550	KIAA0650 protein	KIAA0650 protein
1324	39117_at	KIAA0662	AB014562	KIAA0662 gene product	KIAA0662 protein
1325	41170_at	KIAA0663	AB014563	KIAA0663 gene product	KIAA0663 protein
1326	31826_at	KIAA0674	AB014574	KIAA0674 protein	KIAA0674 protein
1327	39403_at	KIAA0678	AB014578	KIAA0678 protein	KIAA0678 protein
1328	39519_at	KIAA0692	AB014592	KIAA0692 protein	KIAA0692 protein
1329	39380_at	KIAA0697	AB014597	KIAA0697 protein	KIAA0697 protein
1330	39705_at	KIAA0700	AB014600	KIAA0700 protein	KIAA0700 protein
1331	41620_at	KIAA0716	AB018259	KIAA0716 gene product	KIAA0716 protein
1332	33835_at	KIAA0721	AB018264	KIAA0721 protein	KIAA0721 protein
1333	35177_at	KIAA0725	AB018268	KIAA0725 protein	KIAA0725 protein
1334	41218_at	KIAA0729	AB018272	KIAA0729 protein	KIAA0729 protein
1335	38694_at	KIAA0738	AB018281	KIAA0738 gene product	KIAA0738 protein
1336	39771_at	KIAA0740	AB018283	KIAA0740 gene product	KIAA0740 protein
1337	41585_at	KIAA0746	AB018289	KIAA0746 protein	KIAA0746 protein
1338	38424_at	KIAA0747	AB018290	KIAA0747 protein	KIAA0747 protein
1339	40848_g_at	KIAA0750	AB018293	KIAA0750 gene product	KIAA0750 protein
1340	32224_at	KIAA0769	AB018312	KIAA0769 gene product	KIAA0769 protein
1341	36474_at	KIAA0776	AB018319	KIAA0776 protein	KIAA0776 protein
1342	33251_at	KIAA0779	AB018322	KIAA0779 protein	KIAA0779 protein
1343	35999_r_at	KIAA0781	AB018324	KIAA0781 protein	KIAA0781 protein

Gis 21



	A	B	C	D	E
1344	41224_at	KIAA0788	AB018331	KIAA0788 protein	KIAA0788 protein
1345	34285_at	KIAA0795	AB018338	KIAA0795 protein	KIAA0795 protein
1346	39614_at	KIAA0802	AB018345	KIAA0802 protein	KIAA0802 protein
1347	36588_at	KIAA0810	AB018353	KIAA0810 protein	KIAA0810 protein
1348	40492_at	KIAA0826	AB020633	KIAA0826 protein	KIAA0826 protein
1349	40455_at	KIAA0830	AB020637	KIAA0830 protein	KIAA0830 protein
1350	41372_at	KIAA0831	AB020638	KIAA0831 protein	KIAA0831 protein
1351	36888_at	KIAA0841	AB020648	KIAA0841 protein	KIAA0841 protein
1352	39597_at	KIAA0843	AB020650	KIAA0843 protein	KIAA0843 protein
1353	41503_at	KIAA0854	AB020661	KIAA0854 protein	KIAA0854 protein
1354	38730_at	KIAA0864	AB020671	KIAA0864 protein	KIAA0864 protein
1355	39021_at	KIAA0877	AB020684	KIAA0877 protein	KIAA0877 protein
1356	32215_i_at	KIAA0878	AB020685	KIAA0878 protein	KIAA0878 protein
1357	38254_at	KIAA0882	AB020689	KIAA0882 protein	KIAA0882 protein
1358	35720_at	KIAA0893	AB020700	KIAA0893 protein	KIAA0893 protein
1359	40423_at	KIAA0903	AB020710	KIAA0903 protein	KIAA0903 protein
1360	41421_at	KIAA0909	AB020716	KIAA0909 protein	KIAA0909 protein
1361	41498_at	KIAA0911	AB020718	KIAA0911 protein	KIAA0911 protein
1362	39777_at	KIAA0916	AF075587	KIAA0916 protein	protein associated with Myc
1363	32735_at	KIAA0931	AB023148	KIAA0931 protein	KIAA0931 protein
1364	33408_at	KIAA0934	AB023151	KIAA0934 protein	KIAA0934 protein
1365	35369_at	KIAA0937	AB023154	KIAA0937 protein	KIAA0937 protein
1366	33235_at	KIAA0938	AB023155	KIAA0938 protein	KIAA0938 protein
1367	32740_at	Rab11-FIP2	AB023158	KIAA0941 protein	KIAA0941 protein
1368	35794_at	KIAA0942	AB023159	KIAA0942 protein	KIAA0942 protein
1369	41595_at	KIAA0947	AB023164	KIAA0947 protein	KIAA0947 protein
1370	38649_at	KIAA0970	AB023187	KIAA0970 protein	KIAA0970 protein
1371	34396_at	KIAA0978	AB023195	KIAA0978 protein	KIAA0978 protein
1372	32085_at	KIAA0981	AB023198	KIAA0981 protein	KIAA0981 protein
1373	35199_at	KIAA0982	AB023199	KIAA0982 protein	KIAA0982 protein
1374	32769_at	KIAA0993	AB023210	KIAA0993 protein	KIAA0993 protein
1375	34751_at	KIAA0997	AI970189	KIAA0997 protein	KIAA0997 protein
1376	34808_at	KIAA0999	AB023216	KIAA0999 protein	KIAA0999 protein
1377	33193_at	KIAA1001	AW052084	KIAA1001 protein	KIAA1001 protein
1378	36002_at	KIAA1012	AB023229	KIAA1012 protein	KIAA1012 protein
1379	35802_at	KIAA1014	AB023231	KIAA1014 protein	KIAA1014 protein

Fig 21

	A	B	C	D	E
1380	39615_at	KIAA1026	AB028949	KIAA1026 protein	KIAA1026 protein
1381	34089_at	KIAA1030	AB028953	KIAA1030 protein	KIAA1030 protein
1382	41651_at	KIAA1033	AB028956	KIAA1033 protein	KIAA1033 protein
1383	41708_at	KIAA1034	AB028957	KIAA1034 protein	KIAA1034 protein
1384	35163_at	KIAA1041	AB028964	KIAA1041 protein	KIAA1041 protein
1385	38778_at	KIAA1046	AB028969	KIAA1046 protein	KIAA1046 protein
1386	41268_g_at	KIAA1049	AB028972	KIAA1049 protein	KIAA1049 protein
1387	40855_at	KIAA1053	AB028976	KIAA1053 protein	KIAA1053 protein
1388	39400_at	KIAA1055	AB028978	KIAA1055 protein	KIAA1055 protein
1389	33877_s_at	KIAA1067	AB028990	KIAA1067 protein	KIAA1067 protein
1390	34688_at	KIAA1078	AB029001	KIAA1078 protein	KIAA1078 protein
1391	33924_at	KIAA1091	AB029014	KIAA1091 protein	KIAA1091 protein
1392	32508_at	KIAA1096	AL096857	KIAA1096 protein	hypothetical protein
1393	41179_at	KIAA1100	AB029023	KIAA1100 protein	KIAA1100 protein
1394	34839_at	KIAA1104	AB029027	KIAA1104 protein	KIAA1104 protein
1395	33457_at	RAP140	AB029028	KIAA1105 protein	KIAA1105 protein
1396	36814_at	KIAA1109	AB029032	KIAA1109 protein	KIAA1109 protein
1397	34274_at	KIAA1116	AB029039	KIAA1116 protein	KIAA1116 protein
1398	37617_at	KIAA1128	U90912	KIAA1128 protein	
1399	33358_at	KIAA1157	W29087	KIAA1157 protein	
1400	40308_at	KIAA1240	AI830496	KIAA1240 protein	
1401	33811_at	KIAA1254	AI761567	KIAA1254 protein	
1402	38674_at	KIAA1354	AA115140	KIAA1354 protein	
1403	32730_at	KIAA1750	AL080059	KIAA1750 protein	
1404	32171_at	KIAA1856	AL080102	KIAA1856 protein	hypothetical protein
1405	39897_at	KIAA1966	N36997	KIAA1966 protein	
1406	32846_s_at	KTN1	D13629	kinectin 1 (kinesin receptor)	kinectin 1
1407	39057_at	KNS2	L04733	kinesin 2 (60-70kD)	kinesin light chain
1408	32079_at	KIF13B	AB014539	kinesin family member 13B	KIAA0639 protein
1409	33345_at	KIF3C	AF035621	kinesin family member 3C	kinesin-related protein
1410	34294_at	KIFC3	AL041493	kinesin family member C3	
1411	41474_at	KIF2	Y08319	kinesin heavy chain member 2	kinesin-2
1412	40779_at	KIFAP3	U59919	kinesin-associated protein 3	SMAP
1413	34216_at	KLF7	AA478904	Kruppel-like factor 7 (ubiquitous)	
1414	38768_at	HADHSC	X96752	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain	3-hydroxyacyl-CoA dehydrogenase

Fig 21

	A	B	C	D	E
1415	41485_at	LDHA	X02152	lactate dehydrogenase A	lactate dehydrogenase A
1416	288_s_at	LBR	L25931	lamin B receptor	lamin B receptor
1417	256_s_at	LAMR1	M14199	laminin receptor 1 (67kD, ribosomal protein SA)	laminin receptor 1
1418	37671_at	LAMA4	S78569	laminin, alpha 4	laminin alpha 4 chain
1419	581_at	LAMB1	M61916	laminin, beta 1	laminin B1
1420	39441_at	LANCL1	Y11395	LanC lamibiotic synthetase component C-like 1 (bacterial)	lanthionine synthetase C-like protein 1
1421	1495_at	LTBP1	M34057	latent transforming growth factor beta binding protein 1	latent transforming growth factor beta binding protein 1 precursor
1422	37906_at	LTBP2	Z37976	latent transforming growth factor beta binding protein 2	LTBP-2 precursor
1423	33412_at	LGALS1	A1535946	lectin, galactoside-binding, soluble, 1 (galectin 1)	
1424	35367_at	LGALS3	AB006780	lectin, galactoside-binding, soluble, 3 (galectin 3)	galectin-3
1425	37754_at	LGALS3BP	L13210	lectin, galactoside-binding, soluble, 3 binding protein	Mac-2 binding protein
1426	1846_at	LGALS8	L78132	lectin, galactoside-binding, soluble, 8 (galectin 8)	prostate carcinoma tumor antigen
1427	34267_r_at	LEPR	U50748	leptin receptor	leptin receptor
1428	33830_at	HSOBRGRP	AW026535	leptin receptor gene-related protein	
1429	33829_at	HSOBRGRP	Y12670	leptin receptor gene-related protein	leptin receptor gene-related protein
1430	38985_at	LEPROTL1	AF063605	leptin receptor overlapping transcript-like 1	brain my047 protein
1431	41320_s_at	LRRFIP1	U69609	leucine rich repeat (in FLII) interacting protein 1	transcription repressor
1432	39967_at	LDOC1	AB019527	leucine zipper, down-regulated in cancer 1	LDOC1 protein
1433	41754_at	LRPPRC	M92439	leucine-rich PPR-motif containing	leucine-rich PPR-motif containing protein
1434	37470_at	LAIR1	AF013249	leukocyte-associated Ig-like receptor 1	leukocyte-associated Ig-like receptor-1
1435	38081_at	LTA4H	J03459	leukotriene A4 hydrolase	leukotriene A4 hydrolase
1436	36062_at	LPXN	AF062075	leupaxin	leupaxin
1437	35278_at	RPS29	A1541542	libtest16.A02.r bvnorm Homo sapiens cDNA 5', mRNA sequence.	
1438	39687_at	E46L	A1524873	like mouse brain protein E46	

Gis 21

A	B	C	D	E
1439 39686_g_at	E46L	AL050282	like mouse brain protein E46	hypothetical protein
1440 39685_at	E46L	AL050282	like mouse brain protein E46	hypothetical protein
1441 39163_at	KIDINS220	W27233	likely homolog of rat kinase D-interacting substance of 220 kDa	
1442 32669_at	SOCS5	AB014571	likely ortholog of mouse suppressors of cytokine signalling 5	KIAA0671 protein
1443 40555_at	TC10	AL043108	likely ortholog of mouse TC10-alpha	
1444 40844_at	TSBP	D63875	likely ortholog of mouse TPR-containing, SH2-binding phosphoprotein	KIAA0155 gene product
1445 41248_at	CSTF2T	AB014589	likely ortholog of mouse variant polyadenylation protein CSTF-64	KIAA0689 protein
1446 35805_at	GRASP55	AA447263	likely ortholog of rat golgi stacking protein homolog GRASP55	
1447 39232_at	LIMS1	U09284	LIM and senescent cell antigen-like domains 1	PINCH protein
1448 36181_at	LASP1	X82456	LIM and SH3 protein 1	LIM and SH3 domain protein
1449 38617_at	LIMK2	D45906	LIM domain kinase 2	LIMK-2
1450 1452_at	LMO4	U24576	LIM domain only 4	breast tumor autoantigen
1451 31936_s_at	LKAP	AB007890	limkain b1	KIAA0430 protein
1452 38745_at	LIPA	X76488	lipase A, lysosomal acid, cholesterol esterase (Wolman disease)	lysosomal acid lipase
1453 38098_at	LPIN1	D80010	lipin 1	
1454 37542_at	LHFPL2	D86961	lipoma HMGIC fusion partner-like 2	
1455 41209_at	LPL	M15856	lipoprotein lipase	lipoprotein lipase precursor
1456 1798_at	LIV-1	U41060	LIV-1 protein, estrogen regulated liver form; Homo sapiens glycogen phosphorylase (PYGL) gene, exon 20 and complete cds.	estrogen regulated LIV-1 protein
1457 37215_at	PYGL	AF046798		glycogen phosphorylase

Gy 21

A	B	C	D	E
1458 40493_at	CD44	L05424	long tailed isoform; individual exons 6-14 are alternative exons any of which can be spliced out of the mRNA.; putative; long tailed isoform; putative; long tailed isoform; hemopoietic variant; putative; long tailed isoform; epithelial form; putative; Human cell surface glycoprotein CD44 (CD44) gene, 3' end of long tailed isoform.	cell surface glycoprotein CD44
1459 36194_at	LRPAP1	M63959	low density lipoprotein-related protein-associated protein 1 (alpha-2-macroglobulin receptor-associated protein 1)	alpha-2-macroglobulin receptor-associated protein
1460 34400_at	QP-C	A1540957	low molecular mass ubiquitinone-binding protein (9.5kD)	
1461 37025_at	PIG7	AL120815	LPS-induced TNF-alpha factor	
1462 39017_at	LSM1	AJ238094	Lsm1 protein	Lsm1 protein
1463 38038_at	LUM	U21128	lumican	lumican
1464 38115_at	FUS1	AF055479	lung cancer candidate	lung cancer candidate FUS1
1465 39428_at	LNK	AF055581	lymphocyte adaptor protein	adaptor protein Lnk
1466 39396_at	LYPLA1	AF081281	lysophospholipase I	lysophospholipase
1467 33788_at	LYSAL1	AB002390	lysosomal apyrase-like 1	lysosomal apyrase-like 1
1468 39758_f_at	LAMP1	J04182	lysosomal-associated membrane protein 1	lysosomal membrane glycoprotein-1
1469 38403_at	LAMP2	X77196	lysosomal-associated membrane protein 2	lysosome-associated membrane protein-2
1470 38402_at	LAMP2	U36336	lysosomal-associated membrane protein 2	lysosome-associated membrane protein-2b
1471 39019_at	LAPTM4A	D14696	lysosomal-associated protein	lysosomal-associated protein
1472 33127_at	LOXL2	U89942	transmembrane 4 alpha	transmembrane 4 alpha
1473 34336_at	KARS	D32053	lysyl oxidase-like 2	lysyl oxidase-related protein
1474 32832_at	MAEA	AF084928	lysyl-tRNA synthetase	Lysyl tRNA Synthetase
			macrophage erythroblast attachment	erythroblast macrophage protein EMP
1475 36174_at	MACMARCKS	X70326	macrophage myristoylated alanine-rich C kinase substrate	macrophage myristoylated alanine-rich C kinase substrate

Fig 21

A	B	C	D	E
1476 1453_at	MADH2	U68018	MAD, mothers against decapentaplegic homolog 2 (Drosophila)	mad protein homolog
1477 38944_at	MADH3	U68019	MAD, mothers against decapentaplegic homolog 3 (Drosophila)	mad protein homolog
1478 1433_g_at	MADH3	U68019	MAD, mothers against decapentaplegic homolog 3 (Drosophila)	mad protein homolog
1479 36953_at	MADH4	U44378	MAD, mothers against decapentaplegic homolog 4 (Drosophila)	Dpc4
1480 1013_at	MADH5	U59913	MAD, mothers against decapentaplegic homolog 5 (Drosophila)	Smad5
1481 1955_s_at	MADH6	AF035528	MAD, mothers against decapentaplegic homolog 6 (Drosophila)	Smad6
1482 1857_at	MADH7	AF010193	MAD, mothers against decapentaplegic homolog 7 (Drosophila)	MAD-related gene SMAD7
1483 41237_at	HLA-A	D32129	major histocompatibility complex, class I, A	HLA-A26
1484 41609_at	HLA-DMB	U15085	major histocompatibility complex, class II, DM beta	HLA-DMB
1485 38096_f_at	HLA-DPB1	M83664	major histocompatibility complex, class II, DP beta 1	HLA-DPB1
1486 38095_i_at	HLA-DPB1	M83664	major histocompatibility complex, class II, DP beta 1	HLA-DPB1
1487 37039_at	HLA-DRA	J00194	major histocompatibility complex, class II, DR alpha	major histocompatibility complex, class II, DR alpha precursor
1488 33261_at	HLA-DRB1	M16941	major histocompatibility complex, class II, DR beta 1	
1489 34425_at	HLALS	AF031469	major histocompatibility complex, class I-like sequence	MHC class I-related protein 1 isoform D
1490 34003_at	CD4	U47924	major receptor for HIV-1; member of immunoglobulin supergene family; T cell surface glycoprotein T4	protein 'A', isoform 1
1491 36608_at	MDH1	D55654	malate dehydrogenase 1, NAD (soluble)	cytosolic malate dehydrogenase
1492 837_s_at	ME1	U43944	malic enzyme 1, NADP(+)-dependent, cytosolic	cytosolic NADP(+)-dependent malic enzyme

Gis 21

A	B	C	D	E
1493 36599_at	ME2	M55905	malic enzyme 2, NAD(+)-dependent, mitochondrial	mitochondrial NAD(P)+ -dependent malic enzyme
1494 36673_at	MPI	X76057	mannose phosphate isomerase	phosphomannose isomerase
1495 35299_at	MKNK1	AB000409	MAP kinase-interacting serine/threonine kinase 1	MNK1
1496 40826_at	MARK3	M80359	MAP/microtubule affinity-regulating kinase 3	protein p78
1497 41506_at	MAPKAPK5; PRA	AF032437	MAPK-activated protein kinase; PRK; Homo sapiens mitogen activated protein kinase activated protein kinase gene, complete cds.	mitogen activated protein kinase activated protein kinase
1498 37009_at	CAT	AL035079	match proteins: Sw:P04040 Sw:P04762 Sw:P24270 Tr:O62839 Sw:P00432 Sw:P17336 Tr:P90682 Tr:Q27487 Sw:O61235 Tr:O18193 Tr:O77229 Tr:Q49133 Sw:P26901 Sw:P55306 Sw:P30263 Tr:P95631 Sw:P44390 Tr:Q27710 Sw:Q96528 Sw:O13289 Sw:P07820 Sw:P30265 Sw:P77872 Tr:Q59602 Tr:P77924 Sw:Q59170 Sw:P15202 Tr:Q59296 Tr:O33613 Sw:Q92405 Sw:Q59635 Sw:P81138 match ESTs: W94164 N28621 match to ESTs AA316181 (NID:g3165221), AA032221 (NID:g1502183), and AI167942 (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from 7q21, complete sequence.	dJ53C18.1 (Catalase)
1499 40297_at	WUGSC:H_RG04	AC005053		six transmembrane epithelial antigen of the prostate

C's 21

A	B	C	D	E
1500 34860_g_at	BCG1	Z98046	match: cDNAs X67055 X14690 D89287 X70393 S82800 X16260 M18192 Y11283 D38535 D38595 match: proteins Q06033 P97280 O54882 O35802 Q61704 Q14624 P79263 Q63416 O42141 P19823 O02668 Q61703 P97279 Q29052	hepatocellular carcinoma associated protein; breast cancer associated gene 1
1501 35336_at	HS50815A	AL021707	match: cDNAs: Em:AL050345 match: ESTs: Em:AA304885 Em:AA447346 Em:AA314213 Em:AA209368 Em:AA209372 Em:T84723 Em:H23039 Em:AA542125 Em:W41686 Em:AA384854 Em:AA492678	chromosome 22 open reading frame 2
1502 32658_at	dJ1033B10.1	AL031228	match: protein O15214	BING4
1503 31545_at	dJ1033B10.1	AL031228	match: protein O15214	BING4
1504 36986_at	dJ886K2.1	AL031295	match: protein SPTREMBL: Q14241 match: proteins CE02000 O59733 CE01999; supported by FGENES and GENSCAN	UDP-galactose-4-epimerase
1505 38072_at	dJ465N24.1	AL031432	match: proteins O15037 CE16881 supported by GENSCAN possibly this partial gene and dJ281H8.1 are part of one gene	hypothetical protein dJ465N24.2.1
1506 32478_f_at	dJ281H8.1	AL031133		dJ281H8.2 (PUTATIVE novel protein similar to KIAA0323 and worm C30F12.1)

Fig 21



A	B	C	D	E
150739759_at	dJ51J12.1	AL031781	<p>match: proteins O42476 Q94539; match: protein O88972; match: cDNA AF091047; owing to a different in-frame ORF, the translation of the last coding exon (8 C-terminal amino-acids) differs from that in mouse and is terminated more upstream; match: protein Q61110; Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.</p>	<p>dJ51J12.1 (human ortholog of zebrafish Quaking protein homolog ZKQ-1 (isoform 1)); dJ51J12.1.2 (human ortholog of mouse KH Domain RNA Binding protein QKI-7B (isoform 2)); dJ51J12.1.3 (human ortholog of mouse KH Domain RNA Binding protein QKI-7 (isoform 3))</p>
150839760_at	dJ51J12.1	AL031781	<p>match: proteins O42476 Q94539; match: protein O88972; match: cDNA AF091047; owing to a different in-frame ORF, the translation of the last coding exon (8 C-terminal amino-acids) differs from that in mouse and is terminated more upstream; match: protein Q61110; Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.</p>	<p>dJ51J12.1 (human ortholog of zebrafish Quaking protein homolog ZKQ-1 (isoform 1)); dJ51J12.1.2 (human ortholog of mouse KH Domain RNA Binding protein QKI-7B (isoform 2)); dJ51J12.1.3 (human ortholog of mouse KH Domain RNA Binding protein QKI-7 (isoform 3))</p>
150932573_at	COX6A	AL021546	<p>match: proteins P13182 P12074 P10818 P43024 Q02221 P07471 P10817 P43023 P13182 O13085 O13082</p>	<p>cytochrome c oxidase subunit VIa polypeptide 1</p>

613 21

	A	B	C	D	E
1510	33443_at	HSF2	Z99129	match: proteins P38533 Q03933 P38530 P41154 Q00613 P38529 P38531 Q63717 P38532 Q99472	heat shock transcription factor 2
1511	36133_at	dJ512B11.1	AL031058	match: proteins Q14189 P15924 Q03001 P97395 P97396 P97394; Human DNA sequence from clone 512B11 on chromosome 6p24-25. Contains the Desmoplakin I (DPI) gene, ESTs, STSs and GSSs, complete sequence.	dJ512B11.1 (Desmoplakin I (DPI))
1512	37043_at	E2F-2	AL021154	match: proteins Q14209 Q16254 Q35261 Q00716 Q61501 Q90977 Q01094 Q27368	E2F transcription factor 2
1513	41227_at	OCRL1	AL022162	match: proteins Q15774; match: protein Q01968 P32019; Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.	dJ454M7.1.2 (Lowe Oculocerebrorenal Syndrome protein OCRL-1) (isoform 2); dJ454M7.1.1 (Lowe Oculocerebrorenal Syndrome protein OCRL-1) (isoform 1)
1514	38990_at	dJ341E18.1	AL031178	match: proteins Q62726 P20793 Q04859 Q39423 P43294 Q49669	dJ341E18.1 (Serine/Threonine Protein Kinase (presumptive isolog of Rat protein Q62726))

G's 21

A	B	C	D	E
1515 34782_at	JUMONJI	AL021938	<p>match: proteins Q92833 Q62315; protein Q92833 has a different stop codon 19 aa further downstream because it jumps frame twice, circumventing the stopcodon in this entry. This could be due to a sequence error in the cDNA sequence; Homo sapiens DNA sequence from PAC 232K4 on chromosome 6p22.3. Contains the JUMONJI gene for a hypothetical 141.7 kD protein. Contains ESTs, STSs, a CA repeat polymorphism and genomic marker D6S260, complete sequence.</p>	dJ232K4.1 (hypothetical 141.7 kD protein JUMONJI)
1516 37350_at	dJ889N15.1	AL031177	<p>match: proteins Q99795 Q91665 Q91664 O09052 P78310 P97792 Q91667 O60939 P54900 Q62861 Q61148 O00426 P06907 P25189 Q92677 P20938 P27573 P10522 P37301 match: patented sequence I80040 supported by GENSCAN and FGENES</p>	dJ889N15.1 (novel protein similar to X. laevis Cortical Thymocyte Marker CTX)
1517 39738_at	APOL2	Z82215	match: proteins: Sw:O14791	apolipoprotein L
1518 31824_at	ME1	AL049699	<p>match: proteins: Sw:P06801 Sw:P28227 Sw:Q29558 Sw:P13697 Sw:P40927 Sw:Q16798 Tr:Q16797 Sw:P48163</p>	dJ747H23.1 (malic enzyme 1, soluble (NADP-dependent malic enzyme, malate oxidoreductase, EC 1.1.1.40))
1519 32766_at	OTK27 SSFA1	Z83840	<p>match: proteins: Sw:P12956 match: proteins: Sw:P17861 Tr:O35426; Human DNA sequence from clone CTA-292E10 on chromosome 22q11-12</p>	non-histone chromosome protein 2 (S. cerevisiae)-like 1
1520 39756_g_at	XBP1	Z93930	<p>Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs, GSSs and a putative CpG island, complete sequence.</p>	bK292E10.1 (X-box binding protein 1 (TREB5))

Fig 21

	A	B	C	D	E
1521	39755_at	XBP1	Z93930	<p>match: proteins: Sw:P17861 Tr:O35426; Human DNA sequence from clone CTA-292E10 on chromosome 22q11-12</p> <p>Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs, GSSs and a putative CpG island, complete sequence.</p> <p>match: proteins: Sw:P26038 Tr:O35763 Sw:P26041 Sw:P26042 Sw:P26044 Sw:P35241 Sw:P26043 Sw:P15311 Sw:P31976 Sw:P26040 Tr:Q26520 Tr:Q24788 Tr:Q24796 Tr:Q94815; Human DNA sequence from clone 376D21 on chromosome Xq11.1-12 Contains the MSN gene for Moesin (Membrane-organizing Extension Spike protein), ESTs, STSs, GSSs, genomic marker DXS8029 and a putative CpG island, complete sequence.</p>	bK292E10.1 (X-box binding protein 1 (TREB5))
1522	40771_at	MSN	Z98946		dJ376D21.1 (Moesin (Membrane-organizing Extension Spike protein))
1523	31722_at	RPL3	AL022326	<p>match: proteins: Sw:P39023 Sw:O16797 Sw:P21531 Sw:P39872 Sw:P27659 Sw:Q92901 Sw:P49149 Sw:P22738 Sw:P35684 Sw:P17094 Wp:CE05598</p> <p>match: proteins: Sw:P50550 Sw:O09181 Tr:O62622 Sw:P40984 Sw:P50623 Tr:Q42551 Tr:O24240 Tr:Q42973 Sw:P52478 Sw:Q02159 Sw:P15732 Sw:O00102 Tr:O76542 Sw:P27949 Sw:P49427 Tr:O17424 Sw:P25867 Sw:P52490</p>	ribosomal protein L3
1524	33136_at	UBE21	AL031714		C358B7.1 (ubiquitin-conjugating enzyme E2) (homologous to yeast UBC9))
1525	36607_at	bK250D10.3	Z99716	<p>match: proteins: Sw:Q12772 Sw:Q60429 Sw:P36956 Sw:Q60416 Tr:O15352</p>	sepin 3
1526	38399_at	SNRNP2	AL034428	<p>match: proteins: Sw:Q28038 Sw:Q16674 Tr:P97591 Sw:Q61865</p>	small nuclear ribonucleoprotein polypeptide B"

Fig 21

	A	B	C	D	E
				match: proteins: Tr:O54791 Sw:Q90595 Sw:Q61827 Sw:Q90596 Tr:O54790 Tr:O15525 Sw:Q90889 Tr:O73679 Tr:O75444 Sw:P54844 Sw:P54843 Sw:Q00056 Sw:Q10060 Sw:Q15427	chromosome 22 open reading frame 5 chromobox homolog 6
1527 36711_at	HS506A DKFZP5	AL021977		match: proteins: Tr:O54793 Tr:O44229	dJ738P15.2 (CD39-like 2 (a nucleoside phosphatase))
1528 39561_at	DNAL4	AL008583		match: proteins: Tr:O75354 Tr:O75356 Tr:Q9QYCY8 Tr:Q9WUZ9 Tr:O70214 Tr:Q9QYCY9	dJ347H13.1 (aconitase 2, mitochondrial (Aconitate Hydratase, EC 4.2.1.3, Citrate Hydrolase))
1529 39876_at	dJ738P15.1	AL035252		match: proteins: Tr:Q94136 Sw:Q99798 Sw:P49609 Sw:P20004 Sw:P16276 Tr:O75809 Tr:O74699 Wp:CE00516 Sw:P19414 Tr:O75944 Sw:O13966	activating transcription factor 4 dJ117516.1 (Ras inhibitor JC265 (Ras association (RalGDS/AF-6) domain containing protein))
1530 37189_at	ACO2	AL023553		match: proteins: Tr:P70386 Sw:Q02527 Sw:Q10470 Sw:Q09327	RNA-binding protein (autoantigenic) long isoform
1531 41235_at	TAXREB67 TXRE	AL022312		match: proteins: Tr:Q00425 Sw:Q13671 Tr:O15010 Tr:P97680	dJ483K16.1.1 (novel protein (isoform 1)) maternal G10 transcript
1532 36550_at	dJ117516.1	AL049538		match: proteins: Tr:Q14621 Tr:Q64012 Sw:P07910 Sw:P19600 Tr:O60812 Sw:Q14011 Sw:P26686	ROX protein MAX interacting protein 1, isoform a; MAX interacting protein 1, isoform b MAX interacting protein 1, isoform a; MAX interacting protein 1, isoform b
1533 39368_at	P542	AL031668		match: proteins: Tr:Q9Y3M0 Tr:Q9WU14 Sw:P39540 Tr:Q9Y396	KIAA0572 protein
1534 33821_at	dJ483K16.1	AL034374		maternal G10 transcript	
1535 39029_at	G10	U11861		MAX binding protein	
1536 35145_at	MNT	X96401		MAX interacting protein 1	
1537 39072_at	MXI1	L07648		MAX interacting protein 1	
1538 654_at	MXI1	L07648		MCM2 minichromosome maintenance deficient 2, mitotin (S. cerevisiae)	
1539 35312_at	MCM2	D21063		MCM3 minichromosome maintenance deficient 3 (S. cerevisiae) associated protein	
1540 40469_at	MCM3AP	AB011144			

Fig 21

	A	B	C	D	E
1541	40117_at	MCM6	D84557	MCM6 minichromosome maintenance deficient 6 (MIS5 homolog, <i>S. pombe</i> ) ( <i>S. cerevisiae</i> )	HsMcm6
1542	41388_at	MEIS2	AF017418	Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse)	homeobox protein MEIS2
1543	37486_f_at	MEIS3	U68385	Meis1, myeloid ecotropic viral integration site 1 homolog 3 (mouse)	Meis1-related protein 2
1544	35340_at	MEL	AI819948	mel transforming oncogene (derived from cell line NK14)- RAB8 homolog	
1545	36500_at	MAGEA2A	AF027974	melanoma antigen, family A, 2, copy a; similar to GenBank Accession Number L18920	melanoma antigen family A2a
1546	41139_at	MAGED1	W26633	melanoma antigen, family D, 1	
1547	39327_at	D2S448	D86983	Melanoma associated gene	
1548	38441_s_at	MCP	X59408	membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen)	membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen)
1549	39471_at	M11S1	Z48042	membrane component, chromosome 11, surface marker 1	GPI-anchored protein p137
1550	33444_at	M17S2	D30756	membrane component, chromosome 17, surface marker 2 (ovarian carcinoma antigen CA125)	membrane component, chromosome 17, surface marker 2
1551	1389_at	MME	J03779	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)	membrane metallo-endopeptidase
1552	40399_r_at	MEOX2	AI743406	mesenchyme homeo box 2 (growth arrest-specific homeo box)	
1553	37697_s_at	por		Met at bp 326 also used as initiation codon in vitro; Met at bp 248 also used as initiation codon in vitro; Homo sapiens porin (por) mRNA, complete cds and truncated cds.	porin
1554	40244_s_at	MPPE1	L08666 AI743654	metallo phosphoesterase	

Fig 21

A	B	C	D	E
1555 31975_at			metallothionein (MT)-like gene; H.sapiens pseudogene for metallothionein and AG/CT repetitive element.	metallothionein
1556 39081_at	MT2A	X55503	metallothionein 2A	
1557 38945_at	MTF1	AI547258	metal-regulatory transcription factor 1	metal-regulatory transcription factor
1558 1643_g_at	MTA1	X78710	metastasis associated 1	metastasis associated protein
1559 35642_at	MTX2	U35113	metaxin 2	metaxin 2
1560 39342_at	MARS	AF053551	methionine-tRNA synthetase	yeast methionyl-tRNA synthetase homolog
1561 37619_at	METAP1	X94754	methionyl aminopeptidase 1	
1562 41828_at	MBD1	D42084	methy-CpG binding domain protein 1	methy-CpG binding protein
1563 33905_at	MBD2	Y10746	methy-CpG binding domain protein 2	methy-CpG binding protein MBD2
1564 34386_at	MBD4	AF072242	methy-CpG binding domain protein 4	methy-CpG binding protein MBD4
1565 40074_at	MTHFD2	AF072250	methyene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase	methyene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase, precursor
1566 674_g_at	MTHFD1	X16396	methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase	methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase
1567 40105_at	MUT	J04031	methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase	methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase
		M65131	methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase	methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase
1568 35937_at	MICB		MHC class I chain-related gene B; cDNA sequence deposited under GenBank Accession Number X91625; Human MHC class I molecule (MICB) gene, complete cds.	MHC class I molecule
1569 36535_at	MFAP1	U65416	microfibrillar-associated protein 1	associated microfibrillar protein
1570 38228_g_at	MITF	U04209	microphthalmia-associated transcription factor	A-type microphthalmia associated transcription factor
1571 820_at	MGST2	AB006909	microsomal glutathione S-transferase 2	microsomal glutathione S-transferase 2
1572 38704_at	MACF1	U77604	microtubule-actin crosslinking factor 1	KIAA0465 protein
1573 35917_at	MAP1A	AB007934	microtubule-associated protein 1A	
1574 33850_at	MAP4	W26631	microtubule-associated protein 4	
		W28892		

Fig 21

	A	B	C	D	E
1575	33456_at	MAPRE1	U24166	microtubule-associated protein, RP/EB family, member 1	EB1
1576	39370_at	MAP1A/1BLC3	W28807	microtubule-associated proteins 1A/1B light chain 3	
1577	34296_at	MID1	AF041210	midline 1 (Opitz/BBB syndrome)	midline 1 fetal kidney isoform 3
1578	34403_at	MFIGE8	U58516	milk fat globule-EGF factor 8 protein	BA46
1579	40027_at	ATPW	W52999	mitochondrial ATP synthase regulatory component factor B	
1580	37174_at	MRPL19	D14660	mitochondrial ribosomal protein L19	mitochondrial ribosomal protein L19
1581	37726_at	MRPL3	X06323	mitochondrial ribosomal protein L3	mitochondrial ribosomal protein L3
1582	39717_g_at	MRPL33	AI597616	mitochondrial ribosomal protein L33	
1583	32221_at	MRPS18B	AL050361	mitochondrial ribosomal protein S18B	mitochondrial ribosomal protein S18B
1584	38899_s_at	MFN1	U95822	mitofusin 1	putative transmembrane GTPase KIAA0214 protein
1585	34369_at	MFN2	D86987	mitofusin 2	KIAA0214 protein
1586	36577_at	MIG2	Z24725	mitogen-inducible 2	mitogen-inducible gene mig-2
1587	37733_at	MAPK14	L35263	mitogen-activated protein kinase 14	CSaids binding protein
1588	36926_at	MAPK6	X80692	mitogen-activated protein kinase 6	p97mapk
1589	38431_at	MAPK9	U09759	mitogen-activated protein kinase 9	protein kinase
1590	1238_at	MAPK9	U09759	mitogen-activated protein kinase 9	protein kinase
1591	1130_at	MAP2K1	L11284	mitogen-activated protein kinase kinase 1	mitogen-activated protein kinase kinase 1
1592	1327_s_at	MAP3K5	U67156	mitogen-activated protein kinase kinase kinase 5	mitogen-activated kinase kinase kinase 5
1593	36905_at	MAP3K7	AB009356	mitogen-activated protein kinase kinase kinase 7	TGF-beta activated kinase 1a
1594	38980_at	MAP3K7IP2	AB018276	mitogen-activated protein kinase kinase kinase 7 interacting protein 2	KIAA0733 protein
1595	35694_at	MAP4K4	AB014587	mitogen-activated protein kinase kinase kinase 4	KIAA0687 protein
1596	36179_at	MAPKAPK2	U12779	mitogen-activated protein kinase-activated protein kinase 2	MAP kinase activated protein kinase 2
1597	1637_at	MAPKAPK3	U09578	mitogen-activated protein kinase-activated protein kinase 3	MAPKAP kinase
1598	41220_at	MSF	AB023208	MLL septin-like fusion	KIAA0991 protein
1599	38437_at	MLN51	X80199	MLN51 protein	MLN51 protein

Fig 21



	A	B	C	D	E
1600 35273_at	MMS19L		AF007151	MMS19-like (MET18 homolog, <i>S. cerevisiae</i> )	MMS19 (MET18 <i>S. cerevisiae</i> )-like
1601 34767_at	MAP-1		A1670788	modulator of apoptosis 1	
1602 41771_g_at	MAOA		AA420624	monoamine oxidase A	
1603 41772_at	MAOA		M68840	monoamine oxidase A	monoamine oxidase A
1604 41770_at	MAOA		AA420624	monoamine oxidase A	
1605 37628_at	MAOB		M69177	monoamine oxidase B	monoamine oxidase B
1606 37565_at	MMD		X85750	monocyte to macrophage differentiation-associated	monocyte to macrophage differentiation-associated, precursor
1607 40861_at	MRGX		D14812	MORF-related gene X	MORF-related gene X
1608 33797_at	MPHOSPH10		X98494	M-phase phosphoprotein 10 (U3 small nuclear ribonucleoprotein)	M phase phosphoprotein 10
1609 34306_at	MBNL		AB007888	muscleblind-like (Drosophila)	muscleblind (Drosophila)-like
1610 35992_at	MSC		AF087036	musculin (activated B-cell factor-1)	musculin
1611 31884_at	MLH3		L40399	mutL homolog 3 ( <i>E. coli</i> )	mutL homolog 3
1612 860_at	MSH2		U03911	mutS homolog 2, colon cancer, nonpolyposis type 1 ( <i>E. coli</i> )	mutS homolog 2
1613 2003_s_at	MSH6		U28946	mutS homolog 6 ( <i>E. coli</i> )	G/T mismatch binding protein
1614 33769_at	MPZL1		AF087020	myelin protein zero-like 1	protein zero related protein
1615 33146_at	MCL1		L08246	myeloid cell leukemia sequence 1 (BCL2-related)	myeloid cell leukemia sequence 1 (BCL2-related)
1616 277_at	MCL1		L08246	myeloid cell leukemia sequence 1 (BCL2-related)	myeloid cell leukemia sequence 1 (BCL2-related)
1617 39037_at	MLLT2		L13773	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, <i>Drosophila</i> ); translocated to, 2	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, <i>Drosophila</i> ); translocated to, 2
1618 41637_at	MYLE		AF108145	MYLE protein	DEXI
1619 41439_at	MYO1B		AJ001381	myosin IB	myh-1c
1620 35729_at	MYO1D		AB018270	myosin ID	KIAA0727 protein
1621 37631_at	MYO1E		U14391	myosin IE	myosin-IC
1622 38251_at	MLC1SA		A1127424	myosin light chain 1 slow a	
1623 41187_at	MLC-B		U26162	myosin regulatory light chain	myosin regulatory light chain
1624 35362_at	MYO10		AB018342	myosin X	KIAA0799 protein
1625 33447_at	MLCB		X54304	myosin, light polypeptide, regulatory, non-sarcomeric (20kD)	myosin, light polypeptide, regulatory, non-sarcomeric (20kD)
1626 35739_at	MTMR3		AB002369	myotubularin related protein 3	myotubularin related protein 3

Fig 21

	A	B	C	D	E
1627	39707_at	MTMR4	AB014547	myotubularin related protein 4	KIA0647 protein
1628	38035_at	MTMR6	AF072928	myotubularin related protein 6	myotubularin related protein 6
1629	39607_at	MTMR8	AL080178	myotubularin related protein 8	hypothetical protein
1630	36692_at	MTMR8	AF052099	myotubularin related protein 8	
1631	32434_at	MARCKS	D10522	myristoylated alanine-rich protein kinase C substrate	80K-L protein
1632	39267_at	AGM1	AF102265	N-acetylglucosamine-phosphate mutase	N-acetylglucosamine-phosphate mutase
1633	36938_at	ASAH	U70063	N-acylsphingosine amidohydrolase (acid ceramidase)	acid ceramidase
1634	461_at	ASAH	U70063	N-acylsphingosine amidohydrolase (acid ceramidase)	acid ceramidase
1635	36169_at	NDUFA1	N47307	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1 (7.5kD, MWFE)	
1636	40546_s_at	NDUFA2	AF047185	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (8kD, B8)	NADH-ubiquinone oxidoreductase subunit C1
1637	38462_at	NDUFA5	U64028	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 (13kD, B13)	B8
1638	32752_at	NDUFA7	W72440	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (14.5kD, B14.5a)	NADPH:ubiquinone oxidoreductase subunit B13
1639	38605_at	NDUFB1	AI345944	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1 (7kD, MNLL)	
1640	38981_at	NDUFB3	AA203354	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3 (12kD, B12)	
1641	32232_at	NDUFB5	AF047181	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5 (16kD, SGDH)	NADH-ubiquinone oxidoreductase subunit C1
1642	32774_at	NDUFB8	AI541050	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASH)	SGDH
1643	38485_at	NDUFC1	AA760866	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1 (6kD, KFYI)	
1644	38395_at	NDUFS1	X61100	NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase)	75 kDa subunit NADH dehydrogenase precursor
1645	38695_at	NDUFS4	AA203303	NADH dehydrogenase (ubiquinone) Fe-S protein 4 (18kD) (NADH-coenzyme Q reductase)	

Fig 21

A	B	C	D	E
1646 38060_at	NDUFS5	A1541336	NADH dehydrogenase (ubiquinone) Fe-S protein 5 (15kD) (NADH-coenzyme Q reductase)	
1647 34893_at	NDUFV2	A1557064	NADH dehydrogenase (ubiquinone) flavoprotein 2 (24kD)	
1648 34519_at	NPR3	M59305	natriuretic peptide receptor C/guanylate cyclase C (atrialnatriuretic peptide receptor C)	atrial natriuretic peptide clearance receptor
1649 34234_f_at	NKTR	A1688640	natural killer-tumor recognition sequence	
1650 41795_at	NCK1	X17576	NCK adaptor protein 1	NCK adaptor protein 1
1651 33357_at	NCKAP1	AB011159	NCK-associated protein 1	KIAA0587 protein
1652 36073_at	NDN	U35139	necdin homolog (mouse)	NECDIN related protein
1653 34202_at	DKFZP566B0846	AL050071	necdin 3	hypothetical protein
1654 34264_at	NESCA	AB026894	nesca protein	NESCA
1655 38719_at	NSF	U03985	N-ethylmaleimide-sensitive factor	N-ethylmaleimide-sensitive factor
1656 39356_at	NEDD4L	AB007899	neural precursor cell expressed, developmentally down-regulated 4-like	ubiquitin-protein ligase NEDD4-like
1657 40281_at	NEDD5	D63878	neural precursor cell expressed, developmentally down-regulated 5	neural precursor cell expressed, developmentally down-regulated 5
1658 1695_at	NEDD8	D23662	neural precursor cell expressed, developmentally down-regulated 8	ubiquitin-like protein
1659 37005_at	NBL1	D28124	neuroblastoma, suppression of tumorigenicity 1	neuroblastoma, suppression of tumorigenicity 1
1660 31896_at	NAG	AL050281	neuroblastoma-amplified protein	hypothetical protein
1661 37286_at	NRCAM	AB002341	neuronal cell adhesion molecule	neuronal cell adhesion molecule
1662 37673_at	NSMAF	X96586	neural sphingomyelinase (N-SMase)	FAN protein
1663 38692_at	NAB1	AF045451	activation associated factor	
1664 34835_at	NCSTN	D87442	NGF1-A binding protein 1 (EGR1 binding protein 1)	transcriptional regulatory protein p54
1665 37032_at	NNMT	U08021	nicastrin	
1666 41722_at	NINT	U40490	nicotinamide N-methyltransferase	nicotinamide N-methyltransferase
1667 35366_at	NID	M30269	nicotinamide nucleotide transhydrogenase	nicotinamide nucleotide transhydrogenase
1668 753_at	NID2	D86425	nidogen (enactin)	nidogen
			nidogen 2	osteonidogen

Fig 21

A	B	C	D	E
1669 37047_at	NPC1	AF002020	Niemann-Pick disease, type C1	Niemann-Pick C disease protein
1670 980_at	NPC1	AF002020	Niemann-Pick disease, type C1	Niemann-Pick C disease protein
1671 39345_at	NPC2	AI525834	Niemann-Pick disease, type C2	
1672 35153_at	NBS1	AF058696	Nijmegen breakage syndrome 1 (nibrin)	cell cycle regulatory protein p95
1673 36047_at	NEK1	AL050385	NIMA (never in mitosis gene a)-related kinase 1	
1674 35843_at	Nek8	L40402	NIMA-related kinase Nek8	
1675 40866_at	NIPSNAP1	AJ001258	nipsnap homolog 1 (C. elegans)	NIPSNAP1 protein
1676 33916_at	NISCH	AB023192	nischarin	KIAA0975 protein
1677 39165_at	NIFU	U47101	nitrogen fixation cluster-like	NifU-like protein
1678 36472_at	NMI	U32849	N-myc (and STAT) interactor	Nmi
1679 36933_at	NDRG1	D87953	N-myc downstream regulated gene 1	RTP
1680 41656_at	NMT2	AF043325	N-myristoyltransferase 2	N-myristoyltransferase 2
1681 39040_at	NCUBE1	W28360	non-canonical ubiquitin conjugating enzyme 1	
1682 39039_s_at	NCUBE1	AI557497	non-canonical ubiquitin conjugating enzyme 1	
1683 1521_at	NME1	X17620	non-metastatic cells 1, protein (NM23A) expressed in	Nm23 protein
1684 33415_at	NME2	X58965	non-metastatic cells 2, protein (NM23B) expressed in	NM23-H2 protein
1685 1980_s_at	NME2	X58965	non-metastatic cells 2, protein (NM23B) expressed in	NM23-H2 protein
1686 38527_at	NONO	U02493	non-POU domain containing, octamer-binding	54 kDa protein
1687 38750_at	NOTCH3	U97669	Notch homolog 3 (Drosophila)	Notch3
1688 34781_at	WS-3	D84145	novel RGD-containing protein	novel RGD-containing protein
1689 40122_at	NSAP1	AF037448	NS1-associated protein 1	Gry-rbp
1690 33752_at	NS1-BP	AB020657	NS1-binding protein	KIAA0850 protein
1691 35626_at	SGSH	U30894	N-sulfoglucosamine sulfohydrolase (sulfamidase)	N-sulfoglucosamine sulfohydrolase
1692 37352_at	SP100	M60618	nuclear antigen Sp100	nuclear autoantigen
1693 37353_g_at	SP100	M60618	nuclear antigen Sp100	nuclear autoantigen
1694 40901_at	GS2NA	U17989	nuclear autoantigen	GS2NA
1695 32789_at	NCBP2	AA149428	nuclear cap binding protein subunit 2, 20kD	

Fig 21

A	B	C	D	E
1696 35836_at	NUDC	AB019408	nuclear distribution gene C homolog (A. nidulans)	nuclear distribution gene C (A. nidulans) homolog
1697 39782_at	C1D	X95592	nuclear DNA-binding protein	C1D protein
1698 40063_at	NDP52	U22897	nuclear domain 10 protein	NDP52
1699 853_at	NFE2L2	S74017	nuclear factor (erythroid-derived 2)-like 2	Nr12
1700 38354_at	CEBPB; LAP; CRI	X52560	nuclear factor NF-IL6 (AA 1-345); Human gene for nuclear factor NF-IL6.	CCAAT/enhancer binding protein (C/EBP), beta
1701 40822_at	NFATC3	L41067	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3
1702 38438_at	NFKB1	M58603	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	nuclear factor kappa-B DNA binding subunit
1703 1377_at	NFKB1	M58603	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	nuclear factor kappa-B DNA binding subunit
1704 1461_at	NFKBIA	M69043	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha
1705 37544_at	NFIL3	X64318	nuclear factor, interleukin 3 regulated	nuclear factor, interleukin 3 regulated
1706 38648_at	GIZ	U80760	nuclear matrix transcription factor 4	CAGH1 alternate open reading frame
1707 40816_at	PWP1	L07758	nuclear phosphoprotein similar to S. cerevisiae PWP1	IEF SSP 9502
1708 34312_at	NCOA2	AI040324	nuclear receptor coactivator 2	Amplified in Breast Cancer
1709 33381_at	NCOA3	AF012108	nuclear receptor coactivator 3	Rel fused gene
1710 39174_at	NCOA4	X77548	nuclear receptor coactivator 4	nuclear factor RIP140
1711 40088_at	NR1P1	X84373	nuclear receptor interacting protein 1	
1712 39397_at	NR2F2	M64497	nuclear receptor subfamily 2, group F, member 2	apolipoprotein AI regulatory protein-1
1713 36690_at	NR3C1	M10901	nuclear receptor subfamily 3, group C, member 1	nuclear receptor subfamily 3, group C, member 1
1714 35302_at	NXF1	AJ132712	nuclear RNA export factor 1	nuclear RNA export factor 1
1715 37928_at	NFYB	AA621555	nuclear transcription factor Y, beta	
1716 34667_at	NFX1	U15306	nuclear transcription factor, X-box binding 1	NFX1
1717 33413_at	PRL-1	AF051160	nuclear; Homo sapiens tyrosine phosphatase (PRL-1) gene, complete cds.	tyrosine phosphatase

fig. 21

	A	B	C	D	E
1718	32340_s_at	NSEP1	M85234	nuclease sensitive element binding protein 1	nuclease sensitive element binding protein-1
1719	35643_at	NUCB2	X76732	nucleobindin 2	NEFA protein
1720	36597_at	NOLC1	D21262	nucleolar and coiled-body phosphoprotein 1	ORF
1721	37520_at	HSA6591	AJ006591	nucleolar cysteine-rich protein	cysteine-rich protein
1722	36930_at	HUMAUANTIG	L05425	nucleolar GTPase	nucleolar GTPase
1723	39390_at	NUP133	AF052123	nucleoporin 133kD	
1724	32850_at	NUP153	Z25535	nucleoporin 153kD	nuclear pore complex protein hnup153
1725	39024_at	NUP98	AF042357	nucleoporin 98kD	
1726	571_at	NAP1L1	M86667	nucleosome assembly protein 1-like 1	nucleosome assembly protein 1-like 1
1727	743_at	NAP1L3	D50370	nucleosome assembly protein 1-like 3	nucleosome assembly protein
1728	32575_at	NAP1L4	U77456	nucleosome assembly protein 1-like 4	nucleosome assembly protein 2
1729	36127_g_at	NBP	U18919	nucleotide binding protein	nucleotide binding protein
1730	41584_at	NUDT3	AF062529	nudix (nucleoside diphosphate linked moiety X)-type motif 3	diphosphoinositol polyphosphate phosphohydrolase
1731	37693_at	NUMB	L40393	numb homolog (Drosophila)	numb homolog
1732	35916_s_at	INHBC	AA877215	ob15e02.s1 NCL CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1323770 3' similar to SW:ROA3_HUMAN P51991 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A3 :: mRNA sequence.	
1733	34169_s_at	OCRL	U57627	oculocerebrorenal syndrome of Lowe	ocrl1
1734	31921_at	OLF3	U56421	olfactory receptor; Human olfactory receptor (OLF3) gene, complete cds.	HsOLF3
1735	39507_at	OGT	AL050366	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	hypothetical protein
1736	40332_at	OGFR	AF109134	opoid growth factor receptor	Jul-60
1737	39745_at	OPA1	AB011139	optic atrophy 1 (autosomal dominant)	KIAA0567 protein
1738	41744_at	OPTN	AF070533	optineurin	optineurin
1739	34539_at	OR7E12P	AF065854	OR11-3; olfactory receptor; Homo sapiens OR7E12P pseudogene, complete sequence.	

Fig-21

	A	B	C	D	E
1740	AFFX-BioC-3_at	bioA	J04423	ORF 1	7,8-diamino-pelargonic acid aminotransferase
1741	AFFX-BioB-M_at	bioA	J04423	ORF 1	7,8-diamino-pelargonic acid aminotransferase
1742	AFFX-BioDn-5_a	bioA	J04423	ORF 1	7,8-diamino-pelargonic acid aminotransferase
1743	AFFX-BioDn-3_a	bioA	J04423	ORF 1	7,8-diamino-pelargonic acid aminotransferase
1744	AFFX-BioC-5_at	bioA	J04423	ORF 1	7,8-diamino-pelargonic acid aminotransferase
1745	32412_at	RPS14	M13934	ORF; putative; Human ribosomal protein S14 gene, complete cds.	unknown protein; ribosomal protein S14
1746	1315_at	OAZ1	D78361	ORF1; ORF 2; no start codon; Human mRNA for ornithine decarboxylase antizyme, ORF 1 and ORF 2.	ornithine decarboxylase antizyme 1
1747	32800_at	RXRA; NR2B1	U66306	ORF-2; ORF-3; Human retinoid X receptor alpha mRNA, 3' UTR, partial sequence.	retinoid X receptor, alpha
1748	38155_at	ORC5L	U92538	origin recognition complex, subunit 5-like (yeast)	origin recognition complex subunit 5 homolog
1749	36636_at	OAT	M12267	ornithine aminotransferase (gyrate atrophy)	ornithine aminotransferase
1750	1959_at	OAZIN	D88674	ornithine decarboxylase antizyme inhibitor	antizyme inhibitor
1751	33367_s_at	OAZIN	D88674	ornithine decarboxylase antizyme inhibitor	antizyme inhibitor
1752	1081_at	ODC1	M33764	ornithine decarboxylase; Human ornithine decarboxylase gene, complete cds.	ornithine decarboxylase 1
1753	31700_at	GPR35	AF027957	orphan G protein-coupled receptor; Homo sapiens G protein-coupled receptor (GPR35) gene, complete cds.	G protein-coupled receptor
1754	1451_s_at	OSF-2	D13666	osteoblast specific factor 2 (fasciclin 1-like)	osteoblast specific factor 2
1755	39774_at	OXA1L	X80695	oxidase (cytochrome c) assembly 1-like	oxidase (cytochrome c) assembly 1-like

Fig-21

A	B	C	D	E
1756 39136_at	OSR1	AB017642	oxidative-stress responsive 1	oxidative-stress responsive 1
1757 41438_at	OSBPL8	AL049923	oxysterol binding protein-like 8	oxysterol-binding protein-like protein 8
1758 34329_at	PAK2	N25547	p21 (CDKN1A)-activated kinase 2	
1759 39710_at	P311	U30521	P311 protein	P311 HUM
1760 36136_at	PIG11	AF010315	p53-induced protein	Pig11
1761 40441_g_at	PAI-RBP1	AL080119	PAI-1 mRNA-binding protein	hypothetical protein
1762 40440_at	PAI-RBP1	AL080119	PAI-1 mRNA-binding protein	hypothetical protein
1763 32001_s_at	PACE4	M80482	paired basic amino acid cleaving system 4	subtilisin-like protease
				paired box gene 8, isoform PAX8A; paired box gene 8, isoform PAX8B; paired box gene 8, isoform PAX8C; paired box gene 8, isoform PAX8D; paired box gene 8, isoform PAX8E
1764 121_at	PAX8	X69699	paired box gene 8	homeobox protein
1765 40127_at	PMX1	M95929	paired mesoderm homeo box 1	KIAA0992 protein
1766 41191_at	KIAA0992	AB023209	palladin	paraoxonase
1767 40504_at	PON2	AF001601	paraoxonase 2	
			partially supported by FGENES and GENSCAN	hypothetical protein
1768 36032_at	dJ167A19.1	AL031427		Dfs70
1769 39243_s_at	PSIP2	U94319	PC4 and SFRS1 interacting protein 2	KIAA0824 protein
1770 41665_at	PCF11	AB020631	PCF11p homolog	
1771 38758_at	PDAP1	R98910	PDGFA associated protein 1	
1772 36937_s_at	PDLIM1	U90878	PDZ and LIM domain 1 (elfin)	carboxyl terminal LIM domain protein
			PDZ domain containing guanine nucleotide exchange factor(GEF)1	PDZ domain containing guanine nucleotide exchange factor(GEF)1
1773 32026_s_at	PDZ-GEF1	AB002311	nucleotide exchange factor(GEF)1	
1774 34745_at	PDZ-GEF1	AF070570	PDZ domain containing guanine nucleotide exchange factor(GEF)1	
			PEDF; Human pigment epithelium-derived factor gene, complete cds.	pigment epithelium-derived factor
1775 40856_at	SERPINF1; PEDF	U29953	factor gene, complete cds.	
			pentaxin-related gene, rapidly induced by IL-1 beta	tumor necrosis factor
1776 1491_at	PTX3	M31166		peptidylglycine alpha-amidating monooxygenase
1777 38465_at	PAM	M37721	peptidylglycine alpha-amidating monooxygenase	
1778 35823_at	PPIB	M63573	peptidylprolyl isomerase B (cyclophilin B)	secreted cyclophilin-like protein

fig-21



	A	B	C	D	E
1779 37422_at	PPIC	S71018	peptidylprolyl isomerase C (cyclophilin C)	cyclophilin C	
1780 37385_at	PPIG	U40763	peptidyl-prolyl isomerase G (cyclophilin G)	CARS-Cyp	
1781 36829_at	PER1	AF022991	period homolog 1 (Drosophila)	Rigli	
1782 35835_at	PDL-108	AB019409	periodontal ligament fibroblast protein		
			peripheral benzodiazepine receptor; Human peripheral benzodiazepine receptor (hpb) mRNA, complete cds.	peripheral benzodiazepine receptor; peripheral benzodiazepine receptor short form	
1783 32806_at	BZRP; MBR; PBR	M36035		PMP-22(PAS-11/SR13/Gas-3)	
1784 38653_at	PMP22	D11428	peripheral myelin protein 22	peroxiredoxin 1	
1785 41213_at	PRDX1	X67951	peroxiredoxin 1	Aop1_Human, MER5(Aop1_Mouse)-like protein	
1786 36631_at	PRDX3	D49396	peroxiredoxin 3	antioxidant enzyme AOE37-2	
1787 38435_at	PRDX4	U25182	peroxiredoxin 4	peroxisomal biogenesis factor	
1788 37900_at	PEX11B	AF093670	peroxisomal biogenesis factor 11B	Pex3 protein	
1789 36864_at	PEX3	AJ001625	peroxisomal biogenesis factor 3	peroxisomal long-chain acyl-coA thioesterase	
1790 36625_at	ZAP128	L40401	peroxisomal long-chain acyl-coA thioesterase	peroxisome assembly factor-1	
1791 33265_at	PXMP3	M86852	peroxisomal membrane protein 3 (35kD, Zellweger syndrome)	KIAA0834 protein	
1792 36502_at	PFTK1	AB020641	PFTAIRE protein kinase 1	PHD finger protein 3	
1793 37694_at	PHF3	D87685	PHD finger protein 3		
1794 39381_at	XAP135	AF055030	PHD zinc finger protein XAP135	PHD zinc finger protein XAP135, isoform a; PHD zinc finger protein XAP135, isoform b	
1795 1434_at	PTEN	U92436	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	MMAC1	
1796 34797_at	PPAP2A	AF014402	phosphatidic acid phosphatase type 2A	type-2 phosphatidic acid phosphatase alpha- 1	
1797 33862_at	PPAP2B	AF017786	phosphatidic acid phosphatase type 2B	phosphatidic acid phosphohydrolase homolog	
1798 40783_s_at	PIK4CA	L36151	phosphatidylinositol 4-kinase, catalytic, alpha polypeptide	phosphatidylinositol 4-kinase	
1799 37685_at	PICALM	U45976	phosphatidylinositol binding clathrin assembly protein	CALM	

Fig-21

A	B	C	D	E
1800 39993_at	PIGA	D11466	phosphatidylinositol glycan, class A (paroxysmal nocturnal hemoglobinuria)	PIG-A protein
1801 314_at	PIGB	D42138	phosphatidylinositol glycan, class B	PIG-B
1802 751_at	PIGC	D85418	phosphatidylinositol glycan, class C	phosphatidylinositol-glycan-class C (PIG-C)
1803 776_at	PIGF	D13435	phosphatidylinositol glycan, class F	PIG-F
1804 40629_at	PIGH	L19783	phosphatidylinositol glycan, class H	phosphatidylinositol glycan, class H
1805 38297_at	PITPNM	X98654	phosphatidylinositol transfer protein, membrane-associated	homologue of Drosophila retinal degeneration B gene
1806 35741_at	PIP5K2B	U85245	phosphatidylinositol-4-phosphate 5-kinase, type II, beta	phosphatidylinositol-4-phosphate 5-kinase type II beta
1807 37320_at	PTDSS1	D14694	phosphatidylserine synthase 1	phosphatidylserine synthase 1
1808 33705_at	PDE4B	L20971	phosphodiesterase 4B, cAMP-specific (Drosophila)	phosphodiesterase
1809 39422_at	PDE4DIP	AB007923	phosphodiesterase 4D interacting protein (myomegalin)	KIAA0454 protein
1810 37676_at	PDE8A	AF056490	phosphodiesterase 8A	cAMP-specific phosphodiesterase 8A
1811 37188_at	PCK2	X92720	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	phosphoenolpyruvate carboxykinase (GTP)
1812 39175_at	PFKP	D25328	phosphofructokinase, platelet	platelet-type phosphofructokinase
1813 32210_at	PGM1	M83088	phosphoglucomutase 1	phosphoglucomutase 1
1814 36963_at	PGD	U30255	phosphogluconate dehydrogenase	phosphogluconate dehydrogenase
1815 37677_at	PGK1	V00572	phosphoglycerate kinase 1	phosphoglycerate kinase 1
1816 41221_at	PGAM1	J04173	phosphoglycerate mutase 1 (brain)	phosphoglycerate mutase 2
1817 35665_at	PIK3C3	Z46973	phosphoinositide-3-kinase, class 3	phosphatidylinositol 3-kinase
1818 1269_at	PIK3R1	M61906	phosphoinositide-3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)	
1819 37961_at	PIK3R3	U90907	phosphoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma)	
1820 32775_r_at	PLSCR1	AB006746	phospholipid scramblase 1	phospholipid scramblase 1
1821 32260_at	PEA15	X86809	phosphoprotein enriched in astrocytes 15	
1822 36489_at	PRPS1	D00860	phosphoribosyl pyrophosphate synthetase 1	phosphoribosyl pyrophosphate synthetase subunit 1

Fig. 21

A	B	C	D	E
1823 37338_at	PRPSAP1	D61391	phosphoribosyl pyrophosphate synthetase-associated protein 1	phosphoribosyl pyrophosphate synthetase-associated protein 39
1824 39056_at	PAICS	X53793	phosphoribosylaminimidazole carboxylase,	phosphoribosylaminimidazole carboxylase,
1825 37392_at	PHKB	X84908	phosphoribosylaminimidazole succinocarboxamide synthetase	phosphoribosylaminimidazole succinocarboxamide synthetase
1826 36667_at	PYGB	U47025	phosphorylase kinase, beta	phosphorylase kinase
1827 32724_at	PHYH	AF023462	phosphorylase, glycogen; brain	glycogen phosphorylase B
1828 33543_s_at	PNN	U77718	phytanoyl-CoA hydroxylase (Refsum disease)	peroxisomal phytanoyl-CoA alpha-hydroxylase
1829 39003_at	PTTG1IP	Z50022	pinin, desmosome associated protein	pinin
1830 34793_s_at	PLS3	M22299	pituitary tumor-transforming 1 interacting protein	putative surface glycoprotein
1831 32569_at	PAFAH1B1	L13385	platelet-activating factor acetylhydrolase, isoform 1b, alpha subunit (45kD)	platelet-derived growth factor receptor A chain
1832 1731_at	PDGFRA	M21574	platelet-derived growth factor receptor, alpha polypeptide	cytohesin 1, isoform 1; cytohesin 1, isoform 2
1833 38666_at	PSCD1	M85169	pleckstrin homology, Sec7 and coiled/coiled domains 1 (cytohesin 1)	cytohesin-2
1834 38741_at	PSCD2	U70728	pleckstrin homology, Sec7 and coiled/coiled domains 2 (cytohesin-2)	C2H2 zinc finger protein PLAGL1
1835 36943_r_at	PLAGL1	U81992	pleiomorphic adenoma gene-like 1	plexin B2
1836 34780_at	PLXNB2	AB002313	plexin B2	VESPR
1837 32193_at	PLXNC1	AF030339	plexin C1	poly(ADP-ribose) glycohydrolase
1838 38270_at	PARG	AF005043	poly (ADP-ribose) glycohydrolase	polyadenylate binding protein II
1839 31951_s_at	PABPC1	Z48501	poly(A) binding protein, cytoplasmic 1	poly(A) binding protein, cytoplasmic 1
1840 31950_at	PABPC1	Y00345	poly(A) binding protein, cytoplasmic 1	poly(A)-specific ribonuclease
1841 36003_at	PARN	AJ005698	poly(A)-specific ribonuclease (deadenylation nuclease)	poly(A)-specific ribonuclease sub2.3
1842 34305_at	PCBP1	Z29505	poly(rC) binding protein 1	hnRNP-E2
1843 35746_r_at	PCBP2	X78136	poly(rC) binding protein 2	hnRNP-E2
1844 35745_f_at	PCBP2	X78136	poly(rC) binding protein 2	
1845 39868_at	PCBP3	AL046394	poly(rC) binding protein 3	

Fig. 21

A	B	C	D	E
1846 38120_at	PKD2	U50928	polycystic kidney disease 2 (autosomal dominant)	polycystin 2
1847 33380_at	POLS	AB005754	polymerase (DNA directed) sigma	LAK-1
1848 38702_at	POLE3	AF070640	polymerase (DNA directed), epsilon 3 (p17 subunit)	polymerase (DNA directed), epsilon 3 (p17 subunit)
1849 40791_at	POLR2A	X63564	polymerase (RNA) II (DNA directed) polypeptide A (220kD)	RNA polymerase II largest subunit
1850 39746_at	POLR2B	X63563	polymerase (RNA) II (DNA directed) polypeptide B (140kD)	RNA polymerase II 140 kDa subunit
1851 36027_at	POLR2F	AA418779	polymerase (RNA) II (DNA directed) polypeptide F	
1852 35631_at	POLR2H	U37689	polymerase (RNA) II (DNA directed) polypeptide H	RNA polymerase II subunit
1853 1248_at	POLR2H	U37689	polymerase (RNA) II (DNA directed) polypeptide H	RNA polymerase II subunit
1854 503_at	POLR2L	U37690	polymerase (RNA) II (DNA directed) polypeptide L (7.6kD)	RNA polymerase II subunit
1855 35841_at	POLR2L	N24355	polymerase (RNA) II (DNA directed) polypeptide L (7.6kD)	
1856 34320_at	PTRF	AL050224	polymerase I and transcript release factor	
1857 34005_at	PIGR	X73079	polymeric immunoglobulin receptor	Polymeric immunoglobulin receptor
1858 40593_at	PTBP1	X66975	polypyrimidine tract binding protein 1	nuclear ribonucleoprotein
1859 31600_s_at	PMS2L1	D38435	postmeiotic segregation increased 2-like 1	
1860 AFFX-CreX-5_at			pot. ORF1 (aa 1-73); ORF2, put. cre protein (aa 1-343); Bacteriophage P1 cre gene for recombinase protein.	
1861 AFFX-CreX-3_at		X03453	pot. ORF1 (aa 1-73); ORF2, put. cre protein (aa 1-343); Bacteriophage P1 cre gene for recombinase protein.	
1862 315_at	PRDM2	D45132	PR domain containing 2, with ZNF domain	zinc-finger DNA-binding protein
1863 32696_at	PBX3	X59841	pre-B-cell leukemia transcription factor 3	homeobox protein

Fig. 21

A	B	C	D	E
			precursor; Human prolyl 4-hydroxylase beta-subunit and disulfide isomerase (P4HB) gene, exon 11, clones 6B-(1,3,5,6).	
1864 36666_at	P4HB	M22806		prolyl 4-hydroxylase beta-subunit
1865 34321_i_at	GS3786	D87120	predicted osteoblast protein	GS3786
1866 41003_at	PFDN4	U41816	prefoldin 4	C-1
1867 38698_at	PREI3	AL080070	preimplantation protein 3	hypothetical protein
1868 40269_at	PRP18	U51990	pre-mRNA processing factor 18	hPrp18
1869 38291_at	PENK	J00123	preproenkephalin (; Human enkephalin gene: exon 3 and 3'lank.	proenkephalin
1870 641_at	PSN1	L76517	presenilin 1 (Alzheimer disease 3)	presenilin 1
1871 40621_at	PAWR	U63809	PRKC, apoptosis, WT1, regulator	prostate apoptosis response protein par-4
1872 41773_at	PCOLN3	U58048	procollagen (type III) N-endopeptidase	PRSM1
1873 31609_s_at	PCOLCE	L33799	procollagen C-endopeptidase enhancer	procollagen C-proteinase enhancer protein
1874 34795_at	PLOD2	U84573	procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2	lysyl hydroxylase isoform 2
			procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI)	lysyl hydroxylase
1875 36184_at	PLOD	L06419	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I
1876 37037_at	P4HA1	M24486	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide II	
1877 34390_at	P4HA2	U90441		prolyl 4-hydroxylase alpha (II) subunit
			procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55)	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55)
1878 691_g_at	P4HB	J02783	profilin 2	profilin II
1879 38840_s_at	PFN2	L10678	profilin 2	profilin 2 isoform b; profilin 2 isoform a
1880 38839_at	PFN2	AL096719	progesterone receptor membrane component 1	putative progesterone binding protein
1881 38802_at	PGRMC1	Y12711	progesterone receptor membrane component 2	progesterone binding protein
1882 38821_at	PGRMC2	AJ002030		

Fig. 21

A	B	C	D	E
1883 39035_at	DD5	AF06010	progesterone induced protein	progesterone induced protein
1884 39036_g_at	DD5	AF06010	progesterone induced protein	progesterone induced protein
1885 35218_at	PDCD10	AF02385	programmed cell death 10	TFAR15
1886 37569_at	PDCD6	AF035606	programmed cell death 6	calcium binding protein
1887 32212_at	PDCD8	AL049703	programmed cell death 8 (apoptosis-inducing factor)	hypothetical protein
1888 36592_at	PHB	S85655	prohibitin	prohibitin
1889 1884_s_at	PCNA	M15796	proliferating cell nuclear antigen	proliferating cell nuclear antigen
1890 41600_at	PA2G4	U59435	proliferation-associated 2G4, 38kD	cell cycle protein p38-2G4 homolog
1891 35978_at	PRRG1	AF09242	proline-rich Gla (G-carboxyglutamic acid) polypeptide 1	proline-rich Gla protein 1
1892 36023_at	PRH1	AI864120	proline-rich protein HaeIII subfamily 1	
1893 40803_at	PORIMIN	AL050161	pro-oncogene receptor inducing membrane injury gene	pro-oncogene receptor inducing membrane injury gene
1894 1348_s_at	PCCA	S79219	propionyl Coenzyme A carboxylase, alpha polypeptide	Propionyl-Coenzyme A carboxylase, alpha polypeptide precursor
1895 36561_at	PCCB	X73424	propionyl Coenzyme A carboxylase, beta polypeptide	propionyl-CoA carboxylase
1896 41032_at	PCSK5	U56387	proprotein convertase subtilisin/kexin type 5	protease PC6 isoform A
1897 36795_at	PSAP	J03077	prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)	prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)
1898 38406_f_at	PTGDS	AI207842	prostaglandin D2 synthase (21kD, brain)	
1899 828_at	PTGER2	U19487	prostaglandin E receptor 2 (subtype EP2), 53kD	prostaglandin E2 receptor
1900 1890_at	PLAB	AB000584	prostate differentiation factor	TGF-beta superfamily protein
1901 32611_at	PBP	X75252	prostatic binding protein	phosphatidylethanolamine binding protein
1902 719_g_at	PRSS11	D87258	protease, serine, 11 (IGF binding)	serine protease with IGF-binding motif
1903 718_at	PRSS11	D87258	protease, serine, 11 (IGF binding)	serine protease with IGF-binding motif
1904 33368_at	PRSS15	X76040	protease, serine, 15	Lon protease-like protein
1905 40078_at	SPUVE	AF015287	protease, serine, 23	serine protease
1906 39845_at	PRSS25	AF020760	protease, serine, 25	serine protease
1907 688_at	PSMC1	L02426	proteasome (prosome, macropain) 26S subunit, ATPase, 1	26S protease (S4) regulatory subunit

Fig. 21

A	B	C	D	E
1908 35353_at	PSMC2	D11094	proteasome (prosome, macropain) 26S subunit, ATPase, 2	MSS1 protein
1909 592_at	PSMC3	M34079	proteasome (prosome, macropain) 26S subunit, ATPase, 3	proteasome (prosome, macropain) 26S subunit, ATPase, 3
1910 37766_s_at	PSMC5	AF035309	proteasome (prosome, macropain) 26S subunit, ATPase, 5	
1911 949_s_at	PSMC6	D78275	proteasome (prosome, macropain) 26S subunit, ATPase, 6	proteasome subunit p42
1912 1314_at	PSMD1	D44466	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	proteasome subunit p112
1913 1192_at	PSMD12	AB003103	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	26S proteasome subunit p55
1914 32240_at	PSMD5	D31889	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5
1915 945_at	PSMD7	D50063	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog)	proteasome subunit p40 / Mov34 protein
1916 40276_at	PSMD7	D50063	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog)	proteasome subunit p40 / Mov34 protein
1917 32584_at	PSMD8	D38047	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	26S proteasome subunit p31
1918 36492_at	PSMD9	A1347155	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	
1919 41171_at	PSME2	D45248	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)	proteasome activator hPA28 suunit beta
1920 1184_at	PSME2	D45248	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)	proteasome activator hPA28 suunit beta
1921 36974_at	PSMF1	D88378	proteasome (prosome, macropain) inhibitor subunit 1 (PI31)	proteasome inhibitor hPI31 subunit
1922 38371_at	PSMA1	M64992	proteasome (prosome, macropain) subunit, alpha type, 1	prosomeal protein P30-33K
1923 1446_at	PSMA2	D00760	proteasome (prosome, macropain) subunit, alpha type, 2	proteasome (prosome, macropain) subunit, alpha type, 2
1924 1448_at	PSMA3	D00762	proteasome (prosome, macropain) subunit, alpha type, 3	proteasome (prosome, macropain) subunit, alpha type, 3

Fig 21

	A	B	C	D	E
1925	1450_g_at	PSMA4	D00763	proteasome (prosome, macropain) subunit, alpha type, 4	proteasome (prosome, macropain) subunit, alpha type, 4
1926	1449_at	PSMA4	D00763	proteasome (prosome, macropain) subunit, alpha type, 4	proteasome (prosome, macropain) subunit, alpha type, 4
1927	37046_at	PSMA5	A1246726	proteasome (prosome, macropain) subunit, alpha type, 5	
1928	36122_at	PSMA6	X59417	proteasome (prosome, macropain) subunit, alpha type, 6	prosome P27K protein
1929	1447_at	PSMB1	D00761	proteasome (prosome, macropain) subunit, beta type, 1	proteasome (prosome, macropain) subunit, beta type, 1
1930	1310_at	PSMB2	D26599	proteasome (prosome, macropain) subunit, beta type, 2	proteasome subunit HsC7-1
1931	33154_at	PSMB4	D26600	proteasome (prosome, macropain) subunit, beta type, 4	proteasome subunit HsN3
1932	1311_at	PSMB4	D26600	proteasome (prosome, macropain) subunit, beta type, 4	proteasome subunit HsN3
1933	37666_at	PSMB5	D29011	proteasome (prosome, macropain) subunit, beta type, 5	proteasome subunit X
1934	941_at	PSMB6	D29012	proteasome (prosome, macropain) subunit, beta type, 6	proteasome subunit Y
1935	39060_at	PSMB7	D38048	proteasome (prosome, macropain) subunit, beta type, 7	proteasome subunit z
1936	1313_at	PSMB7	D38048	proteasome (prosome, macropain) subunit, beta type, 7	proteasome subunit z
1937	38287_at	PSMB9	AA089961	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protease 2)	
1938	41750_at	P5	D49489	protein disulfide isomerase-related protein	human P5
1939	32558_at	PIAS3	AB021868	protein inhibitor of activated STAT3	protein inhibitor of activated STAT3
1940	34376_at	PKIG	AB019517	protein kinase (cAMP-dependent, catalytic) inhibitor gamma	protein kinase inhibitor gamma
1941	36957_at	PRKCBP1	W22296	protein kinase C binding protein 1	
1942	1602_at	PRKCI	L33881	protein kinase C, iota	protein kinase C iota
1943	1603_g_at	PRKCI	L33881	protein kinase C, iota	protein kinase C iota
1944	36835_at	PRKCL2	U33052	protein kinase C-like 2	PRK2

fig. 21



	A	B	C	D	E
1945	41768_at	PRKAR1A	M33336	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	cAMP-dependent protein kinase type I-alpha subunit
1946	227_g_at	PRKAR1A	M33336	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	cAMP-dependent protein kinase type I-alpha subunit
1947	226_at	PRKAR1A	M33336	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	cAMP-dependent protein kinase type I-alpha subunit
1948	32205_at	PRKRA	AF072860	protein kinase, interferon-inducible double stranded RNA dependent activator	protein activator of the interferon-induced protein kinase
1949	37725_at	PPP1CC	X74008	protein phosphatase 1, catalytic subunit, gamma isoform	serine/threonine specific protein phosphatase
1950	40438_at	PPP1R12A	D87930	protein phosphatase 1, regulatory (inhibitor) subunit 12A	myosin phosphatase target subunit 1
1951	39366_at	PPP1R3C	N36638	protein phosphatase 1, regulatory (inhibitor) subunit 3C	
1952	41540_at	PPP1R7	Z50749	protein phosphatase 1, regulatory subunit 7	yeast sds22 homolog
1953	857_at	PPM1A	S87759	protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform	protein phosphatase 2C alpha
1954	36501_at	PPM1A	S87759	protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform	protein phosphatase 2C alpha
1955	37107_at	PPM1D	U78305	protein phosphatase 1D magnesium-dependent, delta isoform	Wip1
1956	924_s_at	PPP2CB	J03805	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	
1957	41167_at	PPP2R2A	M64929	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform	protein phosphatase-2A subunit-alpha
1958	1383_at	PPP2R2A	M64929	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform	protein phosphatase-2A subunit-alpha
1959	32734_at	PPP2R5E	L76703	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform	protein phosphatase B56-epsilon

Fig-21

A	B	C	D	E
1960 40786_at	PPP2R5C	U37352	protein phosphatase 2, regulatory subunit B (B56), gamma isoform	protein phosphatase 2A B'alpha1 regulatory subunit
1961 176_at	PPP2R5C	U37352	protein phosphatase 2, regulatory subunit B (B56), gamma isoform	protein phosphatase 2A B'alpha1 regulatory subunit
1962 39127_f_at	PPP2R4	X73478	protein phosphatase 2A, regulatory subunit B' (PR 53)	phosphotyrosyl phosphatase activator
1963 38277_at	PPP3CB	M29550	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform (calcineurin A beta)	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform (calcineurin A beta)
1964 32541_at	PPP3CC	S46622	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma)	calcineurin A catalytic subunit
1965 34371_at	PPP4R1	U79267	protein phosphatase 4, regulatory subunit 1	
1966 37581_at	PPP6C	X92972	protein phosphatase 6, catalytic subunit	protein phosphatase 6
1967 35752_s_at	PROS1	M15036	protein S (alpha)	protein S (alpha)
1968 32564_at	SEC61B	AA083129	protein translocation complex beta	
1969 1064_at	PTK9	U02680	protein tyrosine kinase 9	protein tyrosine kinase
1970 843_at	PTP4A1	U48296	protein tyrosine phosphatase type IVA, member 1	protein tyrosine phosphatase PTPCAAX1
1971 38415_at	PTP4A2	U14603	protein tyrosine phosphatase type IVA, member 2	protein-tyrosine phosphatase
1972 1241_at	PTP4A2	U14603	member 2	protein-tyrosine phosphatase
1973 40137_at	PTPN1	M31724	protein tyrosine phosphatase, non-receptor type 1	protein tyrosine phosphatase, non-receptor type 1
1974 1463_at	PTPN12	M93425	protein tyrosine phosphatase, non-receptor type 12	protein tyrosine phosphatase
1975 34198_at	PTPN13	U12128	protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)	protein tyrosine phosphatase 1E
1976 1496_at	PTPRA	M34668	protein tyrosine phosphatase, receptor type, A	protein tyrosine phosphatase, receptor type, A, isoform 1 precursor; protein tyrosine phosphatase, receptor type, A, isoform 2 precursor

Fig. 21

A	B	C	D	E
1977 36204_at	PTPRF	Y00815	protein tyrosine phosphatase, receptor type, F	put. LAR preprotein (AA -16 to 1881)
1978 41780_at	PPFIA1	U22816	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1	LAR-interacting protein 1b
1979 1488_at	PTPRK	L77886	protein tyrosine phosphatase, receptor type, K	protein tyrosine phosphatase
1980 995_g_at	PTPRM	X58288	protein tyrosine phosphatase, receptor type, M	protein-tyrosine phosphatase
1981 31892_at	PTPRM	X58288	protein tyrosine phosphatase, receptor type, M	protein-tyrosine phosphatase
1982 41141_at	PRKRIR	AL049970	protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor)	hypothetical protein
1983 37737_at	PCMT1	D25547	protein-L-isoaspartate (D-aspartate) O-methyltransferase	PIMT isozyme I
1984 37736_at	PCMT1	D13892	protein-L-isoaspartate (D-aspartate) O-methyltransferase	carboxyl methyltransferase
1985 32227_at	PRG1	X17042	proteoglycan 1, secretory granule	proteoglycan 1, secretory granule
1986 38590_r_at	PTMA	M14630	prothymosin, alpha (gene sequence 28)	prothymosin, alpha (gene sequence 28)
1987 38589_i_at	PTMA	M14630	prothymosin, alpha (gene sequence 28)	prothymosin, alpha (gene sequence 28)
1988 37936_at	HRP4P	AI184802	PRP4/STKWD splicing factor	
1989 31697_s_at	FTHP1	J04755	pseudoferritin H protein; Human ferritin H processed pseudogene, complete cds.	
1990 36117_at	PTK2	L13616	PTK2 protein tyrosine kinase 2	focal adhesion kinase
1991 40048_at	PUM1	D43951	pumilio homolog 1 (Drosophila)	KIAA0099 protein
1992 35359_at	PUM2	D87078	pumilio homolog 2 (Drosophila)	KIAA0235 protein
1993 35221_at	PURA	X91648	purne-rich element binding protein A	
1994 33341_at	GNB1	X04526	put. ORFX (AA 1-75); beta subunit (AA 1-340); Human liver mRNA for beta-subunit signal transducing proteins Gs/Gi (beta-G).	guanine nucleotide-binding protein, beta-1 subunit
1995 33720_at	LOC56902	L48692	putative 28 kDa protein	
1996 39363_at	BC-2	AF042384	putative breast adenocarcinoma marker (32kD)	BC-2 protein

Fig. 21

A	B	C	D	E
1997 39884_g_at	HSA9761	AF091078	putative dimethyladenosine transferase	putative dimethyladenosine transferase
1998 38841_at	GDBR1	AF068195	putative glioblastoma cell differentiation-related	putative glioblastoma cell differentiation-related protein
1999 41188_at	LC27	W28186	putative integral membrane transporter	
2000 38984_at	KIAA0436	AB007896	putative L-type neutral amino acid transporter	
2001 39116_at	LOC54499	AF070626	putative membrane protein	
2002 35286_r_at	RY1	X76302	putative nucleic acid binding protein RY-1	nucleic acid binding protein
2003 36852_at	N33	U42349	Putative prostate cancer tumor suppressor	
2004 33710_at	C3F	U72515	putative protein similar to nessy (Drosophila)	C3f
2005 40203_at	SUI1	AJ012375	putative translation initiation factor	putative translation initiation factor
2006 37678_at	NMA	U23070	putative transmembrane protein	putative transmembrane protein
2007 35326_at	54TM	AF004876	putative transmembrane protein; homolog of yeast Golgi membrane protein Yif1p (Yip1p-interacting factor)	54TMp
2008 35697_at	PTS	L76259	putative; Homo sapiens PTS gene, complete cds.	6-pyruvoyltetrahydropterin synthase
2009 40887_g_at	PTI-1	L41498	putative; originally identified as an 'oncogene', product renamed by NCBI staff; Homo sapiens longation factor 1-alpha 1 (PTI-1) mRNA, complete cds.	longation factor 1-alpha 1
2010 40886_at	PTI-1	L41498	putative; originally identified as an 'oncogene', product renamed by NCBI staff; Homo sapiens longation factor 1-alpha 1 (PTI-1) mRNA, complete cds.	longation factor 1-alpha 1
2011 33219_at	VDU1	AB029020	pVHL-interacting deubiquitinating enzyme 1	KIAA1097 protein
2012 36164_at	PDX1	U82328	Pyruvate dehydrogenase complex, lipoyl-containing component X; E3-binding protein	pyruvate dehydrogenase complex protein X subunit precursor
2013 32378_at	PKM2	M26252	pyruvate kinase, muscle	pyruvate kinase, muscle
2014 260_at	QDPR	M16447	quinoid dihydropteridine reductase	quinoid dihydropteridine reductase

Fig. 21

	A	B	C	D	E
2015	36610_at	R3HDM	D21852	R3H domain (binds single-stranded nucleic acids) containing	KIAA0029 protein
2016	39030_at	RABAC1	AJ133534	Rab acceptor 1 (prenylated)	prenylated Rab acceptor 1 (PRA1)
2017	37703_at	RABGGTB	Y08201	Rab geranyltransferase, beta subunit	rab geranyltransferase
2018	38264_at	RABIF	U74324	RAB interacting factor	guanine nucleotide exchange factor mss4
2019	36660_at	RAB11A	AF000231	RAB11A, member RAS oncogene family	rab11a
2020	35325_at	RAB14	AF052113	RAB14, member RAS oncogene family	
2021	34393_r_at	RAB1A	AL050268	RAB1A, member RAS oncogene family	hypothetical protein
2022	34392_s_at	RAB1A	AL050268	RAB1A, member RAS oncogene family	hypothetical protein
2023	33326_at	RAB21	D42087	RAB21, member RAS oncogene family	RAB21, member RAS oncogene family
2024	809_at	RAB27A	U57094	RAB27A, member RAS oncogene family	Rab27a
2025	33371_s_at	RAB31	U59877	RAB31, member RAS oncogene family	low-Mr GTP-binding protein Rab31
2026	36110_at	RAB5A	M28215	RAB5A, member RAS oncogene family	GTP-binding protein
2027	35289_at	GAPCENA	AJ011679	rab6 GTPase activating protein (GAP and centrosome-associated)	Rab6 GTPase activating protein, GAPCena
2028	35304_at	RAB6A	AF052130	RAB6A, member RAS oncogene family	
2029	39628_at	RAB9A	AI671547	RAB9A, member RAS oncogene family	
2030	41716_at	RC3	AB020663	rabconnectin-3	KIAA0856 protein
2031	37543_at	ARHGEF6	D25304	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	
2032	36857_at	RAD1	AF084513	RAD1 homolog (S. pombe)	DNA repair exonuclease
2033	38114_at	RAD21	D38551	RAD21 homolog (S. pombe)	RAD21 homolog
2034	1874_at	RAD23B	D21090	RAD23 homolog B (S. cerevisiae)	XP-C repair complementing protein (p58/HHR23B)
2035	32757_at	RAE1	U84720	RAE1 RNA export 1 homolog (S. pombe)	mRNA export protein
2036	1524_at			RAGE-4 ORF2: one of 2 possible coding regions; RAGE-4 ORF3: one of 2 possible coding regions; Human renal cell carcinoma antigen RAGE-4 mRNA, complete putative cds.	
2037	36628_at	RALBP1	U46194	ralA binding protein 1	RLIP76 protein
2038	37539_at	RGL	L42542	RalGDS-like gene	KIAA0959 protein
			AB023176		

Fig. 21

	A	B	C	D	E
2039	41342_at	RANBP1	D38076	RAN binding protein 1	Ran-BP1 (Ran-binding protein 1)
2040	40824_at	RANBP16	AB018288	RAN binding protein 16	KIAA0745 protein
2041	41174_at	RANBP2L1	AF012086	RAN binding protein 2-like 1	Ran binding protein 2
2042	35255_at	RANBP7	AF098799	RAN binding protein 7	RanBP7/importin 7
2043	32602_at	RAP1GDS1	X63465	RAP1, GTP-GDP dissociation stimulator 1	smg GDS
2044	1848_at	RAP1A	M22995	RAP1A, member of RAS oncogene family	ras-related protein
2045	40146_at	RAP1B	AL080212	RAP1B, member of RAS oncogene family	hypothetical protein
2046	39601_at	RASSF1	AF061836	Ras association (RalGDS/AF-6) domain family 1	putative tumor suppressor protein
2047	37598_at	RASSF2	D79990	Ras association (RalGDS/AF-6) domain family 2	Ras association (RalGDS/AF-6) domain family 2
2048	1659_s_at	RHEB2	D78132	Ras homolog enriched in brain 2	ras-related GTP-binding protein
2049	37309_at	ARHA	L09159	ras homolog gene family, member A	multidrug resistance protein
2050	1394_at	ARHA	L25080	ras homolog gene family, member A	GTP-binding protein
2051	35803_at	ARHE	S82240	ras homolog gene family, member E	RhoE
2052	36935_at	RASA1	M23379	RAS p21 protein activator (GTPase activating protein) 1	GTPase-activating protein
2053	1675_at	RASA1	M23379	RAS p21 protein activator (GTPase activating protein) 1	GTPase-activating protein
2054	35793_at	G3BP2	AB014560	Ras-GTPase activating protein SH3 domain-binding protein 2	KIAA0660 protein
2055	40864_at	RAC1	D25274	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	
2056	2050_s_at	RAC1	M29870	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	ras-related C3 botulinum toxin substrate 1 isoform Rac1; ras-related C3 botulinum toxin substrate 1 isoform Rac1b
2057	35316_at	RAGA	U41654	Ras-related GTP-binding protein	adenovirus E3-14.7K interacting protein 1
2058	33234_at	BCAA	AA887480	RBP1-like protein	
2059	41407_at	RDBP	L03411	RD RNA-binding protein	RD protein
2060	34684_at	RECQL	L36140	RecQ protein-like (DNA helicase Q1-like)	DNA helicase

Fig. 21

A	B	C	D	E
2061 34685_at	RECQL	A1685944	RecQ protein-like (DNA helicase Q1-like) regulated at the translational level; contains l-mfa domain; utilizes unique GTG start codon; Homo sapiens HIC protein isoform p40 and HIC protein isoform p32 mRNAs, complete cds.	HIC protein isoform p40; HIC protein isoform p32
2062 37842_at	HIC	AF054589	regulator of G-protein signalling 19 interacting protein 1	RGS-GAIP interacting protein GIPC
2063 35756_at	RGS19IP1	AF089816	regulator of G-protein signalling 2, 24kD	helix-loop-helix phosphoprotein
2064 37701_at	RGS2	L13463	regulator of nonsense transcripts 2	hypothetical protein
2065 35722_at	RENT2	AL080198	related RAS viral (r-ras) oncogene homolog 2	
2066 32827_at	RRAS2	A1365215	remainder of gene in clone 549K18 (AL023654)	CGI-51 protein
2067 34845_at	dJ79617.4	AL035398	replication factor C (activator 1) 4 (37kD)	replication factor C, 37-kDa subunit
2068 1055_g_at	RFC4	M87339	replication protein A1 (70kD)	replication protein A, 70-kDa subunit
2069 38481_at	RPA1	M63488	replication protein A3 (14kD)	replication protein A 14kDa subunit
2070 652_g_at	RPA3	L07493	REST corepressor	REST corepressor
2071 37651_at	RCOR	D31888	restin (Reed-Steinberg cell-expressed intermediate filament-associated protein)	
2072 34350_at	RSN	X64838	ret finger protein 2	restin
2073 31851_at	RFP2	AJ224819	reticulocalbin 1, EF-hand calcium binding domain	tumor suppressor
2074 40556_at	RCN1	D42073	reticulocalbin 2, EF-hand calcium binding domain	reticulocalbin
2075 37727_i_at	RCN2	X78669	reticulocalbin 2, EF-hand calcium binding domain	EF-hand protein
2076 37728_r_at	RCN2	X78669	reticulocalbin 2, EF-hand calcium binding domain	EF-hand protein
2077 31536_at	RTN4	AB020693	reticulon 4	KIAA0886 protein
2078 39964_at	RP2	AJ007590	retinitis pigmentosa 2 (X-linked recessive)	XRP2 protein
2079 38164_at	RPGR	U57629	retinitis pigmentosa GTPase regulator retinoblastoma 1 (including osteosarcoma)	retinitis pigmentosa GTPase regulator
2080 2044_s_at	RB1	M15400		retinoblastoma 1 (including osteosarcoma)

Fig. 21

	A	B	C	D	E
2081	35227_at	RBBP8	U72066	retinoblastoma binding protein 8	CBP interacting protein CIP
2082	33860_at	RBAF600	AB007931	retinoblastoma-associated factor 600	KIAA0462 protein
2083	32597_at	RBL2	X76061	retinoblastoma-like 2 (p130)	130K protein
2084	35848_at	RAI17	AL049432	retinoic acid induced 17	
				retropseudogene; Human	
2085	31672_g_at	RBMS1P; MSSP1	D82351	retropseudogene MSSP-1 DNA, complete cds.	MSSP-1
2086	38908_s_at	REV3L	AL096744	REV3-like, catalytic subunit of DNA polymerase zeta (yeast)	hypothetical protein
2087	35236_g_at	RECK	AA099265	reversion-inducing-cysteine-rich protein with kazal motifs	
2088	35235_at	RECK	AA099265	reversion-inducing-cysteine-rich protein with kazal motifs	
2089	35234_at	RECK	D50406	reversion-inducing-cysteine-rich protein with kazal motifs	RECK protein precursor
2090	553_g_at	ARHGAP1	U02570	Rho GTPase activating protein 1	CDC42 GTPase-activating protein
2091	39700_at	ARHGAP1	AI961929	Rho GTPase activating protein 1	
2092	34180_at	ARHGEF10	AB002292	Rho guanine nucleotide exchange factor (GEF) 10	Rho guanine nucleotide exchange factor 10
2093	40828_at	ARHGEF7	D63476	Rho guanine nucleotide exchange factor (GEF) 7	PAK-interacting exchange factor beta
2094	40100_at	ARHGEF2	U72206	rho/rac guanine nucleotide exchange factor (GEF) 2	guanine nucleotide regulatory factor
2095	36537_at	P114-RHO-GEF	AB011093	Rho-specific guanine nucleotide exchange factor p114	KIAA0521 protein
2096	41040_at	RPP38	U77664	ribonuclease P (38kD)	RNaseP protein P38
2097	32664_at	RNASE4	D37931	ribonuclease, RNase A family, 4	RNase 4
2098	36187_at	RNH	X13973	ribonuclease/angiogenin inhibitor	ribonuclease/angiogenin inhibitor
2099	34314_at	RRM1	X59543	ribonucleotide reductase M1 polypeptide	M1 subunit of ribonucleotide reductase
2100	2016_s_at	RPL10	M64241	ribosomal protein L10	Wilm's tumor-related protein
2101	41178_at	RPL11	X79234	ribosomal protein L11	ribosomal protein L11
2102	33668_at	RPL12	AF037643	ribosomal protein L12	ribosomal protein L13
2103	31509_at	RPL13	X64707	ribosomal protein L13	23 kD highly basic protein
2104	35119_at	RPL13A	X56932	ribosomal protein L13a	ribosomal protein L14
2105	31907_at	RPL14	D87735	ribosomal protein L14	

Fig. 21



	A	B	C	D	E
2106	32432_f_at	RPL15	L25899	ribosomal protein L15	ribosomal protein L10
2107	32440_at	RPL17	X53777	ribosomal protein L17	ribosomal protein L17
2108	31546_at	RPL18	L11566	ribosomal protein L18	ribosomal protein L18
2109	33614_at	RPL18A	X80822	ribosomal protein L18a	ribosomal protein L18a
2110	32435_at	RPL19	X63527	ribosomal protein L19	ribosomal protein L19
2111	32337_at	RPL21	U25789	ribosomal protein L21	ribosomal protein L21
2112	33451_s_at	RPL22	AI526079	ribosomal protein L22	
2113	32395_r_at	RPL23	X55954	ribosomal protein L23	HL23 ribosomal protein
2114	32394_s_at	RPL23	X55954	ribosomal protein L23	HL23 ribosomal protein
2115	32341_f_at	RPL23A	U37230	ribosomal protein L23a	ribosomal protein L23a
2116	33677_at	RPL24	M94314	ribosomal protein L24	ribosomal protein L30
2117	32444_at	RPL26	X69392	ribosomal protein L26	ribosomal protein L26
2118	39830_at	RPL27	AA044823	ribosomal protein L27	
2119	32436_at	RPL27A	U14968	ribosomal protein L27a	ribosomal protein L27a
2120	31708_at	RPL30	L05095	ribosomal protein L30	ribosomal protein L30
2121	33676_at	RPL31	X15940	ribosomal protein L31	ribosomal protein L31
2122	32276_at	RPL32	X03342	ribosomal protein L32	ribosomal protein L32
2123	33657_at	RPL34	L38941	ribosomal protein L34	ribosomal protein L34
2124	41765_at	RPL35	AI541285	ribosomal protein L35	
2125	41152_f_at	RPL36A	T89651	ribosomal protein L36a	
2126	33656_at	RPL37	D23661	ribosomal protein L37	ribosomal protein L37
2127	31962_at	RPL37A	L06499	ribosomal protein L37a	ribosomal protein L37a
2128	34085_at	RPL38	Z26876	ribosomal protein L38	ribosomal protein
2129	33485_at	RPL4	D23660	ribosomal protein L4	ribosomal protein
					human homologue to yeast ribosomal protein YL41
2130	32466_at	RPL41	Z12962	ribosomal protein L41	protein YL41
2131	33660_at	RPL5	U14966	ribosomal protein L5	ribosomal protein L5
2132	31952_at	RPL6	X69391	ribosomal protein L6	ribosomal protein L6
2133	36333_at	RPL7	X57958	ribosomal protein L7	ribosomal protein L7
2134	31505_at	RPL8	Z28407	ribosomal protein L8	ribosomal protein L8
2135	31568_at	RPS10	U14972	ribosomal protein S10	ribosomal protein S10
2136	32330_at	RPS11	X06617	ribosomal protein S11	ribosomal protein S11
2137	33116_f_at	RPS12	AA977163	ribosomal protein S12	
2138	33619_at	RPS13	L01124	ribosomal protein S13	ribosomal protein S13
2139	34317_g_at	RPS15A	W52024	ribosomal protein S15a	ribosomal protein S15a
2140	38061_at	RPS16	AI541256	ribosomal protein S16	

Fig. 21

	A	B	C	D	E
2141	34593_g_at	RPS17	M13932	ribosomal protein S17	ribosomal protein S17
2142	34592_at	RPS17	M13932	ribosomal protein S17	ribosomal protein S17
2143	31330_at	RPS19	M81757	ribosomal protein S19	S19 ribosomal protein
2144	31527_at	RPS2	X17206	ribosomal protein S2	ribosomal protein S2
2145	32438_at	RPS20	L06498	ribosomal protein S20	ribosomal protein S20
2146	347_s_at	RPS23	D14530	ribosomal protein S23	ribosomal protein
2147	32315_at	RPS24	M31520	ribosomal protein S24	ribosomal protein S24
2148	31573_at	RPS25	M64716	ribosomal protein S25	ribosomal protein
2149	32748_at	RPS27	A1557852	ribosomal protein S27 (metalloprotein)	
2150	34570_at	RPS27A	S79522	ribosomal protein S27/a	ubiquitin carboxyl extension protein
2151	39798_at	RPS28	R87876	ribosomal protein S28	
2152	34645_at	RPS3	X55715	ribosomal protein S3	ribosomal protein S3
2153	1653_at	RPS3A	M84711	ribosomal protein S3A	v-fos transformation effector protein
2154	34643_at	RPS4X	M58458	ribosomal protein S4, X-linked	ribosomal protein S4X isoform
2155	32437_at	RPS5	U14970	ribosomal protein S5	ribosomal protein S5
2156	31511_at	RPS9	U14971	ribosomal protein S9	ribosomal protein S9
2157	31538_at	RPLP0	M17885	ribosomal protein, large, P0	ribosomal protein P0
2158	31956_f_at	RPLP1	M17886	ribosomal protein, large, P1	ribosomal protein P1
2159	31957_r_at	RPLP1	M17886	ribosomal protein, large, P1	ribosomal protein P1
2160	33213_g_at	RRBP1	AF006751	ribosome binding protein 1 homolog 180kD (dog)	ES/130
2161	38331_at	RIT	Y07566	Ric-like, expressed in many tissues (Drosophila)	Ric-like, expressed in many tissues
2162	35656_at	RNF6	AJ010346	ring finger protein (C3H2C3 type) 6	RING-H2
2163	39150_at	RNF11	U69559	ring finger protein 11	
2164	35811_at	RNF13	AF037204	ring finger protein 13	RING zinc finger protein
2165	33343_at	RNF14	AB022663	ring finger protein 14	ring finger protein.14
2166	33484_at	RNF2	Y10571	ring finger protein 2	ring finger protein 2
2167	37964_at	RNF3	W25793	ring finger protein 3	
2168	35777_at	RNF4	AB000468	ring finger protein 4	zinc finger protein
				ring zinc-finger protein; escapes X chromosome inactivation; Human ring zinc finger protein (ZNF127-Xp) gene and 5' flanking sequence.	
2169	37650_at	ZNF127-Xp	U41315		ZNF127-Xp
2170	37732_at	RYBP	AL049940	RING1 and YY1 binding protein	

Fig. 21

	A	B	C	D	E
2171	38073_at	RNMT	AB007858	RNA (guanine-7-) methyltransferase	RNA (guanine-7-) methyltransferase
2172	41460_at	RBMT4	AF080561	RNA binding motif protein 14	SYT interacting protein SIP
2173	41741_at	RBMT3	U28686	RNA binding motif protein 3	RNPL
2174	35351_at	RBMT4	U89505	RNA binding motif protein 4	Hlark
2175	32804_at	RBMT5	AF091263	RNA binding motif protein 5	RNA binding motif protein 5
2176	40870_g_at	RBMT6	AF069517	RNA binding motif protein 6	RNA binding protein DEF-3
2177	40260_g_at	RBMT9	AL009266	RNA binding motif protein 9	hypothetical protein
2178	39731_at	RBMTX	Z23064	RNA binding motif protein, X chromosome	hnRNP G protein
2179	33867_s_at	RBMTS1	X77494	RNA binding motif, single stranded interacting protein 1	RNA binding motif, single stranded interacting protein 1, isoform a
2180	36186_at	RNPS1	L37368	RNA binding protein S1, serine-rich domain	RNA-binding protein
2181	35202_at	RNGTT	AF025654	RNA guanylyltransferase and 5'-phosphatase	mRNA capping enzyme
2182	33237_at	KIAA0801	AB018344	RNA helicase	KIAA0801 protein
2183	36045_at	RNAH	AJ223948	RNA helicase family	RNA helicase
2184	38762_at	RNAHP	AF083255	RNA helicase-related protein	RNA helicase-related protein
2185	38049_g_at	RBPM5	D84110	RNA-binding protein gene with multiple splicing	RBP-MS/type 4
2186	38047_at	RBPM5	D84109	RNA-binding protein gene with multiple splicing	RBP-MS/type 3
2187	38974_at	DJ-1	AF021819	RNA-binding protein regulatory subunit	RNA-binding protein regulatory subunit
2188	39725_at	RNPC2	L10910	RNA-binding region (RNP1, RRM) containing 2	splicing factor
2189	38011_at	RMP	AB006572	RPB5-mediated protein	RPB5 mediating protein
2190	35195_at	RTCD1	Y11651	RTC domain containing 1	phosphate cyclase
2191	943_at	RUNX1	D43968	runx-related transcription factor 1 (acute myeloid leukemia 1; am1 oncogene)	AML1b protein
2192	40124_at	RUVBL1	Y18418	RuvB-like 1 (E. coli)	erythrocyte cytosolic protein of 54 kDa, ECP-54
2193	35758_at	RUVBL2	AB024301	RuvB-like 2 (E. coli)	RuvB-like DNA helicase TIP49b
2194	39338_at	S100A10	AI201310	S100 calcium binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11))	

Fig. 21

	A	B	C	D	E
2195	36089_at	SAC2	AB023183	Sac domain-containing inositol phosphatase 2	KIAA0966 protein
2196	41101_at	SAC3	D87464	Sac domain-containing inositol phosphatase 3	KIAA0274 gene product
2197	36511_at	SACM1L	AB020658	SAC1 suppressor of actin mutations 1-like (yeast)	KIAA0851 protein
2198	34792_at	AHCYL1	AL049954	S-adenosylhomocysteine hydrolase-like 1	hypothetical protein
2199	41302_at	AHCYL1	R59606	S-adenosylhomocysteine hydrolase-like 1	
2200	36685_at	AMD1	W63793	S-adenosylmethionine decarboxylase 1	S-adenosylmethionine decarboxylase 1 precursor
2201	263_g_at	AMD1	M21154	S-adenosylmethionine decarboxylase 1 sarcoglycan, epsilon	epsilon-sarcoglycan
2202	41449_at	SGCE	AJ000534	S-adenosylmethionine decarboxylase 1 sarcoglycan, epsilon	SAS
2203	36083_at	SAS	U01160	sarcoglycan, epsilon	SAS
2204	36536_at	SCHIP1	AF070614	schwannomin interacting protein 1	schwannomin interacting protein 1
2205	33423_g_at	SEC13L1	AF052155	SEC13-like 1 (S. cerevisiae)	SEC13 (S. cerevisiae)-like 1
2206	33422_at	SEC13L1	AF052155	SEC13-like 1 (S. cerevisiae)	SEC13 (S. cerevisiae)-like 1
2207	36207_at	SEC14L1	D67029	SEC14-like 1 (S. cerevisiae)	SEC14 (S. cerevisiae)-like 1
2208	39099_at	SEC23A	X97064	SEC23 homolog A (S. cerevisiae)	SEC23 protein
2209	34199_at	SEC24A	AJ131244	SEC24 related gene family, member A (S. cerevisiae)	SEC24A protein
2210	35845_at	SEC24B	AJ131245	SEC24 related gene family, member B (S. cerevisiae)	SEC24B protein
2211	32770_at	SEC24D	AB018298	SEC24 related gene family, member D (S. cerevisiae)	KIAA0755 protein
2212	34349_at	SEC63L	AJ011779	SEC63 protein	SEC63 protein
2213	32521_at	SFRP1	AF056087	secreted frizzled-related protein 1	secreted frizzled related protein
2214	34342_s_at	SPP1	AF052124	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)	osteopontin
2215	671_at	SPARC	J03040	secreted protein, acidic, cysteine-rich (osteonectin)	secreted protein, acidic, cysteine-rich (osteonectin)
2216	34265_at	SGNE1	Y00757	secretory granule, neuroendocrine protein 1 (7B2 protein)	secretory granule, neuroendocrine protein 1 (7B2 protein)
2217	37405_at	SELENBP1	U29091	selenium binding protein 1	selenium-binding protein

fig. 21

A	B	C	D	E
2218 39078_at	SPS2	U43286	selenophosphate synthetase 2	selenophosphate synthetase 2
2219 34363_at	SEPP1	Z11793	selenoprotein P, plasma, 1	selenoprotein P
2220 377_g_at	SEMA3C	AB000220	sema domain, immunoglobulin domain (lg), short basic domain, secreted, (semaphorin) 3C	semaphorin E
2221 376_at	SEMA3C	AB000220	sema domain, immunoglobulin domain (lg), short basic domain, secreted, (semaphorin) 3C	semaphorin E
2222 35666_at	SEMA3F	U38276	sema domain, immunoglobulin domain (lg), short basic domain, secreted, (semaphorin) 3F	semaphorin III family homolog
2223 38826_at	2-Sep	D50918	sepin 6	sepin 2
2224 40898_at	SOSTM1	U46751	sequestosome 1	phosphotyrosine independent ligand for the Lck SH2 domain p62
2225 34789_at	SERPINB6	S69272	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6	cytoplasmic aniproteinase
2226 38125_at	SERPINE1	M14083	serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1
2227 39167_r_at	SERPINH2	D83174	serine (or cysteine) proteinase inhibitor, clade H (heat shock protein 47), member 2	collagen binding protein 2
2228 38818_at	SPTLC1	Y08685	serine palmitoyltransferase, long chain base subunit 1	serine palmitoyltransferase, subunit I
2229 40966_at	STK39	AF099989	serine threonine kinase 39 (STE20/SPS1 homolog, yeast)	Ste-20 related kinase SPAK
2230 41737_at	SRRM1	AF048977	serine/arginine repetitive matrix 1	Ser/Arg-related nuclear matrix protein
2231 36019_at	STK19	L26260	serine/threonine kinase 19	RP protein
2232 40473_at	STK24	AF024636	serine/threonine kinase 24 (STE20 homolog, yeast)	STE20-like kinase 3
2233 32142_at	STK3	U26424	serine/threonine kinase 3 (STE20 homolog, yeast)	MST2
2234 32784_at	PRP4	AB011108	serine/threonine-protein kinase PRP4 homolog	KIAA0536 protein

Fig. 21

A	B	C	D	E
2235 40109_at	SRF	J03161	serum response factor (c-fos serum response element-binding transcription factor)	serum response factor (c-fos serum response element-binding transcription factor)
2236 1409_at	SRF	J03161	serum response factor (c-fos serum response element-binding transcription factor)	serum response factor (c-fos serum response element-binding transcription factor)
2237 41544_at	SNK	AF059617	serum-inducible kinase	serum-inducible kinase
2238 34849_at	SARS	X91257	seryl-tRNA synthetase	seryl-tRNA synthetase
2239 40189_at	SET	M93651	SET translocation (myeloid leukemia-associated)	SET translocation (myeloid leukemia-associated)
2240 32160_at	SIAH1	U76247	seven in absentia homolog 1 (Drosophila)	hSIAH1
2241 33799_at	SIAH2	U76248	seven in absentia homolog 2 (Drosophila)	hSIAH2
2242 39088_at	NIFIE14	Y18007	seven transmembrane domain protein	seven transmembrane domain protein
2243 39747_at	rp-7	U52427	seventh largest subunit; Human RNA polymerase II seventh subunit (pb-7)	RNA polymerase II seventh subunit
2244 38518_at	SCML2	Y18004	gene, complete cds.	SCML2 protein
2245 36040_at	SH3BGR	A1337192	sex comb on midleg-like 2 (Drosophila)	
2246 39714_at	SH3BGRL	AF042081	SH3 domain binding glutamic acid-rich protein	SH3 domain binding glutamic acid-rich-like protein
2247 38968_at	SH3BP5	AB005047	SH3 domain binding glutamic acid-rich protein like	
2248 39691_at	SH3GLB1	AB007960	SH3-domain binding protein 5 (BTK-associated)	SH3 binding protein
2249 38118_at	SHC1	U73377	SH3-domain GRB2-like endophilin B1	SH3-containing protein SH3GLB1
2250 34256_at	SIAT9	AB018356	SHC (Src homology 2 domain containing) transforming protein 1	p66shc
2251 39139_at	SPC18	A1357653	sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase)	GM3 synthase
2252 41194_at	SRP14	A1525652	signal peptidase complex (18kD)	
2253 35231_at	SRP19	X12791	signal recognition particle 14kD (homologous Alu RNA binding protein)	signal recognition particle 19kD
2254 36060_at	SRP54	U51920	signal recognition particle 19kD	signal recognition particle

fig-21

	A	B	C	D	E
2255	33837_at	SRP72	AF069765	signal recognition particle 72kD	signal recognition particle 72
2256	36981_at	SRP9	AF070649	signal recognition particle 9kD	signal recognition particle receptor ('docking protein')
2257	36679_at	SRPR	X06272	(docking protein)	transcription factor ISGF-3
2258	AFEX-HUMISGF	STAT1	M97935	signal transducer and activator of transcription 1, 91kD	transcription factor ISGF-3
2259	32860_g_at	STAT1	M97935	signal transducer and activator of transcription 1, 91kD	transcription factor ISGF-3
2260	32859_at	STAT1	M97935	signal transducer and activator of transcription 1, 91kD	transcription factor ISGF-3
2261	33338_at	STAT1	M97936	signal transducer and activator of transcription 1, 91kD	
2262	39708_at	STAT3	L29277	signal transducer and activator of transcription 3 (acute-phase response factor)	DNA-binding protein
2263	160_at	STAM	U43899	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	STAM
2264	35804_at	ASH2L	AB022785	similar to Drosophila ash2 gene; Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene.	
2265	41552_g_at	RER1	AW044624	similar to S. cerevisiae RER1	
2266	41551_at	RER1	AW044624	similar to S. cerevisiae RER1	
2267	33632_g_at	DIM1	AF023612	similar to S. pombe dim1+	Dim1p homolog
2268	35083_at	G1L	AL031670	similar to SW:GOLI DROME Q06003	ring finger protein 24
2269	37178_at	na	M74089	GOLIATH PROTEIN	
2270	40787_at	WIRE	U90911	similar to TB1	
2271	34705_at	BET3	AJ224335	similar to Wiskott-Aldrich syndrome protein interacting protein	
2272	39131_at	UPF3A	N36842	similar to yeast BET3 (S. cerevisiae)	hBET3 protein
2273	41277_at	SAP18	AW021542	similar to yeast Upi3, variant A	
2274	33859_at	SAP18	U96915	sin3-associated polypeptide, 18kD	sin3 associated polypeptide p18
2275	40992_s_at	SAP30	AF055993	sin3-associated polypeptide, 30kD	mSin3A associated polypeptide p30
2276	40004_at	SIX1	X91868	sin3-associated polypeptide, 30kD	sin3 associated polypeptide p30
				sin oculis homeobox homolog 1 (Drosophila)	1

Fig. 21

A	B	C	D	E
2277 39070_at	SNL	U03057	singed-like (fascin homolog, sea urchin) (Drosophila)	actin bundling protein
2278 39086_g_at	SSBP1	AA768912	single-stranded DNA binding protein	
2279 32668_at	SSBP2	AL080076	single-stranded DNA binding protein 2	hypothetical protein
2280 35294_at	SSA2	M25077	Sjogren syndrome antigen A2 (60kD, ribonucleoprotein autoantigen SS-A/Ro)	60kD Ro/SSA autoantigen
2281 35295_g_at	SSA2	M25077	Sjogren syndrome antigen A2 (60kD, ribonucleoprotein autoantigen SS-A/Ro)	60kD Ro/SSA autoantigen
2282 38450_at	SSB	X69804	Sjogren syndrome antigen B (autoantigen La)	Sjogren syndrome antigen B (autoantigen La)
2283 37715_at	SNW1	AF045184	SKI-interacting protein	nuclear receptor coactivator NCoA-62
2284 37389_at	IMAGE145052	AI346580	small acidic protein	
2285 40875_s_at	SNRP70	X06815	small nuclear ribonucleoprotein 70kD polypeptide (RNP antigen)	
2286 38679_g_at	SNRPE	AA733050	small nuclear ribonucleoprotein polypeptide E	hU1-70K-like protein (216 AA)
2287 37337_at	SNRPG	AI803447	small nuclear ribonucleoprotein polypeptide G	
2288 34842_at	SNRPN	U41303	small nuclear ribonucleoprotein polypeptide N	small nuclear ribonucleoprotein particle N
2289 35247_at	SNAPC5	AI557062	small nuclear RNA activating complex, polypeptide 5, 19kD	
2290 32172_at	SHARP	AL096858	SMART/HDAC1 associated repressor protein	hypothetical protein
2291 32849_at	SMC1L1	D80000	SMC1 structural maintenance of chromosomes 1-like 1 (yeast)	
2292 38738_at	SMT3H1	X99584	SMT3 suppressor of mif two 3 homolog 1 (yeast)	SMT3A protein
2293 41185_f_at	SMT3H2	AI971724	SMT3 suppressor of mif two 3 homolog 2 (yeast)	
2294 38288_at	SNAI2	U69196	snail homolog 2 (Drosophila)	
2295 38659_at	SHOC2	AB020669	soc-2 suppressor of clear homolog (C. elegans)	KIAA0862 protein
2296 40928_at	WSB1	W26496	SOCS box-containing WD protein SWIP-1	

fig-21



A	B	C	D	E
2297 36609_at	SLC1A3	D26443	solute carrier family 1 (glial high affinity glutamate transporter), member 3	glutamate transporter
2298 35320_at	SLC11A2	AB004857	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	NPAMP2
2299 33143_s_at	SLC16A3	U81800	solute carrier family 16 (monocarboxylic acid transporters), member 3	monocarboxylate transporter
2300 39260_at	SLC16A4	U59185	solute carrier family 16 (monocarboxylic acid transporters), member 4	solute carrier family 16 (monocarboxylic acid transporters), member 4
2301 36979_at	SLC2A3	M20681	solute carrier family 2 (facilitated glucose transporter), member 3	solute carrier family 2 (facilitated glucose transporter), member 3
2302 32084_at	SLC22A5	AF057164	solute carrier family 22 (organic cation transporter), member 5	organic cation transporter OCTN2
2303 38122_at	SLC23A1	D87075	solute carrier family 23 (nucleobase transporters), member 1	
2304 32822_at	SLC25A4	J02966	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4
2305 37740_r_at	SLC25A5	J02683	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5
2306 40436_g_at	SLC25A6	J03592	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	
2307 40435_at	SLC25A6	J03592	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	
2308 37675_at	SLC25A3	X60036	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3	phosphate carrier protein
2309 33901_at	SLC29A1	U81375	solute carrier family 29 (nucleoside transporters), member 1	equilibrative nucleoside transporter 1
2310 40364_at	SLC31A1	U83460	solute carrier family 31 (copper transporters), member 1	high-affinity copper uptake protein

Fig. 21

A	B	C	D	E
2311 34749_at	SLC31A2	U83461	solute carrier family 31 (copper transporters), member 2	putative copper uptake protein
2312 37895_at	SLC35A1	D87969	solute carrier family 35 (CMP-sialic acid transporter), member 1	CMP-sialic acid transporter
2313 38208_at	SLC35A3	AB021981	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member 3	UDP-N-acetylglucosamine transporter
2314 34936_at	SLC4A7	AB012130	solute carrier family 4, sodium bicarbonate cotransporter, member 7	sodium bicarbonate cotransporter2
2315 34166_at	SLC6A7	S80071	solute carrier family 6 (neurotransmitter transporter, L-proline), member 7	brain-specific L-proline transporter
2316 32186_at	SLC7A5	M80244	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5
2317 39533_at	SLC7A6	D87432	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6
2318 32681_at	SLC9A1	S68616	solute carrier family 9 (sodium/hydrogen exchanger), isoform 1 (antiporter, Na+/H+, amiloride sensitive)	Na+/H+ exchanger NHE-1 isoform
2319 36542_at	SLC9A6	AF030409	solute carrier family 9 (sodium/hydrogen exchanger), isoform 6	sodium-hydrogen exchanger 6
2320 39097_at	SON	X63753	SON DNA binding protein	SON DNA-binding protein
2321 32857_at	SOS2	L13858	son of sevenless homolog 2 (Drosophila)	guanine nucleotide exchange factor
2322 41462_at	SNX2	AF065482	sorting nexin 2	sorting nexin 2
2323 39360_at	SNX3	AF034546	sorting nexin 3	sorting nexin 3
2324 40605_at	SNX4	AA524345	sorting nexin 4	
2325 37808_at	SNX7	AL049989	sorting nexin 7	hypothetical protein
2326 33352_at	H2A	X57985	Source: H.sapiens genes for histones H2B.1 and H2A.	histone H2A
2327 36112_r_at	SC-35	X75755	Source: H.sapiens PR264 gene.	splicing factor, arginine/serine-rich 2
2328 36111_s_at	SC-35	X75755	Source: H.sapiens PR264 gene.	splicing factor, arginine/serine-rich 2

fig. 21

	A	B	C	D	E
2329	1173_g_at		HG172-HT3924	Source: Homo sapiens chromosome 10 clone RP11-96B5, WORKING DRAFT SEQUENCE, 8 unordered pieces.	
2330	40617_at	44M2.1	AC004381	Source: Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.	hypothetical protein FLJ20274
2331	33740_at	COTE1	AF023268	Source: Homo sapiens clk2 kinase (CLK2), propin1, cote1, glucocerebrosidase (GBA), and metaxin genes, complete cds; metaxin pseudogene and glucocerebrosidase pseudogene; and thrombospondin3 (THBS3) gene, partial cds.	chromosome 1 open reading frame 2
2332	41834_g_at	HJTB PAR	AB016492	Source: Homo sapiens hJTB gene, complete cds.	jumping translocation breakpoint
2333	41833_at	HJTB PAR	AB016492	Source: Homo sapiens hJTB gene, complete cds.	jumping translocation breakpoint
2334	32335_r_at	UbC2	AB009010	Source: Homo sapiens mRNA for polyubiquitin UbC, complete cds.	polyubiquitin UbC
2335	32334_f_at	UbC2	AB009010	Source: Homo sapiens mRNA for polyubiquitin UbC, complete cds.	polyubiquitin UbC
2336	32194_at	CBF	M37197	Source: Human CCAAT-box-binding factor (CBF) mRNA, complete cds.	CCAAT-box-binding transcription factor
2337	229_at	CBF	M37197	Source: Human CCAAT-box-binding factor (CBF) mRNA, complete cds.	CCAAT-box-binding transcription factor
2338	41791_at	101F10.3	AC002550	Source: Human Chromosome 16 BAC clone CIT987SK-A-101F10, complete sequence.	hypothetical protein
2339	41488_at	A-211C6.1	AC002394	Source: Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence.	hypothetical protein A-211C6.1
2340	35742_at	A-362G6.1	U95740	Source: Human Chromosome 16 BAC clone CIT987SK-A-362G6, complete sequence.	hypothetical protein A-362G6.1

Fig. 21

	A	B	C	D	E
2341	41733_at	61E3.1	AC003007	Source: Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence.	Unknown gene product (partial)
2342	36894_at		AL031846	Source: Human DNA sequence from clone RP4-742C19 on chromosome 22, complete sequence.	
2343	37383_f_at	HLA class I - locus	X58536	Source: Human mRNA for HLA class I locus C heavy chain.	HLA class I heavy chain
2344	39778_at			Source: Human N-acetylglucosaminyltransferase I (GlcNAc-TI) mRNA, complete cds.	mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase
2345	41573_at	SP3	X68560	Sp3 transcription factor	
2346	32102_at	SACS	AB018273	spastic ataxia of Charlevoix-Saguenay (sacs)	KIAA0730 protein
2347	35171_at	SPG4	AB029006	spastic paraplegia 4 (autosomal dominant; spastin)	KIAA1083 protein
2348	39423_f_at	SPOP	AJ000644	speckle-type POZ protein	SPOP
2349	38924_s_at	SSH3BP1	AF001628	spectrin SH3 domain binding protein 1	interactor protein AbiBP4
2350	33886_at	SSH3BP1	AF006516	spectrin SH3 domain binding protein 1	e3B1
2351	39556_at	SPTBN1	M96803	spectrin, beta, non-erythrocytic 1	beta-spectrin
2352	34304_s_at	SAT	AL050290	spermidine/spermine N1-acetyltransferase	
2353	32574_at	SMPD1	X59960	sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase)	sphingomyelin phosphodiesterase
2354	36142_at	SCA1	X79204	spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1)	ataxin-1
2355	36998_s_at	SCA2	Y08262	spinocerebellar ataxia 2 (olivopontocerebellar ataxia 2, autosomal dominant, ataxin 2)	ataxin 2
2356	38040_at	SPF30	AF107463	splicing factor 30, survival of motor neuron related	splicing factor
2357	36973_at	SF3B2	U41371	splicing factor 3b, subunit 2, 145kD	spliceosome associated protein

fig. 21

	A	B	C	D	E
2358	36224_g_at	SFPQ	AI827895	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	
2359	40638_at	SFPQ	X70944	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	PTB-associated splicing factor
2360	36098_at	SFRS1	M72709	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)
2361	140_s_at	SFRS10	U68063	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)	transformer-2 beta
2362	32183_at	SFRS11	M74002	splicing factor, arginine/serine-rich 11	arginine-rich nuclear protein
2363	35258_l_at	SFRS2IP	AF030234	splicing factor, arginine/serine-rich 2, interacting protein	splicing factor Sip1
2364	40457_at	SFRS3	AF038250	splicing factor, arginine/serine-rich 3	
2365	36991_at	SFRS4	L14076	splicing factor, arginine/serine-rich 4	pre-mRNA splicing factor
2366	40453_s_at	SFRS5	U30826	splicing factor, arginine/serine-rich 5	SRp40-1
2367	40262_at	SRP46	AF031166	Splicing factor, arginine/serine-rich, 46kD	SRp46 splicing factor
2368	35839_at	SQLE	D78130	squalene epoxidase	squalene epoxidase
2369	39047_at	SART3	AB020880	squamous cell carcinoma antigen recognised by T cells 3	squamous cell carcinoma antigen SART-3
2370	41784_at	DKFZp564B0769	AL080186	SR rich protein	hypothetical protein
2371	36091_at	SCAP2	AF051323	src family associated phosphoprotein 2	Src-associated adaptor protein
2372	41354_at	STC1	U25997	stanniocalcin 1	stanniocalcin precursor
2373	32043_at	STC2	AF098462	stanniocalcin 2	stanniocalcin-related protein
2374	41295_at	STARD7	AL041780	START domain containing 7	
2375	38800_at	STMN2	D45352	stathmin-like 2	
2376	41823_at	STAU	AJ132258	staufen, RNA binding protein (Drosophila)	staufen protein
2377	38669_at	SLK	D86959	Ste20-related serine/threonine kinase	KIAA0204 protein
2378	37147_at	SCGF	AF020044	stem cell growth factor; lymphocyte secreted C-type lectin	lymphocyte secreted C-type lectin precursor
2379	36913_at	SLBP	U75679	stem-loop (histone) binding protein	histone stem-loop binding protein
2380	38034_at	STS	M16505	steroid sulfatase (microsomal), arylsulfatase C, isozyme S	steroid sulfatase (microsomal), arylsulfatase C, isozyme S

Fig. 21

A	B	C	D	E
2381 589_at	SRD5A1	M32313	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)
2382 33369_at	SC4MOL	A1535653	sterol-C4-methyl oxidase-like	
2383 33421_s_at	SC5DL	AB016247	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, fungal)-like	sterol-C5-desaturase
2384 40419_at	EPB72	X85116	stomatin; H.sapiens epb72 gene exon 1.	band 7 integral membrane protein
2385 33322_i_at	SFN	X57348	stratiffin	stratiffin
2386 37035_at	SERP1	A1557272	stress-associated endoplasmic reticulum protein 1; ribosome associated membrane protein 4	
2387 35747_at	SDFR1	AF035287	stromal cell derived factor receptor 1	stromal cell derived factor receptor 1 isoform b; stromal cell derived factor receptor 1 isoform a
2388 32666_at	SDF1	U19495	stromal cell-derived factor 1	intercrine-alpha
2389 33834_at	SDF1	L36033	stromal cell-derived factor 1	pre-B cell stimulating factor homologue
2390 41627_at	SDF2	D50645	stromal cell-derived factor 2	SDF2
2391 34826_at	SDHA	L21936	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	succinate dehydrogenase flavoprotein subunit
2392 34385_at	SDHC	U57877	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD	integral membrane protein CII-3
2393 40467_at	SDHD	AB006202	succinate dehydrogenase complex, subunit D, integral membrane protein	cytochrome b small subunit of complex II
2394 40893_at	SUCLA2	AF058953	succinate-CoA ligase, ADP-forming, beta subunit	ATP-specific succinyl-CoA synthetase beta subunit
2395 35832_at	KIAA1077	AB029000	sulfatase FP	KIAA1077 protein
2396 33712_at	SULT4A1	N63574	sulfotransferase family 4A, member 1	
2397 34814_at	UBA2	AL041443	SUMO-1 activating enzyme subunit 2	
2398 37998_at	SKIV2L	U09877	superkiller viralicidic activity 2-like (S. cerevisiae)	helicase-like protein
2399 36620_at	SOD1	X02317	superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))	superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))
2400 40069_at	SVIL	AF051850	supervillin	supervillin
2401 36676_at	GHRF GRF	AL031659	supported by FGENESH	growth hormone releasing hormone

Fig. 21

A	B	C	D	E
2402 33297_at	CBF-B HAP2 NF-AL031778		supported by GENEWISE, GENSCAN and FGENES	nuclear transcription factor Y, alpha, isoform 1
2403 34825_at	TTRAP	AL031775	supported by GENSCAN	TRAF and TNF receptor-associated protein
2404 1640_at	ST13	U17714	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)	putative tumor suppressor ST13
2405 37745_s_at	ST5	U15780	suppression of tumorigenicity 5	p82
2406 37805_at	SRPUL	AF060567	sushi-repeat protein	sushi-repeat protein
2407 31855_at	SRPX	U61374	sushi-repeat-containing protein, X	
2408 31869_at	KIAA0640	AB014540	chromosome	KIAA0640 protein
2409 40213_at	SMARCA1	M88163	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1	transcription activator
2410 40961_at	SMARCA2	X72889	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	HBRM
2411 32579_at	SMARCA4	U29175	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	transcriptional activator
2412 39132_at	SMARCA5	AB010882	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	hSNF2H
2413 34753_at	SYBL1	X92396	synaptobrevin-like 1	synaptobrevin-like 1
2414 41692_at	SYNJ1	AB020717	synaptotagmin 1	KIAA0910 protein
2415 38075_at	SYPL	X68194	synaptophysin-like protein	synaptophysin-like protein
2416 36452_at	KIAA1029	AB028952	synaptopodin	KIAA1029 protein
2417 32178_r_at	SNAP23	AJ011915	synaptosomal-associated protein, 23kD	synaptosome associated protein of 23 kilodaltons, isoform A
2418 39757_at	SDC2	J04621	syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan)	
2419 32092_at	SDC3	AB007937	syndecan 3 (N-syndecan)	KIAA0468 protein
2420 38110_at	SDCBP	AF000652	syndecan binding protein (syntenin)	syntenin
2421 38685_at	STX12	AL035306	syntaxin 12	hypothetical protein
2422 38381_at	STX3A	U32315	syntaxin 3A	syntaxin 3

Fig. 2

A	B	C	D	E
2423 38774_at	STX7	U77942	syntaxin 7	syntaxin 7
2424 37510_at	STX8	AF036715	syntaxin 8	syntaxin 8
2425 33942_s_at	STXBP1	AF004563	syntaxin binding protein 1	hUNC18b
2426 37962_r_at	STXBP3	D63506	syntaxin binding protein 3	unc-18homologue
2427 33315_at		M29204	Synthetic construct chimeric DNA-binding factor mRNA, complete cds.	chimeric DNA-binding factor
2428 192_at	TAF7	U18062	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 55 kD	TFIID subunit TAFII55
2429 193_at	TAF9	U21858	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32 kD	TAFII32 precursor
2430 37620_at	TAF12; TAF2J; TAF15	U57693	TAF120; contains homology to histone H2B; TFIID subunit; TAFII15; contains homology to histone H2B; TFIID subunit; Human TFIID subunits TAF20 and TAF15 mRNA, complete cds.	TAF20; TAF15
2431 32166_at	TLN1	AB028950	talin 1	KIAA1027 protein
2432 39765_at	TLN2	AB002318	talin 2	tapasin
2433 41168_at	TAPBP	AF029750	TAP binding protein (tapasin)	TAR RNA loop binding protein
2434 39779_at	TARBP1	U38847	TAR (HIV) RNA binding protein 1	hypothetical protein
2435 32241_at	TARDBP	AL050265	TAR DNA binding protein	Tax interaction protein 1
2436 39416_at	TIP-1	U90913	Tax interaction protein 1	tax1-binding protein TXBP151
2437 498_at	TAX1BP1	U33821	Tax1 (human T-cell leukemia virus type I) binding protein 1	tax1-binding protein TXBP151
2438 35279_at	TAX1BP1	U33821	Tax1 (human T-cell leukemia virus type I) binding protein 1	TBX19 protein
2439 36702_at	TBX19	AJ010277	T-box 19	KIAA0829 protein
2440 32196_at	TIP120A	AB020636	TBP-interacting protein	t-complex 1
2441 34791_at	TCP1	X52882	t-complex 1	t-complex-associated-testis-expressed 1-like
2442 36921_at	TCTE1L	U02556	t-complex-associated-testis-expressed 1-like	t-complex-associated-testis-expressed 1-like
2443 946_at	TCTEL1	D50663	t-complex-associated-testis-expressed 1-like 1	1

Fig. 21



A	B	C	D	E
2444 38374_at	TIEG, EGRA, KLF AF050110		TEIG; EGRA; Homo sapiens TGFB inducible early protein and early growth response protein alpha genes, complete cds.	TGFB inducible early protein; early growth response protein alpha
2445 32255_i_at	TERF1	U40705	telomeric repeat binding factor (NIMA-interacting) 1	telomeric repeat binding factor 1, isoform 2; telomeric repeat binding factor 1, isoform 1
2446 32134_at	TES	AL050162	testis derived transcript (3 LIM domains)	hypothetical protein
2447 33988_at	TEGT	X75861	testis enhanced gene transcript (BAX inhibitor 1)	testis enhanced gene transcript (BAX inhibitor 1)
2448 32080_at	TETRA	L11669	tetracycline transporter-like protein	tetracycline transporter-like protein
2449 38612_at	TSPAN-3	M69023	tetraspan 3	
2450 37321_at	TTC1	U46570	tetratricopeptide repeat domain 1	tetratricopeptide repeat protein
2451 39065_s_at	TTC3	D83077	tetratricopeptide repeat domain 3	TPRD
2452 224_at	TIEG	S81439	TGFB inducible early growth response	zinc finger transcription factor
2453 38805_at	TGIF	X89750	TGFB-induced factor (TALE family homeobox)	TGIF protein
2454 37319_at	IGFBP3	M35878	The AAs encoded by bases 5728-5736 and 5917-5926 may be ASN-linked glycosylation sites; insulin-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, complete cds.	growth factor-binding protein-3 precursor
2455 1586_at	IGFBP3	M35878	The AAs encoded by bases 5728-5736 and 5917-5926 may be ASN-linked glycosylation sites; insulin-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, complete cds.	growth factor-binding protein-3 precursor

Fig. 21

A	B	C	D	E
			The first in-frame ATG codon is located at nucleotides 17-19, followed by a second ATG codon 52 codons downstream. And the second ATG codon is potential initiation point for translation of NPPase.; Human mRNA for nucleotide	
2456 342_at	ENPP1; M6S1; NFD12485		pyrophosphatase, complete cds.	NPPase
2457 36992_at	TXN	AI653621	thioredoxin	
2458 34768_at	TXNDC	AL080080	thioredoxin domain-containing	hypothetical protein
2459 31508_at	TXNIP	S73591	thioredoxin interacting protein	brain-expressed HHCPA78 homolog VDUP1
2460 39425_at	TXNRD1	X91247	thioredoxin reductase 1	thioredoxin reductase (NADPH)
2461 32214_at	TXNL	AF003938	thioredoxin-like, 32kD	thioredoxin-like protein
2462 38473_at	TARS	M63180	threonyl-tRNA synthetase	threonyl-tRNA synthetase
2463 659_g_at	THBS2	L12350	thrombospondin 2	thrombospondin 2
2464 658_at	THBS2	L12350	thrombospondin 2	thrombospondin 2
2465 40865_at	TDG	U51166	thymine-DNA glycosylase	G/T mismatch-specific thymine DNA glycosylase
2466 31557_at	TMSB4X	M17733	thymosin, beta 4, X chromosome	thymosin, beta 4
2467 32654_g_at	SMAP	AW020536	thyroid hormone receptor coactivating protein	
2468 39699_at	TRIP12	D28476	thyroid hormone receptor interactor 12	thyroid hormone receptor interactor 12
2469 41251_at	TRIP3	L40410	thyroid hormone receptor interactor 3	thyroid receptor interactor
2470 39341_at	TRIP6	AJ001902	thyroid hormone receptor interactor 6	TRIP6
2471 37348_s_at	TRIP7	AA845349	thyroid hormone receptor interactor 7	
2472 41625_at	TRAP240	AB011165	thyroid hormone receptor-associated protein, 240 kDa subunit	KIAA0593 protein
2473 34323_at	TRIP15	AF084260	thyroid receptor interacting protein 15	signalosome subunit 2
2474 33852_at	TIA1	M77142	TIA1 cytotoxic granule-associated RNA binding protein	TIA1 protein, isoform 1; TIA1 protein, isoform 2
2475 41763_g_at	TIAL1	D64015	TIA1 cytotoxic granule-associated RNA binding protein-like 1	T-cluster binding protein
2476 36655_at	TJP2	L27476	tight junction protein 2 (zona occludens 2)	tight junction protein 2 (zona occludens 2)
2477 37801_at	TJ6	AF112972	TJ6 protein	TJ6

Fig-21

A	B	C	D	E
2478 35238_at	TRAF5	AB000509	TNF receptor-associated factor 5	TRAF5
2479 33243_at	GG2-1	AF099935	TNF-induced protein	MDC-3.13 isoform 2
2480 40310_at	TLR2	AF051152	tol-like receptor 2	Toll/interleukin-1 receptor-like protein 4
2481 1030_s_at	TOP1	U07806	topoisomerase (DNA) I	DNA topoisomerase I
2482 36571_at	TOP2B	X68060	topoisomerase (DNA) II beta (180kD)	DNA topoisomerase II
2483 32233_at	TOR1B	AF007872	torsin family 1, member B (torsin B)	torsinB
2484 32219_at	TLK1	D50927	tousled-like kinase 1	KIAA0137 protein
2485 35321_at	TLK2	AB004884	tousled-like kinase 2	PKU-alpha
2486 39742_at	TANK	U59863	TRAF family member-associated NFKB activator	I-TRAF
2487 40051_at	KIAA0057	D31762	TRAM-like protein	TRAM-like protein
2488 1073_at	TCEA1	M81601	transcription elongation factor A (SII), 1	transcription elongation factor SII
2489 38317_at	TCEAL1	M99701	transcription elongation factor A (SII)-like 1	transcription elongation factor A (SII)-like 1
2490 1399_at	TCEB1	L34587	transcription elongation factor B (SIII), polypeptide 1 (15kD, elongin C)	RNA polymerase II elongation factor SIII, p15 subunit
2491 41759_at	TCEB1L	Z47087	transcription elongation factor B (SIII), polypeptide 1-like	RNA polymerase II elongation factor-like protein
2492 39426_at	TCERG1	AF017789	transcription elongation regulator 1 (CA150)	putative transcription factor CA150
2493 33348_at	TCF12	M80627	transcription factor 12 (HTF4, helix-loop-helix transcription factors 4)	helix-loop-helix protein
2494 1373_at	TCF3	M31523	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	
2495 33440_at	TCF8	U19969	transcription factor 8 (represses interleukin 2 expression)	ZEB
2496 39638_at	TFAP4	S73885	transcription factor AP-4 (activating enhancer binding protein 4)	AP-4
2497 37757_at	TFDP1	L23959	transcription factor Dp-1	E2F-related transcription factor
2498 32578_at	TCFL4	AW005997	transcription factor-like 4	
2499 35614_at	TCFL5	AB012124	transcription factor-like 5 (basic helix-loop-helix)	transcription factor-like 5
2500 35749_at	TADA3L	AF069733	transcriptional adaptor 3-like	ADA3-like protein

Fig. 21

	A	B	C	D	E
2501	35297_at	GGA2 VEAR	AC002400	Transcriptional coactivator P15 like	KIAA1080 protein; Golgi-associated, gamma-adaptin ear containing, ARF-binding protein 2
2502	33876_at	TAZ	AL050107	transcriptional co-activator with PDZ-binding motif (TAZ)	hypothetical protein
2503	39358_at	SMRT	U37146	transcriptional co-repressor; Human silencing mediator of retinoid and thyroid hormone action (SMRT) mRNA, complete cds.	silencing mediator of retinoid and thyroid hormone action
2504	37312_at	TRIP-Br2	D50917	transcriptional regulator interacting with the PHS-bromodomain 2	KIAA0127 gene product
2505	40631_at	TOB1	D38305	transducer of ERBB2, 1	Tob
2506	32554_s_at	TBL1	Y12781	transducin (beta)-like 1	transducin (beta) like 1 protein
2507	37324_at	TFRC	X01060	transferrin receptor (p90, CD71)	transferrin receptor (p90, CD71)
2508	39344_at	HSU53209	U53209	transformer-2 alpha (htra-2 alpha)	transformer-2 alpha
2509	39032_at	TSC22	AJ222700	transforming growth factor beta-stimulated protein TSC-22	TSC-22
2510	41445_at	TGFB1	X02812	transforming growth factor, beta 1 (Camurati-Engelmann disease)	transforming growth factor, beta 1 (Camurati-Engelmann disease)
2511	1815_g_at	TGFBR2	D50683	transforming growth factor, beta receptor II (70-80kD)	TGF-betaIIIR alpha
2512	1814_at	TGFBR2	D50683	transforming growth factor, beta receptor II (70-80kD)	TGF-betaIIIR alpha
2513	1385_at	TGFB1	M77349	transforming growth factor, beta-induced, 68kD	transforming growth factor induced protein
2514	40841_at	TACC1	AF049910	transforming, acidic coiled-coil containing protein 1	TACC1
2515	38816_at	TACC2	AF095791	transforming, acidic coiled-coil containing protein 2	TACC2 protein
2516	36931_at	TAGLN	M95787	transgelin	smooth muscle protein
2517	36678_at	TAGLN2	D21261	transgelin 2	transgelin 2
2518	31829_r_at	TGOLN2	AF027515	trans-golgi network protein 2	hTGN48
2519	39124_r_at	TRPC1	X89066	transient receptor potential cation channel, subfamily C, member 1	TRPC1 protein
2520	39123_s_at	TRPC1	X89066	transient receptor potential cation channel, subfamily C, member 1	TRPC1 protein

Fig. 21

A	B	C	D	E
			<p>RETICULUM ATPASE (TER ATPASE) (15S MG(2+)-ATPASE P97 SUBUNIT) (VALOSIN CONTAINING PROTEIN) (VCP); Human homolog of spIQ01853ITERA_MOUSE TRANSITIONAL ENDOPLASMIC RETICULUM ATPASE (TER ATPASE) (15S MG(2+)-ATPASE P97 SUBUNIT) (VALOSIN CONTAINING PROTEIN) (VCP) pirlS25197 transitional endoplasmic reticulum ATPase - mouse gil55217 (Z14044) murine valosin- containing protein; 99% identical to mouse, rat, and pig homologs; X-ray cross complementing gene 9; Putative DNA repair protein; Hypothetical 96.6 kDa putative membrane protein; Most similar to hypothetical proteins in fission and budding yeast, and C. elegans: (AB004539) ORF YLL031c [Schizosaccharomyces pombe] producing hypothetical protein (AL021766) [Schizosaccharomyces pombe]; probable membrane protein YLL031c - yeast (Saccharomyces cerevisiae) gnlPIDle245463 (Z73136) ORF YLL031c [Saccharomyces cerevisiae]; (AF003137) C27A12.9 [Caenorhabditis elegans]; Hypothetical 38.8 kDa putative membrane protein; Most similar to hypothetical proteins: PIDle276130 (Z81072) F30A10.5 [Caenorhabditis elegans]; spIP72655IYB28 [translation factor sui1 homolog translation initiation factor IF2</p>	<p>TERA_HUMAN; XRCC9; P1.11659_3; P1.11659_4; P1.11659_5 GC20 protein KIAA0741 protein 14.5 kDa translational inhibitor protein, p14.5</p>
2521 34380_at	XRCC9	AC004472		
2522 33351_at	GC20	AF064607		
2523 40537_at	IF2	AB018284		
2524 32173_at	UK114	X95384		

Fig. 21

A	B	C	D	E
2525 41051_at	TSNAX	X95073	translin-associated factor X	Translin associated protein X
2526 32831_at	TIMM17A	AA453183	translocase of inner mitochondrial membrane 17 homolog A (yeast)	
2527 36198_at	TOMM20-PENDIN	D13641	translocase of outer mitochondrial membrane 20 (yeast) homolog	mitochondrial outer membrane protein 19
2528 37050_r_at	TOMM34	AI130910	translocase of outer mitochondrial membrane 34	
2529 32853_at	TOMM70A	AB018262	translocase of outer mitochondrial membrane 70 homolog A (yeast)	KIAA0719 protein
2530 34796_at	TRAM	X63679	translocating chain-associating membrane protein	TRAM protein
2531 38100_at	TLOC1	D87127	translocation protein 1	translocation protein-1
2532 950_at	TLOC1	D87127	translocation protein 1	translocation protein-1
2533 41531_at	TM4SF1	AI445461	transmembrane 4 superfamily member 1	
2534 39362_r_at	TM4SF6	AF043906	transmembrane 4 superfamily member 6	T245 protein
2535 32083_at	TM7SF1	AF027826	transmembrane 7 superfamily member 1 (upregulated in kidney)	putative seven pass transmembrane protein
2536 38835_at	TM9SF1	U94831	transmembrane 9 superfamily member 1	multispanning membrane protein
2537 34307_at	TM9SF2	U81006	transmembrane 9 superfamily member 2	p76
2538 37955_at	TMEM4	AB015631	transmembrane protein 4	type II membrane protein
2539 37445_at	TMEM5	AB015633	transmembrane protein 5	type II membrane protein
2540 36128_at	TMP21	L40397	transmembrane trafficking protein	
2541 38982_at	RAP1	W28865	TRF2-interacting telomeric RAP1 protein	
2542 39382_at	TRIM2	AB011089	tripartite motif-containing 2	KIAA0517 protein
2543 36825_at	TRIM22	X82200	tripartite motif-containing 22	gpStat50
2544 38537_at	TRIM32	U18543	tripartite motif-containing 32	zinc-finger protein
2545 32635_at	TRIM33	AB029036	tripartite motif-containing 33	KIAA1113 protein
2546 33107_at	TRIM37	AB020705	tripartite motif-containing 37	KIAA0898 protein
2547 40461_at	TIX1	AB007855	triple homeobox 1	
2548 36791_g_at	TPM1	M19267	tropomyosin 1 (alpha)	tropomyosin 1 (alpha)
2549 36790_at	TPM1	M19267	tropomyosin 1 (alpha)	tropomyosin 1 (alpha)

Fig-21

A	B	C	D	E
2550 36792_at	TPM1	Z24727	tropomyosin 1 (alpha)	tropomyosin isoform
2551 32313_at	TPM2	M12125	tropomyosin 2 (beta)	tropomyosin 2 (beta)
2552 32777_at	WRB	Y12478	tryptophan rich basic protein	congenital heart disease 5 protein
2553 38121_at	WARS	X59892	tryptophanyl-tRNA synthetase	471 aa polypeptide (gamma2)
2554 39867_at	TUFM	S75463	Tu translation elongation factor, mitochondrial	P43
2555 31944_at	TULP3	AI028290	tubby like protein 3	
2556 32272_at	K-ALPHA-1	K00558	tubulin, alpha, ubiquitous	tubulin, alpha, ubiquitous
2557 39332_at	TUBB	AF035316	tubulin, beta polypeptide	
2558 39331_at	TUBB	X79535	tubulin, beta polypeptide	beta tubulin
2559 33346_r_at	TUBG1	M61764	tubulin, gamma 1	gamma-tubulin
2560 36176_at	TBCC	U61234	tubulin-specific chaperone c	cofactor C
2561 35159_at	TBCE	U61232	tubulin-specific chaperone e	cofactor E
2562 37007_at	TDE1	U49188	tumor differentially expressed 1	tumor differentially expressed 1
2563 34892_at	TNFRSF10B	AF016266	tumor necrosis factor receptor superfamily, member 10b	TRAIL receptor 2
2564 41190_at	TNFRSF12	U83598	tumor necrosis factor receptor superfamily, member 12 (translocating chain-association membrane protein)	death domain receptor 3 soluble form
2565 1563_s_at	TNFRSF1A	M58286	tumor necrosis factor receptor superfamily, member 1A	tumor necrosis factor receptor
2566 35150_at	TNFRSF5	X60592	tumor necrosis factor receptor superfamily, member 5	CDw40
2567 37643_at	TNFRSF6	X63717	tumor necrosis factor receptor superfamily, member 6	AP0-1 cell surface antigen precursor
2568 36988_at	TNFAIP1	M80783	tumor necrosis factor, alpha-induced protein 1 (endothelial)	B12 protein
2569 38631_at	TNFAIP2	M92357	tumor necrosis factor, alpha-induced protein 2	B94 protein
2570 595_at	TNFAIP3	M59465	tumor necrosis factor, alpha-induced protein 3	A20
2571 40076_at	TPD52L2	AF004430	tumor protein D52-like 2	hD54+ins2 isoform
2572 1711_at	TP53BP1	U09477	tumor protein p53 binding protein, 1	p53-binding protein
2573 34822_at	TP53BP2	U58334	tumor protein p53 binding protein, 2	Bbp/53BP2
2574 38568_at	TP53BP1	U82939	tumor protein p53-binding protein	p53 binding protein

Fig. 21

	A	B	C	D	E
2575	31584_at	TPT1	X16064	tumor protein, translationally-controlled 1	tumor protein, translationally-controlled 1
2576	31888_s_at	TSSC3	AF001294	tumor suppressing subtransferable candidate 3	IPL
2577	147_at	TSG101	U82130	tumor susceptibility gene 101	tumor susceptibility protein
2578	40328_at	Twist	X99268	twist homolog (acrocephalosyndactyly 3; Saethre-Chotzen syndrome) (Drosophila)	B-HLH DNA binding protein
2579	2086_s_at	TYRO3	D17517	TYRO3 protein tyrosine kinase	Sky
2580	35246_at	TYRO3	U18934	TYRO3 protein tyrosine kinase	receptor tyrosine kinase
2581	32324_at	YWHAH	X57346	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide
2582	409_at	YWHAQ	X56468	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	14.3.3 protein
2583	32530_at	YWHAQ	X56468	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	14.3.3 protein
2584	1235_at	YWHAZ	M86400	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	phospholipase A2
2585	32718_at	TPST1	AF038009	tyrosylprotein sulfotransferase 1	tyrosylprotein sulfotransferase-1
2586	35172_at	TPST2	AF049891	tyrosylprotein sulfotransferase 2	tyrosylprotein sulfotransferase-2
2587	38977_at	YARS	U89436	tyrosyl-tRNA synthetase	tyrosyl-tRNA synthetase
2588	36517_at	U2AF1	M96982	U2(RNU2) small nuclear RNA auxiliary factor 1	U2 snRNP auxiliary factor small subunit
2589	32858_at	UBN1	A1341565	ubiquitin 1	ubiquitin 2
2590	34824_at	UBQLN2	AB015344	ubiquitin 2	ubiquitin 2
2591	38451_at	UQCR	T58471	ubiquinol-cytochrome c reductase (6.4kD) subunit	
2592	39427_at	UQCRB	T79616	ubiquinol-cytochrome c reductase binding protein	
2593	40854_at	UQCRC2	J04973	ubiquinol-cytochrome c reductase core protein II	ubiquinol-cytochrome c reductase core protein II

Fig-21



A	B	C	D	E
2594 36104_at	UQCRH	AA526497	ubiquinol-cytochrome c reductase hinge protein	
2595 1366_i_at	UBC	M26880	ubiquitin C	ubiquitin C
2596 1367_f_at	UBC	M26880	ubiquitin C	ubiquitin C
2597 36990_at	UCHL1	X04741	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)
2598 811_at	UFD1L	U64444	ubiquitin fusion degradation 1-like	ubiquitin fusion-degradation 1 like protein
2599 40623_at	UBE3B	A1749193	ubiquitin protein ligase	
			ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome)	E6-associated protein E6-AP/ubiquitin-protein ligase
2600 41205_at	UBE3A	U84404		ubiquitin specific protease
2601 34383_at	USP1	AB014458	ubiquitin specific protease 1	
2602 37683_at	USP10	D80012	ubiquitin specific protease 10	
2603 162_at	USP11	U44839	ubiquitin specific protease 11	UHX1 protein
			ubiquitin specific protease 14 (tRNA-guanine transglycosylase)	tRNA-Guanine Transglycosylase
2604 36982_at	USP14	U30888		KIAA1063 protein
2605 39866_at	USP22	AB028986	ubiquitin specific protease 22	KIAA1057 protein
2606 35847_at	USP24	AB028980	ubiquitin specific protease 24	
			ubiquitin specific protease 4 (proto-oncogene)	ubiquitin protease
2607 1357_at	USP4	U20657		
			ubiquitin specific protease 5 (isopeptidase T)	isopeptidase T
2608 34405_at	USP5	U47927		herpesvirus associated ubiquitin-specific protease (HAUSP)
2609 37672_at	USP7	Z72499	ubiquitin specific protease 7 (herpes virus-associated)	ubiquitin specific protease 8
2610 39794_at	USP8	D29956	ubiquitin specific protease 8	
			ubiquitin specific protease 9, X	ubiquitin hydrolase
2611 32572_at	USP9X	X98296	chromosome (tat facets-like Drosophila)	
			ubiquitin-activating enzyme E1C (UBA3 homolog, yeast)	UBA3
2612 40066_at	UBE1C	AF046024	ubiquitination factor E4A (UFD2 homolog, yeast)	ubiquitination factor E4A (UFD2 homolog, yeast)
2613 36579_at	UBE4A	D50916	ubiquitination factor E4B (UFD2 homolog, yeast)	ubiquitin-fusion degradation protein 2
2614 41339_at	UBE4B	AF043117		
2615 36959_at	UBE2V1	U49278	ubiquitin-conjugating enzyme E2 variant 1	UEV-1

Fig-21

A	B	C	D	E
2616 890_at	UBE2A	M74524	ubiquitin-conjugating enzyme E2A (RAD6 homolog)	ubiquitin-conjugating enzyme E2A (RAD6 homolog)
2617 37826_at	UBE2D1	AF020761	ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast)	
2618 38705_at	UBE2D2	A1310002	ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast)	
2619 832_at	UBE2D2	U39317	ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast)	UbcH5B
2620 39083_at	UBE2D3	U39318	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	UbcH5C
2621 504_at	UBE2D3	U39318	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	UbcH5C
2622 34850_at	UBE2E3	AB017644	ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast)	ubiquitin-conjugating enzyme E2
2623 32236_at	UBE2G2	AF032456	ubiquitin-conjugating enzyme E2G 2 (UBC7 homolog, yeast)	ubiquitin conjugating enzyme G2
2624 38480_s_at	UBE2I	U66867	ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast)	ubiquitin conjugating enzyme 9
2625 838_s_at	UBE2I	U45328	ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast)	ubiquitin-conjugating enzyme
2626 223_at	UBE2L3	S81003	ubiquitin-conjugating enzyme E2L 3	L-UBC
2627 40505_at	UBE2L6	AA883502	ubiquitin-conjugating enzyme E2L 6	
2628 36604_at	UBE2N	D83004	ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast)	ubiquitin-conjugating enzyme E2 UbcH-ben
2629 457_s_at	UBL1	U67122	ubiquitin-like 1 (septrin)	SUMO-1
2630 155_s_at	UBL1	U61397	ubiquitin-like 1 (septrin)	ubiquitin-homology domain protein PIC1
2631 40839_at	UBL3	AL080177	ubiquitin-like 3	hypothetical protein
2632 37336_at	UBXD2	D87684	UBX domain-containing 2	KIAA0242 protein
2633 40960_at	B4GALT1	D29805	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1	beta-1,4-galactosyltransferase
2634 34177_at	B4GALT2	AF038660	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 2	beta-1,4-galactosyltransferase
2635 39445_at	B4GALT3	AF038661	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3	beta-1,4-galactosyltransferase
2636 40215_at	UGCG	D50840	UDP-glucose ceramide glucosyltransferase	ceramide glucosyltransferase

fig. 21

A		B	C	D	E
2637	35214_at	UGDH	AF061016	UDP-glucose dehydrogenase	UDP-glucose dehydrogenase
2638	37373_at	UGP2	U27460	UDP-glucose pyrophosphorylase 2	uridine diphosphoglucose pyrophosphorylase
2639	38041_at	GALNT1	U41514	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 1 (GalNAc-T1)	UDP-GalNAc:polypeptide N-acetylglucosaminyltransferase
2640	36515_at	GNE	AJ238764	UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine kinase	UDP-N-acetylglucosamine-2-epimerase / N-acetylmannosamine kinase
2641	41242_at	UAP1	AB011004	UDP-N-acetylglucosamine pyrophosphorylase 1	UDP-N-acetylglucosamine pyrophosphorylase
2642	34827_at	ULK1	AF045458	unc-51-like kinase 1 (C. elegans)	serine/threonine kinase ULK1
2643	37315_f_at	BM036	AI057607	uncharacterized bone marrow protein BM036	
2644	35750_at	HT010	AL049948	uncharacterized hypothalamus protein HT010	
2645	41058_g_at	HT012	AI760162	uncharacterized hypothalamus protein HT012	
2646	41057_at	HT012	AI760162	uncharacterized hypothalamus protein HT012	
2647	38610_s_at	KRT10; KPP	X14487	unnamed protein product; Human gene for acidic (type I) cytokeratin 10.	keratin 10
2648	34402_at	UNRIP	AB024327	unr-interacting protein	WD-40 repeat protein
2649	34372_at	UREB1	AB002310	upstream regulatory element binding protein 1	upstream regulatory element binding protein 1
2650	37686_s_at	UNG	Y09008	uracil-DNA glycosylase	uracil-DNA glycosylase
2651	33815_at	UMPS	J03626	uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase)	uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase)
2652	41859_at	UST	AB020316	uronyl-2-sulfotransferase	dermatan/chondroitin sulfate 2-sulfotransferase
2653	39429_at	UVRAG	X99050	UV Radiation Resistance Associated Gene; H.sapiens mRNA; UV Radiation Resistance Associated Gene.	pp63 (processed form)

Fig. 21

A	B	C	D	E
			v-abl Abelson murine leukemia viral oncogene homolog 1	v-abl Abelson murine leukemia viral oncogene homolog 1 isoform a; v-abl
2654 39730_at	ABL1	X16416	v-abl Abelson murine leukemia viral oncogene homolog 1	Abelson murine leukemia viral oncogene homolog 1 isoform b
2655 35779_at	VPS45A	AJ133421	vacuolar protein sorting 45A (yeast)	vacuolar protein sorting
2656 38801_at	VAPA	A1742846	VAMP (vesicle-associated membrane protein)-associated protein A (33kD)	
				vascular cell adhesion molecule 1, isoform a precursor; vascular cell adhesion molecule 1, isoform b precursor
2657 583_s_at	VCAM1	M30257	vascular cell adhesion molecule 1	vascular endothelial growth factor
2658 1953_at	VEGF	AF024710	vascular endothelial growth factor	vascular endothelial growth factor
2659 36100_at	VEGF	AF022375	vascular endothelial growth factor	VEGF related factor isoform VRF186 precursor
2660 37268_at	VEGFB	U43368	vascular endothelial growth factor B	vascular endothelial growth factor related protein
2661 159_at	VEGFC	U43142	vascular endothelial growth factor C	
			VDAC protein; similar to mouse VDAC 3; Homo sapiens voltage dependent anion channel protein mRNA, complete cds.	voltage dependent anion channel protein
2662 36102_at	VDAC3; HD-VDAC	AF038962	vesicle amine transport protein 1	vesicle amine transport protein 1
2663 40147_at	VATI	U18009	vesicle transport-related protein	KIAA0917 protein
2664 33930_at	RA410	AB020724	vesicle-associated membrane protein 2 (synaptobrevin 2)	
2665 32254_at	VAMP2	AL050223	vesicle-associated membrane protein 3 (cellubrevin)	
2666 35783_at	VAMP3	H93123	villin 2 (ezrn)	villin 2
2667 40103_at	VIL2	X51521	vimentin	vimentin
2668 34091_s_at	VIM	Z19554	vinculin	vinculin isoform VCL; VCL isoform meta-VCL
2669 36601_at	VCL	M33308	vitamin A responsive; cytoskeleton related	JWA protein
2670 39091_at	JWA	AF070523	vitamin D (1,25- dihydroxyvitamin D3) receptor	vitamin D (1,25- dihydroxyvitamin D3) receptor
2671 1388_g_at	VDR	J03258	v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogene homolog	K-ras oncogene protein
2672 1940_at	KRAS2	M54968		

fig. 21

	A	B	C	D	E
2673	41504_s_at	MAF	AF055376	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	short form transcription factor C-MAF
2674	32835_at	MAFF	AA725102	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	
2675	40198_at	VDAC1	L06132	voltage-dependent anion channel 1	voltage-dependent anion channel
2676	37696_at	VDAC2	L06328	voltage-dependent anion channel 2	voltage-dependent anion channel
2677	171_at	VBPI	U56833	von Hippel-Lindau binding protein 1	VHL binding protein-1
2678	38743_f_at	RAF1	X06409	v-raf-1 murine leukemia viral oncogene homolog 1	
2679	32776_at	RALB	M35416	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein)	v-ral simian leukemia viral oncogene homolog B
2680	36645_at	RELA	L19067	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian)	NF-kappa-B transcription factor subunit
2681	1295_at	RELA	L19067	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian)	
2682	1674_at	YES1	M15990	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	NF-kappa-B transcription factor subunit
2683	1402_at	LYN	M16038	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1
2684	1058_at	WASF3	S69790	WAS protein family, member 3	
2685	38736_at	WDR1	AL050108	WD repeat domain 1	
2686	41430_at	WDR7	AB011113	WD repeat domain 7	hypothetical protein KIAA0541 protein
2687	36009_at	CL683	AF091092	weakly similar to glutathione peroxidase 2	weakly similar to glutathione peroxidase 2
2688	36909_at	WEE1	X62048	WEE1+ homolog (S. pombe)	wee1 tyrosine kinase
2689	41212_r_at	WBSR1	D26068	Williams-Beuren syndrome chromosome region 1	eukaryotic translation initiation factor 4H, isoform 1; eukaryotic translation initiation factor 4H, isoform 2
2690	41635_at	WTAP	D14661	Wilms' tumour 1-associating protein	Wilms' tumour 1-associating protein
2691	31862_at	WNT5A	L20861	wingless-type MMTV integration site family, member 5A	wingless-type MMTV integration site family, member 5A precursor

Fig. 21

A	B	C	D	E
2692 34225_at	WHSC2	AF101434	Wolf-Hirschhorn syndrome candidate 2	Wolf-Hirschhorn syndrome candidate 2 protein
2693 33438_at	WBP2	AL049981	WW domain binding protein 2	
2694 35213_at	WBP4	AF071185	WW domain binding protein 4 (formin binding protein 21)	formin binding protein 21
2695 39995_s_at	WBOX	U13395	WW domain containing oxidoreductase	oxidoreductase
2696 36822_at	WAC	U51334	WW domain-containing adapter with a coiled-coil region	putative RNA binding protein RBP56
2697 1307_at	XPA	D14533	xeroderma pigmentosum, complementation group A	XPAC protein
2698 1873_at	XPC	D21089	xeroderma pigmentosum, complementation group C	XP-C repair complementing protein (p125)
2699 41756_at	NTPBP	AJ010842	XPA binding protein 1; putative ATP(GTP)-binding protein	ATP(GTP)-binding protein
2700 38733_at	XRCC5	M30938	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen, 80kD)	ATP-dependant DNA helicase II
2701 585_at	XRCC5	M30938	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen, 80kD)	ATP-dependant DNA helicase II
2702 2093_s_at	XRCC5	J04977	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen, 80kD)	ATP-dependant DNA helicase II
2703 35827_at	KIAA0905	AB020712	yeast Sec31p homolog	KIAA0905 protein
2704 40988_at	YME1L1	AJ132637	YME1-like 1 (S. cerevisiae)	ATP-dependent metalloprotease YME1L
2705 891_at	YY1	M77698	YY1 transcription factor	GLI-Krupple related protein
2706 34887_at			zb29g04.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:305046.3, mRNA sequence.	
2707 36308_at	ZIC1	D76435	Zic family member 1 (odd-paired homolog, Drosophila)	Zic protein
2708 35681_r_at	ZFX1B	AB011141	zinc finger homeobox 1b	KIAA0569 protein

fig. 21

A	B	C	D	E
2709 34786_at	TSGA	AB018285	zinc finger protein	KIAA0742 protein
2710 39977_at	ZNF-U69274	U69274	zinc finger protein	zinc finger protein
2711 40140_at	ZFP103	D76444	zinc finger protein 103 homolog (mouse)	zinc finger protein 103 homolog
2712 36295_at	ZNF134	U09412	zinc finger protein 134 (clone pHZ-15)	zinc finger protein ZNF134
2713 32192_g_at	ZNF144	D13969	zinc finger protein 144 (Mel-18)	Mel-18 protein
2714 36928_at	ZNF146	X70394	zinc finger protein 146	zinc finger protein
2715 41532_at	ZNF151	Y09723	zinc finger protein 151 (pHZ-67)	Miz-1 protein
2716 32628_at	ZNF161	D28118	zinc finger protein 161	DB1
2717 41436_at	ZNF198	AJ224901	zinc finger protein 198	ZNF198 protein
2718 40724_at	ZNF200	Y14443	zinc finger protein 200	zinc finger protein
2719 35368_at	ZNF207	AF046001	zinc finger protein 207	zinc finger protein 207
2720 41542_at	ZNF216	AF062346	zinc finger protein 216	zinc finger protein 216 splice variant 1
2721 840_at	ZNF220	U47742	zinc finger protein 220	monocytic leukaemia zinc finger protein
2722 39762_at	ZNF262	AB007885	zinc finger protein 262	zinc finger protein 262
2723 34299_at	ZNF278	AL096880	zinc finger protein 278	hypothetical protein
2724 39005_s_at	ZNF294	AB018257	zinc finger protein 294	KIAA0714 protein
2725 37860_at	ZNF337	AL049942	zinc finger protein 337	hypothetical protein
2726 40448_at	ZFP36	M92843	zinc finger protein 36, C3H type, homolog (mouse)	zinc finger transcriptional regulator
2727 38740_at	ZFP36L1	X79067	zinc finger protein 36, C3H type-like 1	butyrate response factor 1
2728 36046_at	ZNF363	AL050144	zinc finger protein 363	hypothetical protein
2729 32129_at	ZNF364	AL079314	zinc finger protein 364	hypothetical protein, similar to (U06944)
2730 41033_at	ZNF84	M27878	zinc finger protein 84 (HPF2)	PRAJA1 [Mus musculus]
2731 40610_at	ZFR	A1743507	zinc finger RNA binding protein	DNA binding protein
2732 39751_at	ZDHHC3	AF052182	zinc finger, DHHC domain containing 3	
2733 33912_at	ZMPSTE24	Y13834	zinc metalloproteinase (STE24 homolog, yeast)	laminated-proteins converting enzyme 1
2734 36521_at	DZIP1	AB023213	zinc-finger protein DZIP1	KIAA0996 protein
2735 35995_at	ZWINT	AF067656	ZW10 interactor	ZW10 interactor Zwint
2736 706_at		HG4582-HT4987		
2737 960_g_at		HG2463-HT2559		
2738 956_at		HG1980-HT2023		
2739 955_at		HG1862-HT1897		
2740 324_l_at		HG1515-HT1515		

Fig. 21

	A	B	C	D	E
2741	327_f_at		HG1800-HT1823		
2742	333_s_at		HG2639-HT2735		
2743	1840_g_at		HG1112-HT1112		
2744	1664_at		HG3543-HT3739		
2745	1624_at		HG2036-HT2090		
2746	1278_at		HG162-HT3165		
2747	1179_at		HG2855-HT2995		
2748	1180_g_at		HG2855-HT2995		
2749	32243_g_at		AL038340		
2750	311_s_at		HG3044-HT3742		
2751	297_g_at		HG4322-HT4592		
2752	296_at		HG4322-HT4592		
2753	1839_at		HG1112-HT1112		
2754	723_s_at		HG1322-HT5143		
2755	33300_at	dJ283E3.1	AL031282		guanine nucleotide binding protein (G protein), beta polypeptide 1
2756	41249_at	dJ283E3.1	AL031282		guanine nucleotide binding protein (G protein), beta polypeptide 1

Fig-21



	A		B		C		D		E	
	Systematic		Common		Genbank		Description		Product	
1							***ALU WARNING: Human Alu-Sq subfamily consensus sequence.			
2	AFHX-hum_alu_at				U14573		15 kDa selenoprotein		15 kDa selenoprotein	
3	38820_at		15-Sep		AF051894		26S proteasome-associated pad1 homolog		26S proteasome-associated pad1 homolog	
4	33247_at		POH1		U86782		35 kDa protein; Homo sapiens splicing factor, arginine/serine-rich 7 (SFRS7) gene, complete cds.		splicing factor, arginine/serine-rich 7	
5	32165_at		SFRS7		L41887		39 kDa protein; Human N33 protein form 2 (N33) gene, exon 11 and complete cds.		N33 protein form 2	
6	36851_g_at		N33		U42360		3-hydroxy-3-methylglutaryl-Coenzyme A reductase		3-hydroxy-3-methylglutaryl-Coenzyme A reductase	
7	39328_at		HMGCR		M11058		3-oxoacid CoA transferase		succinyl CoA:3-oxoacid CoA transferase precursor	
8	41142_at		OXCT		U62961		3'-phosphoadenosine 5'-phosphosulfate synthase 1		PAPS synthetase	
9	34411_at		PAPSS1		Y10387		5'-nucleotidase, cytosolic II		5'-nucleotidase	
10	738_at		NT5C2		D38524		5'-nucleotidase, cytosolic II		5'-nucleotidase	
11	31794_at		NT5C2		D38524		5-aminimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase		5-aminimidazole-4-carboxamide-1-beta-D-ribonucleotide transformylase/inosinase	
12	38811_at		ATIC		D82348		5-methyltetrahydrofolate-homocysteine methyltransferase		methionine synthase	
13	38383_at		MTR		U73338		6.2 kd protein			
14	39025_at		LOC54543		AI557912					

Fig 21

	A	B	C	D	E
15	40446_at	cICK0721Q.1	AL021366	60S Ribosomal Protein L35A LIKE pseudogene match: proteins P04646 P02434 P18077 P05744 P41056 CE04362 match: cDNAs Y16430 X52966 X03475 V01440 X55030 J00995 match: ESTs AA554649 AA747384 AA572868 AA329139 AA745138 AA330809 AA483371 AA507788 AA483213 D55111 N90267 N91909 AA662153 AA720551 AA836920 AA501529 AA526745 AA608598 AA649846 AA654164 match: genomic DNAs Z32550 X05705 X05706 X05704 I23465 I45758	divalent cation tolerant protein CUTA
16	39059_at	DHCR7	AF034544	7-dehydrocholesterol reductase	delta7-sterol reductase
17	40797_at	ADAM10	AF009615	a disintegrin and metalloproteinase domain 10	ADAM10
18	41601_at	ADAM17	AA142964	a disintegrin and metalloproteinase domain 17 (tumor necrosis factor, alpha, converting enzyme)	
19	34761_r_at	ADAM9	U41766	a disintegrin and metalloproteinase domain 9 (meltrin gamma)	metalloproteinase/disintegrin/cysteine-rich protein precursor
20	37680_at	AKAP12	U81607	A kinase (PRKA) anchor protein (gravin) 12	gravin
21	36633_at	AKAP10	AA114830	A kinase (PRKA) anchor protein 10	
22	34657_at	AKAP11	AB014529	A kinase (PRKA) anchor protein 11	KIAA0629 protein
23	35985_at	AKAP2	AB023137	A kinase (PRKA) anchor protein 2	KIAA0920 protein

Fig 21

	A	B	C	D	E
24	1636_g_at	ABL	U07563	<p>ABL is the cellular homolog proto-oncogene of Abelson's murine leukemia virus and is associated with the t(9;22) chromosomal translocation with the BCR gene in chronic myelogenous and acute lymphoblastic leukemia; alternative splicing using alternative first exon 1b; ABL is the cellular homolog proto-oncogene of Abelson's murine leukemia virus and is associated with the t(9;22) chromosomal translocation with the BCR gene in chronic myelogenous and acute lymphoblastic leukemia; alternative splicing using exon 1a; Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds.</p>	proto-oncogene tyrosine-protein kinase
25	41724_at	DXS1357E	X81817		accessory proteins BAP31/BAP29
26	41530_at	ACAA2	D16294		mitochondrial 3-oxoacyl-CoA thiolase
27	34668_at	ACATN	D88152		
28	36553_at	ASMTL	AA669799		acetyl-Coenzyme A transporter
29	37034_at	ANP32A	U73477		acidic nuclear phosphoprotein pp32
30	38479_at	ANP32B	Y07969		APRIL
31	34397_at	OA48-18	AF069250		okadaic acid-inducible phosphoprotein
32	39168_at	ALTE	AB018328		KIAA0785 protein
33	40077_at	ACO1	Z11559		iron regulatory factor
34	37578_at	AFAP	D25248	actin filament associated protein	actin filament associated protein
35	1718_at	ARPC2	U50523	actin related protein 2/3 complex, subunit 2 (34 kD)	actin related protein 2/3 complex, subunit 2 (34 kD)

F. 521

	A	B	C	D	E
36	34692_r_at	ARPC4	AF006087	actin related protein 2/3 complex, subunit 4 (20 kD)	p20-Arc
37	38392_at	ARPC5	AF006088	actin related protein 2/3 complex, subunit 5 (16 kD)	p16-Arc
38	32755_at	ACTA2	X13839	actin, alpha 2, smooth muscle, aorta	alpha 2 actin
39	AFFX-HSAC07X	ACTB	X00351	actin, beta	beta actin
40	AFFX-HSAC07X	ACTB	X00351	actin, beta	beta actin
41	32318_s_at	ACTB	X63432	actin, beta	mutant beta-actin (beta'-actin)
42	34160_at	ACTG1	X04098	actin, gamma 1	gamma-actin
43	39329_at	ACTN1	X15804	actinin, alpha 1	actinin, alpha 1
44	41753_at	ACTN4	U48734	actinin, alpha 4	alpha actinin
45	38642_at	ALCAM	Y10183	activated leucocyte cell adhesion molecule	MEMD protein
46	36171_at	PC4	AI521453	activated RNA polymerase II transcription cofactor 4	
47	39764_at	ACVR1	Z22534	activin A receptor, type I	ALK-2
48	35162_s_at	ACVR2	D31770	activin A receptor, type II	activin type II A receptor precursor
49	34394_at	ADNP	AB018327	activity-dependent neuroprotector	KIAA0784 protein
50	40673_at	ACADSB	U12778	acyl-Coenzyme A dehydrogenase, short/branched chain	acyl-CoA dehydrogenase
51	40459_at	ACOX1	S69189	acyl-Coenzyme A oxidase 1, palmitoyl	peroxisomal acyl-coenzyme A oxidase
52	40745_at	AP1B1	L13939	adaptor-related protein complex 1, beta 1 subunit	beta-prime-adaptin
53	35275_at	AP1G1	AL050025	adaptor-related protein complex 1, gamma 1 subunit	hypothetical protein
54	39795_at	AP2M1	D63475	adaptor-related protein complex 2, mu 1 subunit	adaptor-related protein complex 2, mu 1 subunit
55	39347_at	AP2S1	X97074	adaptor-related protein complex 2, sigma 1 subunit	clathrin-associated protein
56	32039_at	AP3B1	U81504	adaptor-related protein complex 3, beta 1 subunit	beta-3A-adaptin subunit of the AP-3 complex
57	36172_s_at	AP3D1	AF002163	adaptor-related protein complex 3, delta 1 subunit	delta-adaptin
58	38074_at	AP3S1	U91932	adaptor-related protein complex 3, sigma 1 subunit	AP-3 complex sigma3A subunit
59	33102_at	ADD3	D67031	adducin 3 (gamma)	adducin-like protein

Fig 21

	A	B	C	D	E
60	38014_at	ADAR	X79448	adenosine deaminase, RNA-specific	adenosine deaminase, RNA-specific, isoform ADAR-a; adenosine deaminase, RNA-specific, isoform ADAR-b; adenosine deaminase, RNA-specific, isoform ADAR-c
61	38748_at	ADARB1	U76421	adenosine deaminase, RNA-specific (RED1 homolog rat)	dsRNA adenosine deaminase DRADA2b
62	168_at	ADK	U50196	adenosine kinase	adenosine kinase
63	33865_at	BS69	AA127624	adenovirus 5 E1A binding protein	
64	33134_at	ADCY3	AB011083	adenylate cyclase 3	KIAA0511 protein
65	40585_at	ADCY7	D25538	adenylate cyclase 7	adenylate cyclase 7
66	33800_at	ADCY9	AF036927	adenylate cyclase 9	adenylate cyclase type IX
67	40788_at	AK2	U84371	adenylate kinase 2	adenylate kinase 2A
68	36639_at	ADSL	AF067853	adenylosuccinate lyase	adenylosuccinate lyase
69	935_at	CAP	L12168	adenylate cyclase-associated protein	adenylate cyclase-associated protein
70	33405_at	CAP2	N90755	adenylate cyclase-associated protein 2	
71	34378_at	ADFP	X97324	adipose differentiation-related protein	adipophilin
72	36861_at	DKFZp564I1922	AL049946	adican	hypothetical protein
73	33987_at	ARF1	M36340	ADP-ribosylation factor 1	ADP-ribosylation factor 1
74	39336_at	ARF3	M74491	ADP-ribosylation factor 3	ADP-ribosylation factor 3
75	36585_at	ARF4	M36341	ADP-ribosylation factor 4	ADP-ribosylation factor 4
76	37537_at	ARFD1	L04510	ADP-ribosylation factor domain protein 1, 64kD	nucleotide binding protein
77	39905_i_at	ARFGAP1		ADP-ribosylation factor GTPase activating protein 1	
78	37296_at	ARL1	AA402332	ADP-ribosylation factor-like 1	ADP-ribosylation factor-like 1
79	36572_r_at	ARL6IP	L28997	ADP-ribosylation factor-like 6 interacting protein	
80	41146_at	ADPRT	D31885	ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)	poly(ADP-ribose)transferase
81	1287_at	ADPRT	J03473	ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)	poly(ADP-ribose)transferase
82	34777_at	ADM	J03473	adrenomedullin	adrenomedullin precursor
83	32218_at		D14874	AF034176 Human mRNA (Tripodis and Ragoussis) Homo sapiens cDNA clone ntcon5 contig.	

Fig 21

	A	B	C	D	E
84	34315_at	AFG3L2	Y18314	AFG3 ATPase family gene 3-like 2 (yeast)	paraplegin-like protein
85	33454_at	AGRN	AF016903	agrin	agrin precursor
86	37027_at	AHNAK	M80899	AHNAK nucleoprotein (desmoyokin)	
87	36185_at	AARS	D32050	alanyl-tRNA synthetase	alanyl-tRNA synthetase
88	36686_at	ALDH1A3	U07919	aldehyde dehydrogenase 1 family, member A3	aldehyde dehydrogenase 6
89	32747_at	ALDH2	X05409	aldehyde dehydrogenase 2 family (mitochondrial)	aldehyde dehydrogenase 2 family (mitochondrial)
90	40409_at	ALDH3A2	U46689	aldehyde dehydrogenase 3 family, member A2	aldehyde dehydrogenase
91	37331_g_at	ALDH4A1	U24266	aldehyde dehydrogenase 4 family, member A1	pyroline-5-carboxylate dehydrogenase
92	36132_at	ALDH7A1	S74728	aldehyde dehydrogenase 7 family, member A1	antiquitin
93	33899_at	ALDH9A1	U34252	aldehyde dehydrogenase 9 family, member A1	gamma-aminobutyraldehyde dehydrogenase
94	38780_at	AKR1A1	J04794	aldo-keto reductase family 1, member A1 (aldehyde reductase)	aldo-keto reductase family 1, member A1 (aldehyde reductase)
95	36589_at	AKR1B1	X15414	aldo-keto reductase family 1, member B1 (aldose reductase)	aldo-keto reductase family 1, member B1 (aldose reductase)
96	37399_at	AKR1C3	D17793	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)
97	32510_at	AKR7A2	AF026947	aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase)	aflatoxin aldehyde reductase AFAR
98	39225_at	AGPS	Y09443	alkylglycerone phosphate synthase	alkyl-dihydroxyacetonephosphate synthase precursor
99	36941_at	AF1Q	U16954	ALL1-fused gene from chromosome 1q	AF1Q protein
100	37040_at	G2AN	D42041	alpha glucosidase II alpha subunit	alpha glucosidase II alpha subunit
101	35223_at	KIAA1017	AB023234	alpha integrin binding protein 63	KIAA1017 protein
102	39147_g_at	ATRX	U72936	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)	putative DNA dependent ATPase and helicase

Fig 21

	A	B	C	D	E
103	818_s_at	ATRX	U72936	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)	putative DNA dependent ATPase and helicase
104	34327_at	HLTF	Z46606	alternative translation initiation; H.sapiens HLTF gene for helicase-like transcription factor.	helicase-like transcription factor
105	35761_at	AASDHPPT	AL050073	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	hypothetical protein
106	39431_at	NPEPPS	AJ132583	aminopeptidase puromycin sensitive	puromycin sensitive aminopeptidase
107	41338_at	AES	AI951946	amino-terminal enhancer of split	
108	36996_at	OS-9	U41635	amplified in osteosarcoma	OS-9 precursor
109	38253_at	AGL	U84011	amylase-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)	glycogen debranching enzyme isoform 6
110	41136_s_at	APP	Y00264	amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease)	amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease)
111	40148_at	APBB2	U62325	amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like)	FE65-like protein
112	38471_r_at	APPBP2	D86981	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	KIAA0228 protein
113	38470_i_at	APPBP2	D86981	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	KIAA0228 protein
114	35364_at	APPBP1	U50939	amyloid beta precursor protein binding protein 1, 59kD	amyloid precursor protein-binding protein 1
115	40064_at	ALS2CR3	AB011121	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3	KIAA0549 protein
116	1577_at	AR	M23263	androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease)	androgen receptor
117	38842_at	AMOTL2	AB023206	angiomotin like 2	angiomotin like 2
118	39315_at	ANGPT1	D13628	angiotensinogen 1	angiotensinogen 1
119	1929_at	ANGPT1	U83508	angiotensinogen 1	angiotensinogen 1

Fig 21

	A	B	C	D	E
120	36965_at	ANK3	U13616	ankyrin 3, node of Ranvier (ankyrin G)	ankyrin G
121	37403_at	ANXA1	X05908	annexin A1	annexin I
122	36637_at	ANXA11	L19605	annexin A11	56K autoantigen
123	769_s_at	ANXA2	D00017	annexin A2	lipocortin II
124	31684_at	ANXA2P1	M62896	annexin A2 pseudogene 1	
125	31444_s_at	ANXA2P3	M62895	annexin A2 pseudogene 3	
126	37374_at	ANXA4	M82809	annexin A4	annexin IV (placental anticoagulant protein II)
127	37670_at	ANXA7	J04543	annexin A7	annexin VII isoform 1; annexin VII isoform 2
128	41138_at	MIC2	M16279	antigen identified by monoclonal antibodies 12E7, F21 and O13	antigen
129	40506_s_at	PABPC4; APP1; A	U75686	APP-1; Homo sapiens polyadenylate binding protein mRNA, complete cds.	polyadenylate binding protein
130	34370_at	ARCN1	X81198	archain 1	archain
131	32253_at	REER	AB007927	arginine-glutamic acid dipeptide (RE) repeats	KIAA0458 protein
132	549_at	RARS	S80343	arginyl-tRNA synthetase	arginyl-tRNA synthetase
133	39164_at	ARIH2	AF099149	ariadne homolog 2 (Drosophila)	TRIAD1 type I
134	41729_at	ARIH1	AJ009771	ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila)	putative RING finger protein
135	36057_at	ALEX2	AB011084	armadillo repeat protein ALEX2	KIAA0512 protein
136	40052_at	ACTR1A	X82206	ARP1 actin-related protein 1 homolog A, contractin alpha (yeast)	alpha-centractin
137	35734_at	ACTR2	AI935551	ARP2 actin-related protein 2 homolog (yeast)	
138	35733_at	ACTR2	AF006082	ARP2 actin-related protein 2 homolog (yeast)	Arp2
139	35271_at	ACTR3	AF006083	ARP3 actin-related protein 3 homolog (yeast)	Arp3
140	40516_at	AHR	L19872	aryl hydrocarbon receptor	AH-receptor
141	36671_at	ASNS	M27396	asparagine synthetase	asparagine synthetase
142	41241_at	NARS	D84273	asparaginyl-tRNA synthetase	Asparaginyl tRNA Synthetase
143	38703_at	DNPEP	AF005050	aspartyl aminopeptidase	aspartyl aminopeptidase
144	34181_at	AGA	X55330	aspartylglucosaminidase	aspartylglucosaminidase

Fig 21



	A	B	C	D	E
145	37229_at	ATR	U49844	ataxia telangiectasia and Rad3 related	FRAP-related protein
146	34817_s_at	A2LP	U70671	ataxin 2 related protein	ataxin-2 related protein
147	379_at	APACD	AB006679	ATP binding protein associated with cell differentiation	ATP binding protein
148	40881_at	ACLY	X64330	ATP citrate lyase	ATP-citrate (pro-S)-lyase
149	41228_r_at	ATP5F1	X60221	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	H+-ATP synthase subunit b
150	34811_at	ATP5G3	U09813	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3	mitochondrial ATP synthase subunit 9 precursor
151	35760_at	ATP5H	AF087135	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d	F1FO-type ATPase subunit d
152	38751_i_at	ATP5I	AA426364	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e	
153	36107_at	ATP5J	AA845575	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6	
154	38693_at	ATP5L	AA917672	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g	
155	40115_at	ATP5C1	D16562	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	ATP synthase gamma-subunit
156	39791_at	ATP2A2	M23114	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2
157	39790_at	ATP2A2	M23115	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2
158	38684_at	ATP2C1	AJ010953	ATPase, Ca++ transporting, type 2C, member 1	putative Ca2+-transporting ATPase
159	35831_at	ATP9A	AB014511	ATPase, Class II, type 9A	KIAA0611 protein
160	40853_at	ATP10D	A1478147	ATPase, Class V, type 10D	
161	36635_at	ATP11B	AB023173	ATPase, Class VI, type 11B	KIAA0956 protein
162	36523_at	ATP7A	L06133	ATPase, Cu++ transporting, alpha polypeptide (Menkes syndrome)	Cu++-transporting P-type ATPase
163	33854_at	ATP6M	AA877795	ATPase, H+ transporting, lysosomal (vacuolar proton pump)	

Fig 21

	A	B	C	D	E
164	37395_at	ATP6S14	D49400	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 14kD	vacuolar ATPase
165	36994_at	ATP6L	M62762	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD	vacuolar H+ ATPase proton channel subunit
166	36167_at	ATP6F	D89052	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 21kD	proton-ATPase-like protein
167	37367_at	ATP6E	X76228	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD	vacuolar H+ ATPase E subunit
168	37948_at	ATP6C	J05682	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 42kD	H+ -ATPase C subunit
169	33875_at	ATP6H	A1547262	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 9kD	
170	40903_at	ATP6M8-9	AL049929	ATPase, H+ transporting, lysosomal (vacuolar proton pump) membrane sector associated protein M8-9	hypothetical protein
171	34889_at	ATP6A1	AA056747	ATPase, H+ transporting, lysosomal (vacuolar proton pump), alpha polypeptide, 70kD, isoform 1	
172	40568_at	ATP6B2	L35249	ATPase, H+ transporting, lysosomal (vacuolar proton pump), beta polypeptide, 56/58kD, isoform 2	vacuolar H+-ATPase 56,000 subunit
173	35770_at	ATP6S1	D16469	ATPase, H+ transporting, lysosomal (vacuolar proton pump), subunit 1	ORF
174	37669_s_at	ATP1B1	U16799	ATPase, Na+/K+ transporting, beta 1 polypeptide	Na,K-ATPase beta subunit
175	32563_at	ATP1B3	U51478	ATPase, Na+/K+ transporting, beta 3 polypeptide	sodium/potassium-transporting ATPase beta-3 subunit
176	35717_at	ABCA8	AB020629	ATP-binding cassette, sub-family A (ABC1), member 8	KIAA0822 protein
177	38261_at	ABCC3	AF085692	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	multidrug resistance-associated protein 3B
178	35648_at	KIAA0442	AB007902	autism-related protein 1	autism-related protein 1
179	38068_at	AMFR	M63175	autocrine motility factor receptor	autocrine motility factor receptor
180	38433_at	AXL	M76125	AXL receptor tyrosine kinase	tyrosine kinase receptor
181	35268_at	AXOT	AL050171	axotrophin	hypothetical protein DKFZp586F1122 similar to axotrophin

Fig 21

A	B	C	D	E
182 35350_at	GALNAC4S-6ST	AB011170	B cell RAG associated protein	KIAA0598 protein
183 41562_at	BMI1	L13689	B lymphoma Mo-MLV insertion region (mouse)	murine leukemia viral (bmi-1) oncogene homolog
184 1728_at	BMI1	L13689	B lymphoma Mo-MLV insertion region (mouse)	murine leukemia viral (bmi-1) oncogene homolog
185 36578_at	BIRC2	U37547	baculoviral IAP repeat-containing 2	MIH-B
186 41278_at	BAF53A	AF041474	BAF53	BAF53a
187 33175_at	BBS4	AA156237	Bardet-Biedl syndrome 4	
188 40790_at	BHLHB2	AB004066	basic helix-loop-helix domain containing, class B, 2	1-Dec
189 40108_at	BZAP45	D13630	basic leucine-zipper protein BZAP45	basic leucine-zipper protein BZAP45
190 40202_at	BTEB1	D31716	basic transcription element binding protein 1	GC box binding protein
191 35055_at	BTF3	X53281	basic transcription factor 3	general transcription factor
192 38364_at	BCE-1	AF068197	BCE-1 protein	BCE-1
193 40091_at	BCL6	U00115	B-cell CLL/lymphoma 6 (zinc finger protein 51)	zinc-finger protein
194 37294_at	BTG1	X61123	B-cell translocation gene 1, anti-proliferative	B-cell translocation protein 1
195 32060_at	BNIP2	U15173	BCL2/adenovirus E1B 19kD interacting protein 2	BCL2/adenovirus E1B 19kD-interacting protein 2
196 38010_at	BNIP3	AF002697	BCL2/adenovirus E1B 19kD interacting protein 3	E1B 19K/Bcl-2-binding protein Nip3
197 39436_at	BNIP3L	AF079221	BCL2/adenovirus E1B 19kD interacting protein 3-like	BCL2/adenovirus E1B 19kDa-interacting protein 3a
198 34798_at	BAG1	Z35491	BCL2-associated athanogene	glucocorticoid receptor-associated protein RAP46
199 35291_at	BAG2	AL050287	BCL2-associated athanogene 2	hypothetical protein
200 36463_at	BAG5	AB020680	BCL2-associated athanogene 5	KIAA0873 protein
201 38050_at	BTF	D79986	Bcl-2-associated transcription factor	KIAA0164 gene product
202 38101_at	BDG-29	AB011151	BDG-29 protein	KIAA0579 protein
203 39378_at	BECN1	U17999	beclin 1 (coiled-coil, myosin-like BCL2 interacting protein)	
204 39160_at	PDHB	D90086	beta subunit; Human pyruvate dehydrogenase (EC 1.2.4.1) beta subunit gene, exons 1-10.	pyruvate dehydrogenase (lipoamide) beta

Fig 21

	A	B	C	D	E
205	34644_at	B2M	AB021288	beta-2-microglobulin	beta 2-microglobulin
206	40601_at	BBP	AI057115	beta-amyloid binding protein precursor beta-hexosaminidase alpha chain; Human beta-hexosaminidase alpha chain (HEXA) gene, exon 14.	
207	39340_at	HEXA	M16424	biglycan	hexosaminidase A preproprotein
208	38126_at	BGN	J04599		biglycan preproprotein
209	33198_at	BART1	AA206524	binder of Arl Two	
210	37274_at	Btd	AF018631	biotin-amide amidohydrolase; Homo sapiens biotinidase (BTD) gene, exons 2, 3, and 4 and complete cds.	biotinidase
211	40912_s_at	BPHL	X81372	biphenyl hydrolase-like (serine hydrolase; breast epithelial mucin-associated antigen)	biphenyl hydrolase-related protein
212	35267_g_at	BLCAP	AL049288	bladder cancer associated protein	bladder cancer associated protein
213	35266_at	BLCAP	AL049288	bladder cancer associated protein	bladder cancer associated protein
214	37700_at	BLMH	X92106	bleomycin hydrolase	bleomycin hydrolase
215	39565_at	BMPR1A	Z22535	bone morphogenetic protein receptor, type IA	ALK-3
216	39551_at	BHC80	N98667	BRAF35/HDAC2 complex (80 kDa)	
217	32607_at	BASP1	AF039656	brain abundant, membrane attached signal protein 1	neuronal tissue-enriched acidic protein
218	32606_at	BASP1	AA135683	brain abundant, membrane attached signal protein 1	
219	37945_at	BACH	U91316	brain acyl-CoA hydrolase	acyl-CoA thioester hydrolase
220	37958_at	BCMP1	AL049257	brain cell membrane protein 1	brain cell membrane protein 1
221	40023_at	BDNF	X60201	brain-derived neurotrophic factor	brain-derived neurotrophic factor
222	41683_i_at	BCKDHB	U50708	branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease)	branched chain alpha-ketoacid dehydrogenase E1 beta subunit
223	36812_at	BCAR3	U92715	breast cancer anti-estrogen resistance 3	breast cancer antiestrogen resistance 3 protein
224	38306_at	BIG1	AA477576	brefeldin A-inhibited guanine nucleotide- exchange protein 1	
225	37947_at	BRD3	D26362	bromodomain containing 3	bromodomain containing protein 3
226	31895_at	BACH1	AB002803	BTB and CNC homology 1, basic leucine zipper transcription factor 1	BTB and CNC homology 1, basic leucine zipper transcription factor 1

Fig 21

	A	B	C	D	E
227	36634_at	BTG2	U72649	BTG family, member 2	BTG2
228	37218_at	BTG3	D64110	BTG family, member 3	ANA
229	41547_at	BUB3	AF047472	BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast)	spleen mitotic checkpoint BUB3
230	34783_s_at	BUB3	AF047473	BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast)	testis mitotic checkpoint BUB3
231	32781_f_at	BPAG1	AA058762	bullous pemphigoid antigen 1 (230/240kD)	
232	32780_at	BPAG1	AB018271	bullous pemphigoid antigen 1 (230/240kD)	KIAA0728 protein
233	32629_f_at	BTN3A1	U90552	butyrophilin, subfamily 3, member A1	butyrophilin
234	39357_at	C2F	U72514	C2f protein	C2f
235	40709_at	LOC58502	W27601	C2H2 (Krueppel-type) zinc finger protein	
236	37031_at	C9orf10	D80005	C9orf10 protein	C9orf10 protein
237	33856_at	CXX1	Y13374	CAAX box 1	putative prenylated protein
238	36976_at	CDH11	D21255	cadherin 11, type 2, OB-cadherin (osteoblast)	OB-cadherin-2
239	2087_s_at	CDH11	D21254	cadherin 11, type 2, OB-cadherin (osteoblast)	OB-cadherin-1
240	2053_at	CDH2	M34064	cadherin 2, type 1, N-cadherin (neuronal)	cadherin 2, type 1 preproprotein
241	31670_s_at	CAMK2G	U81554	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	CaM kinase II isoform
242	38716_at	CAMKK2	AB018330	calcium/calmodulin-dependent protein kinase kinase 2, beta	KIAA0787 protein
243	31854_at	CASK	AF035582	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	CASK
244	41738_at	CALD1	M64110	caldesmon 1	caldesmon
245	41739_s_at	CALD1	M83216	caldesmon 1	caldesmon
246	41288_at	CALM1	AL036744	calmodulin 1 (phosphorylase kinase, delta)	
247	911_s_at	CALM2	M19311	calmodulin 2 (phosphorylase kinase, delta)	calmodulin 2 (phosphorylase kinase, delta)
248	40125_at	CANX	L10284	calnexin	calnexin
249	37001_at	CAPN2	M23254	calpain 2, (mII) large subunit	neutral protease large subunit
250	36138_at	CAPNS1	X04106	calpain, small subunit 1	calpain, small subunit 1

Fig 21

	A	B	C	D	E
251	41257_at	CAST	D16217	calpastatin	calpastatin
252	33385_g_at	CAST	U31346	calpastatin	calpastatin
253	40953_at	CNN3	S80562	calponin 3, acidic	acidic calponin
254	37345_at	CALU	AF013759	calumenin	calumein
255	37535_at	CREB1	M27691	cAMP responsive element binding protein 1	cAMP responsive element binding protein 1, isoform A; cAMP responsive element binding protein 1, isoform B
256	40849_s_at	CREB3	U88528	cAMP responsive element binding protein 3 (luman)	transcription factor LZIP
257	39438_at	CREBL2	AF039081	cAMP responsive element binding protein-like 2	Cre binding protein-like 2
258	32065_at	CREM	S68134	cAMP responsive element modulator	cyclic AMP-responsive element modulator beta isoform
259	32067_at	CREM	S68271	cAMP responsive element modulator	cyclic AMP-responsive element modulator
260	32066_g_at	CREM	S68134	cAMP responsive element modulator	cyclic AMP-responsive element modulator beta isoform
261	40910_at	CAPZA1	U56637	capping protein (actin filament) muscle Z-line, alpha 1	capping protein alpha subunit isoform 1
262	36641_at	CAPZA2	U03851	capping protein (actin filament) muscle Z-line, alpha 2	capping protein alpha
263	37012_at	CAPZB	U03271	capping protein (actin filament) muscle Z-line, beta	F-actin capping protein beta subunit
264	32094_at	CHST3	AB017915	carbohydrate (chondroitin 6)	chondroitin 6-sulfotransferase
265	41447_at	CHSY1	AB023207	sulfotransferase 3	KIAA0990 protein
266	41395_at	CHST1	AB003791	carbohydrate (chondroitin) synthase 1	keratan sulfate Gal-6-sulfotransferase
267	37960_at	CHST2	AB014679	carbohydrate (keratan sulfate Gal-6)	N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST)
268	36454_at	CA12	AF037335	sulfotransferase 1	carboxic anhydrase precursor
269	34876_at	CPD	U65090	carbohydrate (N-acetylglucosamine-6-O)	carboxypeptidase D
270	36606_at	CPE	X51405	sulfotransferase 2	carboxypeptidase E precursor
271	35632_at	CBLB	U26710	carboxypeptidase D	cbl-b
272	40184_at	CSNK1A1	L37042	Cas-Br-M (murine) ectropic retroviral transforming sequence b	casein kinase I-alpha
273	36949_at	CSNK1D	U29171	casein kinase 1, alpha 1	casein kinase I delta

Fig 21

	A	B	C	D	E
274	38019_at	CSNK1E	L37043	casein kinase 1, epsilon	casein kinase I-epsilon
275	1211_s_at	CRADD	U84388	CASP2 and RIPK1 domain containing adaptor with death domain	death domain containing protein CRADD
276	1867_at	CFLAR	AF005775	CASP8 and FADD-like apoptosis regulator	caspase-like apoptosis regulatory protein 2
277	195_s_at	CASP4	U28014	caspase 4, apoptosis-related cysteine protease	cysteine protease
278	33774_at	CASP8	X98172	caspase 8, apoptosis-related cysteine protease	MACH-alpha-1
279	41156_g_at	CTNNA1	U03100	catenin (cadherin-associated protein), alpha 1 (102kD)	alpha2(E)-catenin
280	41155_at	CTNNA1	U03100	catenin (cadherin-associated protein), alpha 1 (102kD)	alpha2(E)-catenin
281	2085_s_at	CTNNA1	D14705	catenin (cadherin-associated protein), alpha 1 (102kD)	'human alpha-catenin'
282	2069_s_at	CTNNA1	L23805	catenin (cadherin-associated protein), alpha 1 (102kD)	alpha1(E)-catenin
283	35331_at	CTNNAL1	U97067	catenin (cadherin-associated protein), alpha-like 1	alpha-catenin-like protein
284	40777_at	CTNNB1	X87838	catenin (cadherin-associated protein), beta 1 (98kD)	beta-catenin
285	40444_s_at	CTNND1	AB002382	catenin (cadherin-associated protein), delta 1	
286	38466_at	CTSK	X82153	cathepsin K (pseudosubstososis)	Cathepsin O
287	37391_at	CTSL	X12451	cathepsin L	pro-(cathepsin L)
288	36915_at	CTSO	AI810485	cathepsin O	
289	36119_at	CAV1	AF070648	caveolin 1, caveolae protein, 22kD	
290	339_at	CAV2	AF035752	caveolin 2	caveolin-2
291	33113_at	CITED2	U65093	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	msg-related gene 1
292	1052_s_at	CEBPD	M83667	CCAAT/enhancer binding protein (C/EBP), delta	NF-IL6-beta protein
293	39219_at	CEBPG	U20240	CCAAT/enhancer binding protein (C/EBP), gamma	C/EBP gamma

Fig 21

A	B	C	D	E
294 33861_at	CNOT2	AI123426	CCR4-NOT transcription complex, subunit 2	
295 32820_at	CNOT4	U71267	CCR4-NOT transcription complex, subunit 4	potential transcriptional repressor NOT4Hp
296 34819_at	CD164	D14043	CD164 antigen, sialomucin	MGC-24 precursor
297 34699_at	CD2AP	AL050105	CD2-associated protein	hypothetical protein
298 33823_at	CD36L2	D12676	CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2 (lysosomal integral membrane protein II)	85kDa human lysosomal sialoglycoprotein
299 2036_s_at	CD44	M59040	CD44 antigen (homing function and Indian blood group system)	cell adhesion molecule
300 35282_r_at	CD81	M33680	CD81 antigen (target of antiproliferative antibody 1)	CD81 antigen
301 39389_at	CD9	M38690	CD9 antigen (p24)	CD9 antigen
302 32175_at	CDC10	S72008	CDC10 cell division cycle 10 homolog (S. cerevisiae)	cell division cycle 10
303 40404_s_at	CDC16	U18291	CDC16 cell division cycle 16 homolog (S. cerevisiae)	CDC16Hs
304 31877_at	CDC23	AF053977	CDC23 (cell division cycle 23, yeast, homolog)	cell division cycle protein 23
305 40690_at	CKS2	X54942	CDC28 protein kinase 2	Cks1 protein homologue
306 33362_at	CEP3	AF094521	Cdc42 effector protein 3	MSE55-related protein
307 32833_at	CLK1	M59287	CDC-like kinase 1	
308 41535_at	CDK2AP1	AF006484	CDK2-associated protein 1	putative oral tumor suppressor protein
309 41343_at	CDS2	Y16521	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	CDS2 protein
310 33397_at	CDIPT	AL050383	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)	
311 40591_at	CDC27	S78234	cell division cycle 27	H-NUC
312 450_g_at	CGR19	U66469	cell growth regulatory with ring finger domain	cell growth regulator CGR19
313 36514_at	CGR19	U66469	cell growth regulatory with ring finger domain	cell growth regulator CGR19

Fig 21



A	B	C	D	E
314 35311_at	CREG	AF084523	cellular repressor of E1A-stimulated genes	cellular repressor of E1A-stimulated genes
315 41333_at	CENTB2	D26069	centaurin, beta 2	centaurin, beta 2
316 34676_at	CENTG2	AB029022	centaurin, gamma 2	KIAA1099 protein
317 38410_at	CETN2	X72964	centrin, EF-hand protein, 2	caltractin
318 35232_f_at	CETN3	AI056696	centrin, EF-hand protein, 3 (CDC31 homolog, yeast)	
319 31894_at	CENPC1	M95724	centromere protein C 1	centromere autoantigen C
320 33805_at	CAP350	AB007949	centrosome-associated protein 350	KIAA0480 protein
321 36190_at	CDR2	M63256	cerebellar degeneration-related protein (62kD)	major Yo paraneoplastic antigen
322 32262_at	CGI-01	AL049669	CGI-01 protein	hypothetical protein
323 40931_at	LOC50999	AL080084	CGI-100 protein	
324 38500_at	LOC51014	AB002450	CGI-109 protein	
325 34359_at	LOC51020	AA524058	CGI-130 protein	
326 38667_at	LOC51031	AA189161	CGI-150 protein	
327 41824_at	LOC51096	AI140114	CGI-48 protein	
328 34862_at	LOC51097	AA005018	CGI-49 protein	
329 37199_at	LOC51626	AI760932	CGI-60 protein	
330 41411_at	LOC51103	AI566877	CGI-65 protein	
331 39814_s_at	LOC51635	AI052724	CGI-86 protein	
332 35759_at	CCT2	AF026166	chaperonin containing TCP1, subunit 2 (beta)	chaperonin-containing TCP-1 beta subunit homolog
333 40774_at	CCT3	X74801	chaperonin containing TCP1, subunit 3 (gamma)	gamma subunit of CCT chaperonin
334 32594_at	CCT4	AF026291	chaperonin containing TCP1, subunit 4 (delta)	chaperonin containing t-complex polypeptide 1, delta subunit
335 38416_at	CCT6A	L27706	chaperonin containing TCP1, subunit 6A (zeta 1)	chaperonin-like protein
336 38720_at	CCT7	AF026292	chaperonin containing TCP1, subunit 7 (eta)	chaperonin containing t-complex polypeptide 1, eta subunit
337 39767_at	CCT8	D13627	chaperonin containing TCP1, subunit 8 (theta)	chaperonin containing TCP1, subunit 8 (theta)
338 41000_at	CHES1	U68723	checkpoint suppressor 1	checkpoint suppressor 1
339 37855_at	CTBS	M95767	chitinase, di-N-acetyl-	di-N-acetylchitinase

Fig 21

	A	B	C	D	E
340	38732_at	CLNS1A	X91788	chloride channel, nucleotide-sensitive, 1A	IcIn protein
341	33891_at	CLIC4	AL080061	chloride intracellular channel 4	
342	32363_at	CH25H	AF059214	cholesterol 25-hydroxylase	cholesterol 25-hydroxylase
343	38112_g_at	CSPG2	X15998	chondroitin sulfate proteoglycan 2 (versican)	chondroitin sulfate proteoglycan 2 (versican)
344	38111_at	CSPG2	X15998	chondroitin sulfate proteoglycan 2 (versican)	chondroitin sulfate proteoglycan 2 (versican)
345	34763_at	CSPG6	AF020043	chondroitin sulfate proteoglycan 6 (bamacan)	chromosome-associated polypeptide
346	37304_at	CBX1	U35451	chromobox homolog 1 (HP1 beta homolog Drosophila)	heterochromatin protein p25
347	38085_at	CBX3	A1740522	chromobox homolog 3 (HP1 gamma homolog, Drosophila)	
348	38084_at	CBX3	AA648295	chromobox homolog 3 (HP1 gamma homolog, Drosophila)	
349	36137_at	CHD4	X86691	chromodomain helicase DNA binding protein 4	Mi-2 protein
350	32111_at	CDYL	AL050164	chromodomain protein, Y chromosome-like	hypothetical protein
351	39550_at	C1orf17	AB011156	chromosome 1 open reading frame 17	KIAA0584 protein
352	39033_at	C1orf8	Z78368	chromosome 1 open reading frame 8	
353	32217_at	C12orf22	AF052105	chromosome 12 open reading frame 22	TGF-beta induced apoptosis protein 12
354	40979_at	C14orf3	AJ243310	chromosome 14 open reading frame 3	C14orf3 protein
355	40045_g_at	C18orf1	AF009425	chromosome 18 open reading frame 1	clone 22
356	36860_at	C19orf7	AB028987	chromosome 19 open reading frame 7	KIAA1064 protein
357	34287_at	C21orf80	AB023175	chromosome 21 open reading frame 80	KIAA0958 protein
358	33406_at	C22orf2	AL050345	chromosome 22 open reading frame 2	hypothetical protein
359	33778_at	C22orf4	AL096779	chromosome 22 open reading frame 4	hypothetical protein
360	41758_at	C22orf5	AL096879	chromosome 22 open reading frame 5	hypothetical protein
361	38690_at	C3orf4	AL080097	chromosome 3 open reading frame 4	hypothetical protein
362	36013_at	C4orf1	AF006621	chromosome 4 open reading frame 1	embryonic lung protein
363	36955_at	C5orf8	U10362	chromosome 5 open reading frame 8	GP36b glycoprotein
364	41375_at	C6orf28	AJ245416	chromosome 6 open reading frame 28	G7b protein
365	41454_at	C6orf34	W27949	chromosome 6 open reading frame 34	
366	36139_at	C6orf5	AL050289	chromosome 6 open reading frame 5	hypothetical protein

Fig 21

	A	B	C	D	E
367	35193_at	CHC1L	AF060219	chromosome condensation 1-like	RCC1-like G exchanging factor RLG
368	34292_at	CXorf12	X92475	chromosome X open reading frame 12	chromosome X open reading frame 12
369	41314_at	CS	AF047042	citrate synthase	citrate synthase
370	41159_at	CLTC	D21260	clathrin, heavy polypeptide (Hc)	clathrin heavy chain
371	38657_s_at	CLTA	M20471	clathrin, light polypeptide (Lca)	clathrin, light polypeptide A, isoform a; clathrin, light polypeptide A, isoform b
372	35743_at	CPSF4	U79569	cleavage and polyadenylation specific factor 4, 30kD subunit	no arches
373	32723_at	CSTF1	L02547	cleavage stimulation factor, 3' pre-RNA, subunit 1, 50kD	cleavage stimulation factor
374	41183_at	CSTF3	U15782	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD	cleavage stimulation factor 77kDa subunit
375	38711_at	CLASP2	AB014527	CLIP-associating protein 2	KIAA0627 protein
376	36017_at	LOC57213	AF055016	CLLL6 protein	CLLL6 protein
377	36780_at	CLU	M25915	clusterin (complement lysis inhibitor, SP-40, 40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J)	clusterin (complement lysis inhibitor, SP-40, 40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J)
378	35180_at	LOC113251	AL050205	c-Mpl binding protein	
379	40811_at	COASTER	AB011148	coactivator for steroid receptors	KIAA0576 protein
380	38052_at	F13A1	M14539	coagulation factor XIII, A1 polypeptide	coagulation factor XIII A1 subunit precursor
381	36972_at	RNP24	X92098	coated vesicle membrane protein	transmembrane protein
382	34326_at	COPB	X82103	coatamer protein complex, subunit beta	beta-Coat protein
383	36677_at	COPB2	X70476	coatamer protein complex, subunit beta 2 (beta prime)	subunit of coatamer complex
384	35205_at	COBRA1	AL050280	cofactor of BRCA1	hypothetical protein
385	36648_at	CRSP9	AF031383	cofactor required for Sp1 transcriptional activation, subunit 9 (33kD)	hMed7
386	33659_at	CFL1	X95404	cofilin 1 (non-muscle)	cofilin
387	40879_at	BICD2	AB014599	coiled-coil protein BICD2	KIAA0699 protein
388	39864_at	CIRBP	D78134	cold inducible RNA binding protein	CIRP
389	39839_at	CSDA	M24069	cold shock domain protein A	cold shock domain protein A
390	32307_s_at	COL1A2	V00503	collagen, type I, alpha 2	alpha 2 type I collagen preproprotein
391	32306_g_at	COL1A2	J03464	collagen, type I, alpha 2	alpha 2 type I collagen preproprotein
392	32305_at	COL1A2	J03464	collagen, type I, alpha 2	alpha 2 type I collagen preproprotein

Fig 21

	A	B	C	D	E
393	32488_at			collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)	prepro-alpha-1 type 3 collagen
394	36659_at	COL3A1	X14420	collagen, type IV, alpha 2	alpha (2) chain
395	38420_at	COL4A2	X05610	collagen, type IV, alpha 2	procollagen alpha 2(V)
396	38722_at	COL5A2	Y14690	collagen, type V, alpha 2	alpha-1 collagen VI (AA 574-1009)
397	38077_at	COL6A1	X15880	collagen, type VI, alpha 1	collagen type VI, alpha 3 chain
398	37459_at	COL6A3	X52022	collagen, type VI, alpha 3	alpha 1(VIII) collagen
		COL8A1	X57527	collagen, type VIII, alpha 1	alpha 1 type XI collagen, isoform A
					preproprotein; alpha 1 type XI collagen, isoform B preproprotein; alpha 1 type XI collagen, isoform C preproprotein
399	37892_at	COL11A1	J04177	collagen, type XI, alpha 1	alpha-1 type XVI collagen
400	35168_f_at	COL16A1	M92642	collagen, type XVI, alpha 1	complement component 1, q subcomponent
401	37668_at	C1QBP	M69039	complement component 1, q	binding protein precursor
402	39409_at	C1R	M14058	subcomponent binding protein	complement component 1, r subcomponent
403	40496_at	C1S	J04080	complement component 1, s	complement component 1, s subcomponent
404	36638_at	CTGF	X78947	subcomponent	connective tissue growth factor
405	41202_s_at	OS4	AF000152	connective tissue growth factor	OS-4 protein
406	33770_at	CHUK	AF009225	conserved gene amplified in osteosarcoma	IkB kinase alpha subunit
407	1789_at	COPS5	U65928	conserved helix-loop-helix ubiquitous kinase	Jun activation domain binding protein
408	32539_at	COP9	U51205	COP9 constitutive photomorphogenic homolog subunit 5 (Arabidopsis)	COP9 signalosome subunit 1 CSN1
409	40138_at	MOV34-34KD	U70735	COP9 homolog	34 kDa Mov34 homolog
410	40452_at	CPNE1	U83246	COP9 subunit 6 (MOV34 homolog, 34 kD)	copine I
411	39706_at	CPNE3	AB014536	copine I	KIAA0636 protein
412	37999_at	CPO	D16611	copine III	coproporphyrinogen oxidase
413	37026_at	COPEB	AF001461	coproporphyrinogen oxidase (coproporphyrin, harderoporphyria)	Kruppel-like zinc finger protein Z19
414	41175_at	CBFB	L20298	core promoter element binding protein	transcription factor
415	32803_at	CN1L	AF104398	core-binding factor, beta subunit	cornichon
				cornichon-like	

Fig 21

	A	B	C	D	E
416	34723_at	COX11	U79270	COX11 homolog, cytochrome c oxidase assembly protein (yeast)	COX11 homolog
417	37907_at	F8A; DXS522E	M34677	CpG island protein; Human nested gene protein gene, complete cds.	coagulation factor VIII-associated protein
418	38664_at	CFDP1	AB009285	craniofacial development protein 1	craniofacial development protein 1
419	33831_at	CREBBP	U47741	CREB binding protein (Rubinstein-Taybi syndrome)	CREB-binding protein
420	36948_at	CRI1	AL109701	CREBBP/EP300 inhibitory protein 1	C15orf3
421	38148_at	CRY1	D83702	cryptochrome 1 (photolyase-like)	photolyase
422	37902_at	CRY2	L13278	crystallin, zeta (quinone reductase)	zeta-crystallin
423	40167_s_at	LOC55884	AF038187	CS box-containing WD protein	
424	38804_at	CSE1L	AF053641	CSE1 chromosome segregation 1-like (yeast)	cellular apoptosis susceptibility protein
425	1768_s_at	CSK	X59932	c-src tyrosine kinase	c-src-kinase
426	41309_g_at	CTBP1	U37408	C-terminal binding protein 1	phosphoprotein CtBP
427	40780_at	CTBP2	AF016507	C-terminal binding protein 2	C-terminal binding protein 2
428	39723_at	CUL1	AF062536	cullin 1	cullin 1
429	40141_at	CUL4B	AB014595	cullin 4B	KIAA0695 protein
430	31823_at	CUTL1	M74099	cut-like 1, CCAAT displacement protein (Drosophila)	cut-like 1, CCAAT displacement protein
431	36872_at	ARPP-19	AL120559	cyclic AMP phosphoprotein, 19 kD	
432	41808_at	DMTF1	AF052102	cyclin D binding myb-like transcription factor 1	cyclin D binding myb-like transcription factor 1
433	38418_at	CCND1	X59798	cyclin D1 (PRAD1: parathyroid adenomatosis 1)	cyclin
434	2020_at	CCND1	M73554	cyclin D1 (PRAD1: parathyroid adenomatosis 1)	bcl-1
435	36650_at	CCND2	D13639	cyclin D2	cyclin D2
436	40225_at	GAK	D88435	cyclin G associated kinase	HsGAK
437	37723_at	CCNG2	U47414	cyclin G2	cyclin G2
438	1913_at	CCNG2	U47414	cyclin G2	cyclin G2
439	1924_at	CCNH	U11791	cyclin H	cyclin H
440	1836_at	CCNI	D50310	cyclin I	cyclin I
441	1792_g_at	CDK2	M68520	cyclin-dependent kinase 2	cdc2-related protein kinase

Fig 21

	A	B	C	D	E
442	33317_at	CDK7	L20320	cyclin-dependent kinase 7 (MO15 homolog, <i>Xenopus laevis</i> , cdk-activating kinase)	protein serine/threonine kinase
443	1969_s_at	CDK7	X77743	cyclin-dependent kinase 7 (MO15 homolog, <i>Xenopus laevis</i> , cdk-activating kinase)	CDK activating kinase
444	35140_at	CDK8	R59697	cyclin-dependent kinase 8	
445	2031_s_at	CDKN1A	U03106	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	cyclin-dependent kinase inhibitor 1A
446	33847_s_at	CDKN1B	A1304854	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	
447	36053_at	CDKN2C	AF041248	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	cyclin-dependent kinase inhibitor
448	38700_at	CSRP1	M33146	cysteine and glycine-rich protein 1	cysteine and glycine-rich protein 1
449	41401_at	CSRP2	U57646	cysteine and glycine-rich protein 2	cysteine and glycine-rich protein 2
450	40936_at	CRIM1	A1651806	cysteine-rich motor neuron 1	
451	38772_at	CYR61	Y11307	cysteine-rich, angiogenic inducer, 61	CYR61 protein
452	40408_at	CARS	L06845	cysteinyI-tRNA synthetase	cysteinyI-tRNA synthetase
453	39317_at	CMAH	D86324	cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminic acid hydroxylase)	CMP-N-acetylneuraminic acid hydroxylase
454	34340_at	CYB5-M	AA173896	cytochrome b5 outer mitochondrial membrane precursor	
455	35818_at	HCS	D00265	cytochrome c	cytochrome c
456	39921_at	COX5B	A1526089	cytochrome c oxidase subunit Vb	
457	41206_r_at	COX6A1	A1540925	cytochrome c oxidase subunit VIa	
458	36165_at	COX6C	W51774	polypeptide 1	
459	39031_at	COX7A1	AA152406	cytochrome c oxidase subunit VIc	
460	41760_at	COX7A2	AA978033	cytochrome c oxidase subunit VIIa	
461	34330_at	COX7A2L	AB007618	polypeptide 1 (muscle)	
462	34381_at	COX7C	A1708889	cytochrome c oxidase subunit VIIa	
				polypeptide 2 (liver)	
				polypeptide 2 like	
				polypeptide 2 like	COX7RP
				cytochrome c oxidase subunit VIIc	

Fig 21

	A	B	C	D	E
463	38080_at	COX8	AI525665	cytochrome c oxidase subunit VIII	
464	35819_at	CYC1	X06994	cytochrome c-1	cytochrome c-1
465	33389_at	CYP51	U23942	cytochrome P450, 51 (lanosterol 14-alpha-demethylase)	lanosterol 14-demethylase cytochrome P450
466	859_at	CYP1B1	U03688	cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile)	cytochrome P450
467	40071_at	CYP1B1	U03688	cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile)	cytochrome P450
468	37509_at	CRLF3	AF046059	cytokine receptor-like factor 3	cytokine receptor related protein 4
469	37306_at	KIAA0068	D38549	cytoplasmic FMRP interacting protein 1	
470	1706_at	A-RAF-1	U01337	cytoplasmic; Human Ser/Thr protein kinase (A-RAF-1) gene, complete cds.	Ser/Thr protein kinase
471	34338_at	CKAP1	D49738	cytoskeleton-associated protein 1	cytoskeleton associated protein
472	32529_at	CKAP4	X69910	cytoskeleton-associated protein 4	P63 protein
473	40282_s_at	DF	M84526	D component of complement (adipsin)	adipsin/complement factor D
474	40877_s_at	MN7	AF041080	D15F37 (pseudogene)	
475	1243_at	DDB2	U18300	damage-specific DNA binding protein 2 (48kD)	DDBb p48
476	36616_at	DAZAP2	D31767	DAZ associated protein 2	DAZ associated protein 2
477	37663_at	DDX1	X70649	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1	member of DEAD box protein family
478	35306_at	DDX15	AB001636	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 15	ATP-dependent RNA helicase #46
479	40490_at	DDX21	U41387	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 21	Gu protein
480	39744_at	DDX3	AF000982	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3	dead box, X isoform
481	34647_at	DDX5	X52104	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase, 68kD)	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5
482	36153_at	DDX9	L13848	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 9 (RNA helicase A, nuclear DNA helicase II; leukophysin)	RNA helicase A
483	41872_at	DFNA5	AF073308	deafness, autosomal dominant 5	nonsyndromic hearing impairment protein

Fig 21

185/303

A	B	C	D	E
484 1356_at	DAP3	U18321	death associated protein 3	ionizing radiation resistance conferring protein
485 39114_at	DEPP	AB022718	decidual protein induced by progesterone	DEPP
486 37638_at	DOCK1	D50857	dedicator of cyto-kinesis 1	DOCK180 protein
487 38413_at	DAD1	D15057	defender against cell death 1	DAD-1
488 32824_at	CLN2	AF039704	deficient in late-infantile neuronal ceroid lipofuscinosis; Homo sapiens lysosomal pepstatin insensitive protease (CLN2) gene, complete cds.	lysosomal pepstatin insensitive protease
489 33337_at	DEGS	AF002668	degenerative spermatocyte homolog, lipid desaturase (Drosophila)	MLD
490 38992_at	DEK	X64229	DEK oncogene (DNA binding)	putative oncogene
491 37951_at	DLC1	AF035119	deleted in liver cancer 1	deleted in liver cancer-1
492 33791_at	DLEU1	Y15227	deleted in lymphocytic leukemia, 1	deleted in lymphocytic leukemia, 1
493 38744_at	DSS1	N95406	Deleted in split-hand/split-foot 1 region	
494 36629_at	DSIP1	AI635895	delta sleep inducing peptide, immunoreactor	
495 35814_at	GA17	AF064603	dendritic cell protein	GA17 protein
496 38385_at	DSTN	S65738	desmin (actin depolymerizing factor)	actin depolymerizing factor
497 39410_at	DDEF2	AB007860	development and differentiation enhancing factor 2	development- and differentiation-enhancing factor 2
498 39044_s_at	DGKD	D73409	diacylglycerol kinase, delta (130kD)	diacylglycerol kinase delta
499 38003_s_at	DGKZ	U94905	diacylglycerol kinase, zeta (104kD)	diacylglycerol kinase zeta
500 33920_at	DIAPH1	AF051782	diaphanous homolog 1 (Drosophila)	diaphanous 1
501 37692_at	DBI	AI557240	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein)	
502 39041_at	DLAT	Y00978	dihydrolipoamide S-acetyltransferase (E2 complex)	PDC-E2 precursor (AA -54 to 561)
503 40607_at	DPYSL2	U97105	dihydropyrimidinase-like 2	N2A3
504 36149_at	DPYSL3	D78014	dihydropyrimidinase-like 3	dihydropyrimidinase related protein-3
505 39503_s_at	DPYSL4	AB006713	dihydropyrimidinase-like 4	dihydropyrimidinase related protein 4
506 38220_at	DPYD	U20938	dihydropyrimidine dehydrogenase	dihydropyrimidine dehydrogenase
507 40485_at	HSA249128	AA176780	DIPB protein	

Fig 21



	A	B	C	D	E
508	479_at	DAB2	U53446	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	DOC-2
509	36643_at	DDR1	L20817	discoidin domain receptor family, member 1	tyrosine protein kinase
510	40575_at	DLG5	AB011155	discs, large (Drosophila) homolog 5	KIAA0583 protein
511	33753_at	DAAM1	AB014566	dishevelled associated activator of morphogenesis 1	KIAA0666 protein
512	33150_at	SAS10	AI126004	disrupter of silencing 10	
513	40916_at	dJ635G19.1	AL035494	dJ635G19.1 (LAMR1 (Laminin Receptor 1 (67kD) (RPSA, 40S Ribosomal Protein SA, P40)) pseudogene); match: cDNAs: Em:X15005 Em:J03799 Em:X61156 Em:M64923 Em:X06406 Em:AF140348 Em:J02870 Em:L16589 Em:Z22749 Em:D25224 Em:M14199 Em:M27798; match: ESTs: Em:AA642	dJ635G19.2.1 (novel protein (isoform 1))
514	38456_s_at	dJ734P14.1	AL049650	dJ734P14.1 (KRAB box and C2H2 Zinc finger domain protein pseudogene) match: cDNAs: Em:M27878 Em:M29580 Em:U27186 Em:D31763 Em:AB007872 Em:U09366 Em:U09413 Em:X17617 Em:AF011573 Em:AF020591 Em:X78925 match: proteins: Sw:P52736 Sw:Q06730 Sw:P51523 Tr:Q14585 Sw:P15620 Sw:Q02386 Sw:P51786 Sw:Q99676 Tr:O60792 Sw:Q03923 Sw:O75820 Tr:Q61116 Tr:Q64247	dJ734P14.2.1 (snRNP (small nuclear ribonucleoprotein particle) protein B)

Fig 21

187/303

	A	B	C	D	E
515	38455_at	dJ734P14.1	AL049650	dJ734P14.1 (KRAB box and C2H2 Zinc finger domain protein pseudogene) match: cDNAs: Em:M27878 Em:M29580 Em:U27186 Em:D31763 Em:AB007872 Em:U09366 Em:U09413 Em:X17617 Em:AF011573 Em:AF020591 Em:X78925 match: proteins: Sw:P52736 Sw:Q06730 Sw:P51523 Tr:Q14585 Sw:P15620 Sw:Q02386 Sw:P51786 Sw:Q99676 Tr:O60792 Sw:Q03923 Sw:O75820 Tr:Q61116 Tr:Q64247	dJ734P14.2.1 (snRNP (small nuclear ribonucleoprotein particle) protein B)
516	35809_g_at	dJ862K6.4	AL031681	dJ862K6.4 (pseudogene similar to part of NBP (Nucleotide Binding Protein)) match: proteins: Sw:P53384 Sw:P52920 Sw:P21590 Sw:Q57731 Sw:P40558	dJ862K6.2.2 (splicing factor, arginine/serine-rich 6 (SRP55-2)(isoform 2))
517	35808_at	dJ862K6.4	AL031681	dJ862K6.4 (pseudogene similar to part of NBP (Nucleotide Binding Protein)) match: proteins: Sw:P53384 Sw:P52920 Sw:P21590 Sw:Q57731 Sw:P40558	dJ862K6.2.2 (splicing factor, arginine/serine-rich 6 (SRP55-2)(isoform 2))
518	32433_at	dJ90L6.1	Z97353	dJ90L6.1 (RPL15 (60S Ribosomal Protein L15) pseudogene); match: proteins: Sw:O74895 Sw:P51417 Sw:P39030 Sw:O17445 Sw:P54780 Sw:Q23515 Sw:O65050 Wp:CE12148 Sw:P30736 Sw:P41051 Sw:P54060 Sw:O65082 Sw:P52818 Sw:P79324 Sw:O82712 Sw:O13418 Sw:O82528 Sw:P05748; Human DNA sequence from clone RP1-90L6 on chromosome 22q11.21-11.23 Contains an RPL15 (60S Ribosomal Protein L15) pseudogene, ESTs, STSs and GSSs, complete sequence.	

Fig 21

	A	B	C	D	E
519	34183_at	DKFZP434C171	AL080169	DKFZP434C171 protein	hypothetical protein
520	40801_at	DKFZP434C212	AA643063	DKFZP434C212 protein	
521	38400_at	DKFZP434D1335	A1920820	DKFZP434D1335 protein	
522	33392_at	DKFZP434J154	AL080155	DKFZP434J154 protein	hypothetical protein
523	39411_at	DKFZP434J214	AL080156	DKFZP434J214 protein	hypothetical protein
524	40564_at	DKFZP564A043	N42007	DKFZP564A043 protein	
525	37000_at	DKFZP564B167	AL035304	DKFZP564B167 protein	hypothetical protein
526	33433_at	DKFZP564F0522	AL049943	DKFZP564F0522 protein	hypothetical protein
527	41437_at	DKFZP564F1123	AL080118	DKFZP564F1123 protein	hypothetical protein
528	39442_at	DKFZP564G0222	AL080115	DKFZP564G0222 protein	hypothetical protein
529	40437_at	DKFZP564G2022	AL049944	DKFZP564G2022 protein	hypothetical protein
530	36456_at	DKFZP564I052	AL080063	DKFZP564I052 protein	hypothetical protein
531	38033_at	DKFZP564M1416	AL049934	DKFZP564M1416 protein	hypothetical protein
532	36078_at	DKFZP564O0423	AL080120	DKFZP564O0423 protein	hypothetical protein
533	38256_s_at	DKFZP564O092	W21827	DKFZP564O092 protein	
534	39034_at	DKFZP564O123	AL080122	DKFZP564O123 protein	hypothetical protein
535	41662_at	DKFZP566B183	AL050272	DKFZP566B183 protein	hypothetical protein
536	32807_at	DKFZP566C134	AF004292	DKFZP566C134 protein	
537	38687_at	DKFZP566D193	AL050051	DKFZP566D193 protein	hypothetical protein
538	33776_at	DKFZP566K023	AL050062	DKFZP566K023 protein	hypothetical protein
539	41335_at	DC8	AL050084	DKFZP566O1646 protein	hypothetical protein
540	36961_at	DKFZP586A011	AL050286	DKFZP586A011 protein	hypothetical protein
541	38717_at	DKFZP586A0522	AL050159	DKFZP586A0522 protein	hypothetical protein
542	40831_at	DKFZP586B0923	AL050190	DKFZP586B0923 protein	hypothetical protein
543	34821_at	DKFZP586D0623	AL050197	DKFZP586D0623 protein	hypothetical protein
544	39986_at	DKFZP586D0919	AL050100	DKFZP586D0919 protein	hypothetical protein
545	34269_at	DKFZP586F1019	AL050102	DKFZP586F1019 protein	hypothetical protein
546	35736_at	DKFZP586F1918	AL050091	DKFZP586F1918 protein	hypothetical protein
547	40832_s_at	DKFZP586G011	AL050126	DKFZP586G011 protein	hypothetical protein
548	36007_at	DKFZP586L151	AL050137	DKFZP586L151 protein	hypothetical protein
549	34833_at	DKFZP586O0120	AL050157	DKFZP586O0120 protein	hypothetical protein
550	37333_at	DNMT1	X63692	DNA (cytosine-5)-methyltransferase 1	DNA (cytosine-5)-methyltransferase
551	40891_f_at	DXS9879E	X92896	DNA segment on chromosome X (unique) 9879 expressed sequence	ITBA2 protein DNA segment on chromosome X and Y
552	34215_at	DXYS155E	IL03426	DNA segment on chromosome X and Y (unique) 155 expressed sequence	(unique) 155 expressed sequence

Fig 21

	A	B	C	D	E
553	1252_at	D5S346	M73547	DNA segment, single copy probe LNS-CAI/LNS-CAII (deleted in polyposis)	polyposis locus-encoded protein
554	37162_at	D10S170	S72869	DNA segment, single copy, probe pH4 (transforming sequence, thyroid-1,	DNA segment, single copy, probe pH4 (transforming sequence, thyroid-1,
555	39118_at	DNAJA1	L08069	DnaJ (Hsp40) homolog, subfamily A, member 1	DNAJ homologue-2
556	276_at	DNAJA1	L08069	DnaJ (Hsp40) homolog, subfamily A, member 1	DNAJ homologue-2
557	41233_at	DNAJB6	AB014888	DnaJ (Hsp40) homolog, subfamily B, member 6	MRJ
558	35799_at	DNAJB9	AL080081	DnaJ (Hsp40) homolog, subfamily B, member 9	hypothetical protein
559	36166_at	DNAJC8	AF083190	DnaJ (Hsp40) homolog, subfamily C, member 8	SPF31
560	816_g_at	DOK1	U70987	docking protein 1, 62kD (downstream of tyrosine kinase 1)	GAP binding protein p62dok
561	34433_at	DOK1	AF035299	docking protein 1, 62kD (downstream of tyrosine kinase 1)	docking protein 1
562	34879_at	DPM1	AF007875	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit	dolichol monophosphate mannosase synthase
563	38957_at	DCAMKL1	AB002367	doublecortin and CaM kinase-like 1	doublecortin and CaM kinase-like 1
564	32168_s_at	DSCR1	U85267	Down syndrome critical region gene 1	Down syndrome critical region protein 1
565	36088_at	DSCR2	AJ006291	Down syndrome critical region gene 2	leucine rich protein
566	35166_at	DSCR3	D87343	Down syndrome critical region gene 3	DCRA
567	32621_at	DR1	M97388	down-regulator of transcription 1, TBP-binding (negative cofactor 2)	TATA binding protein-associated phosphoprotein
568	37981_at	DBN1	D17530	drebrin 1	drebrin E
569	40920_at	cdc14B	AF023158	dual specific protein; Homo sapiens tyrosine phosphatase (cdc14B) mRNA, complete cds.	tyrosine phosphatase
570	39727_at	DUSP11	AF023917	dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	PIR1
571	38272_at	DUSP14	AF038844	dual specificity phosphatase 14	MKP-1 like protein tyrosine phosphatase
572	41225_at	DUSP3	AL049417	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	

Fig 21

	A	B	C	D	E
573	41193_at	DUSP6	AB013382	dual specificity phosphatase 6	DUSP6
574	36946_at	DYRK1A	D86550	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A	serine/threonine protein kinase
575	1512_at	DYRK1A	D86550	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A	serine/threonine protein kinase
576	760_at	DYRK2	Y09216	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 isoform 1
577	39931_at	DYRK3	Y12735	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	Dyrk3 protein
578	38368_at	DUT	U31930	dUTP pyrophosphatase	deoxyuridine nucleotidohydrolase
579	38475_at	DCTN2	U50733	dynactin 2 (p50)	dynamitin
580	34891_at	PLN	A1540958	dynein, cytoplasmic, light polypeptide	
581	34829_at	DKC1	U59151	dyskeratosis congenita 1, dyskerin	Cbl5p homolog
582	32234_at	DYT1	AF007871	dystonia 1, torsion (autosomal dominant; torsin A)	torsinA
583	36989_at	DAG1	L19711	dystroglycan 1 (dystrophin-associated glycoprotein 1)	dystroglycan
584	40488_at	DMD	M18533	dystrophin (muscular dystrophy, Duchenne and Becker types)	dystrophin
585	40106_at	E1B-AP5	AJ007509	E1B-55kDa-associated protein 5	E1B-55kDa-associated protein
586	33354_at	SMURF2	AA630312	E3 ubiquitin ligase SMURF2	
587	40375_at	EGR3	X63741	early growth response 3	transcription factor
588	36135_at	EBNA1BP2	U86602	EBNA1 binding protein 2	nucleolar protein p40
589	37730_at	p100	U22055	EBNA-2 co-activator (100kD)	100 kDa coactivator
590	33254_at	EVI5	AF008915	ecotropic viral integration site 5	EVI-5 homolog
591	39542_at	ENC1	AF059611	ectodermal-neural cortex (with BTB-like domain)	nuclear matrix protein NRP/B
592	41124_r_at	ENPP2	L35594	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	autotaxin
593	41123_s_at	ENPP2	L35594	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	autotaxin
594	32551_at	EFEMP1	U03877	EGF-containing fibulin-like extracellular matrix protein 1	extracellular protein

Fig 21

	A	B	C	D	E
595	36488_at	EGFL5	AB011542	EGF-like-domain, multiple 5	MEGF9
596	40509_at	ETFA	J04058	electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II)	electron transfer flavoprotein, alpha polypeptide
597	36881_at	ETFB	X71129	electron-transfer-flavoprotein, beta polypeptide	electron transfer flavoprotein beta subunit
598	1288_s_at	EEF1A	J04617	elongation factor EF-1-alpha; Human	eukaryotic translation elongation factor 1 alpha 1
599	31853_at	EED	AF080227	complete cds. embryonic ectoderm development	embryonic ectoderm development protein
600	39861_at	EMS1	M98343	ems1 sequence (mammary tumor and squamous cell carcinoma-associated (p80/85 src substrate) end of last exon based on GENSCAN prediction presumably this gene and dJ477H23.2 are part of the same gene match: ESTs: Em:AA354647	amplixin
601	41478_at	dJ477H23.1	AL033538	endocytic receptor (macrophage mannose receptor family)	dJ477H23.1 (novel protein)
602	37408_at	ENDO180	AB014609	endosome-associated FYVE-domain protein	KIAA0709 protein
603	37914_at	ENDOFIN	AB002303	endosulfine alpha	endosome-associated FYVE-domain protein
604	39010_at	ENSA	AI658639	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2	lysophosphatidic acid receptor homolog
605	40387_at	EDG2	U80811		
606	40874_at	EDF1	AJ005259	endothelial differentiation-related factor 1 enhancer of rudimentary homolog (Drosophila)	endothelial differentiation-related factor 1 human protein homologous to DROER protein
607	39079_at	ERH	D85758	enolase 1, (alpha)	c-myc binding protein
608	2035_s_at	ENO1	M55914	ephrin-B2	
609	34335_at	EFNB2	AI765533	epidermal growth factor receptor pathway substrate 15	epidermal growth factor receptor pathway substrate 15
610	37731_at	EPS15	Z29064	epidermal growth factor receptor pathway substrate 8	epidermal growth factor receptor kinase substrate
611	1467_at	EPS8	U12535	epithelial membrane protein 1	progression associated protein
612	37762_at	EMP1	Y07909	epithelial membrane protein 2	XMP
613	39631_at	EMP2	U52100		

Fig 21

A	B	C	D	E
614 35816_at	cystatin B	U46692	EPM1 disease gene; cysteine protease inhibitor; Human cystatin B gene, complete cds.	cystatin B
615 32585_at	EPB41L2	AF027299	erythrocyte membrane protein band 4.1-like 2	protein 4.1-G
616 38375_at	ESD	AF112219	esterase D/formylglutathione hydrolase	esterase D
617 38283_at	EBAG9	AB007619	estrogen receptor binding site associated, antigen, 9	EBAG9
618 37161_at		W28948	ESTs	
619 40885_s_at		N30151	ESTs	
620 33328_at	C1S	W28612	ESTs	
621 33453_at	ATP6S1	AI400326	ESTs	
622 31801_at		AI808712	ESTs	
623 41598_at		AA890010	ESTs	
624 32744_at	RPS21	AI526078	ESTs, Highly similar to RS21_HUMAN 40S RIBOSOMAL PROTEIN S21 [H.sapiens]	
625 39750_at		W61005	ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]	
626 34906_g_at		AA977136	ESTs, Moderately similar to GLK5_HUMAN GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 5 PRECURSOR [H.sapiens]	
627 35787_at		AI986201	ESTs, Moderately similar to T46365 hypothetical protein DKFZp434A1518.1 [H.sapiens]	
628 41463_at		AL042729	ESTs, Weakly similar to 0903209A peptide PD,basic Pro rich [H.sapiens]	
629 41273_at		AL046940	ESTs, Weakly similar to N-WASP [H.sapiens]	
630 38097_at	PIG8	AF010313	eloposide-induced mRNA	PIG8
631 40888_f_at	EEF1A1	W28170	eukaryotic translation elongation factor 1 alpha 1	

Fig 21

	A	B	C	D	E
632	35175_f_at	EEF1A2	X70940	eukaryotic translation elongation factor 1 alpha 2	elongation factor 1 alpha-2
633	35748_at	EEF1B2	X60489	eukaryotic translation elongation factor 1 beta 2	elongation factor-1-beta
634	41256_at	EEF1D	Z21507	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	human elongation factor-1-delta
635	1676_s_at	EEF1G	M55409	eukaryotic translation elongation factor 1 gamma	pancreatic tumor-related protein
636	36587_at	EEF2	Z11692	eukaryotic translation elongation factor 2	human elongation factor 2
637	663_at	EIF1A	L18960	eukaryotic translation initiation factor 1A	protein synthesis factor
638	34278_at	EIF1A	L18960	eukaryotic translation initiation factor 1A	protein synthesis factor
639	1154_at	EIF2S1	J02645	eukaryotic translation initiation factor 2, subunit 1 (alpha, 35kD)	eukaryotic translation initiation factor 2, subunit 1 (alpha, 35kD)
640	40515_at	EIF2B2	AF035280	eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD)	eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD)
641	1644_at	EIF3S2	U36764	eukaryotic translation initiation factor 3, subunit 2 (beta, 36kD)	TGF-beta receptor interacting protein 1
642	35327_at	EIF3S3	U54559	eukaryotic translation initiation factor 3, subunit 3 (gamma, 40kD)	translation initiation factor eIF3 p40 subunit
643	32576_at	EIF3S5	U94855	eukaryotic translation initiation factor 3, subunit 5 (epsilon, 47kD)	translation initiation factor 3 47 kDa subunit
644	38681_at	EIF3S6	U62962	eukaryotic translation initiation factor 3, subunit 6 (48kD)	murine mammary tumor integration site 6 (oncogene homolog)
645	35298_at	EIF3S7	U54558	eukaryotic translation initiation factor 3, subunit 7 (zeta, 66/67kD)	translation initiation factor eIF3 p66 subunit
646	35323_at	EIF3S9	U78525	eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD)	eukaryotic translation initiation factor
647	41785_at	EIF4G2	U73824	eukaryotic translation initiation factor 4 gamma, 2	p97
648	33907_at	EIF4G3	AF012072	eukaryotic translation initiation factor 4 gamma, 3	eIF4GII

Fig 21



	A	B	C	D	E
649	1420_s_at	EIF4A2	D30655	eukaryotic translation initiation factor 4A, isoform 2	eukaryotic initiation factor 4All
650	37752_at	EIF4E	M15353	eukaryotic translation initiation factor 4E	cap-binding protein
651	35263_at	EIF4EBP2	N73769	eukaryotic translation initiation factor 4E binding protein 2	
652	167_at	EIF5	U49436	eukaryotic translation initiation factor 5	translation initiation factor 5
653	37318_at	ETF1	X81625	eukaryotic translation termination factor 1	C11 protein
654	1885_at	ERCC3	M31899	excision repair cross-complementing rodent repair deficiency, complementation group 3 (xeroderma pigmentosum group B complementing)	excision repair cross-complementing rodent repair deficiency, complementation group 3 (xeroderma pigmentosum group B complementing)
655	2063_at	ERCC5	L20046	excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group G (Cockayne syndrome))	excision repair protein
656	33734_at	HSD11B1	AL022398	exons 1-4 beyond this clone; match: proteins P28845 P50172 P51975 Q29608	dJ434O14.1 (Hydroxysteroid (11-beta) Dehydrogenase 1 (EC 1.1.1.146))
657	222_at	EXT1	S79639	exostoses (multiple) 1	exostoses (multiple) 1
658	36526_at	EXTL2	AF000416	exostoses (multiple)-like 2	EXT-like protein 2
659	38809_s_at	EXTL3	AB011091	exostoses (multiple)-like 3	KIAA0519 protein
660	37729_at	XPO1	Y08614	exportin 1 (CRM1 homolog, yeast)	exportin 1
661	38753_at	XPOT	AF039022	exportin, tRNA (nuclear export receptor for tRNAs)	exportin t
662	39673_i_at	ECM2	AB011792	extracellular matrix protein 2, female organ and adipocyte specific	extracellular matrix protein
663	39674_r_at	ECM2	AB011792	extracellular matrix protein 2, female organ and adipocyte specific	extracellular matrix protein
664	35226_at	EYA2	U71207	eyes absent homolog 2 (Drosophila)	Eab1
665	38318_at	FAM8A1	AL050128	family with sequence similarity 8, member A1	
666	31879_at	FUBP3	U69127	far upstream element (FUSE) binding protein 3	FUSE binding protein 3

Fig 21

	A	B	C	D	E
667	37325_at	FDPS	D14697	farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase)	farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase)
668	34848_at	FDFT1	X69141	farnesyl-diphosphate farnesyltransferase 1	farnesyl-diphosphate farnesyltransferase
669	1499_at	FNTA	L10413	farnesyltransferase, CAAX box, alpha	farnesyl-protein transferase alpha-subunit
670	38755_at	FADD	X84709	Fas (TNFRSF6)-associated via death domain	mediator of receptor induced toxicity
671	37743_at	FEZ1	U60060	fasciculation and elongation protein zeta 1 (zygin I)	FEZ1
672	38651_at	FEZ2	U60061	fasciculation and elongation protein zeta 2 (zygin II)	FEZ2
673	40454_at	FAT	X87241	FAT tumor suppressor homolog 1 (Drosophila)	homologue of Drosophila Fat protein
674	40082_at	FACL2	D10040	fatty-acid-Coenzyme A ligase, long-chain 2	long-chain acyl-CoA synthetase
675	33880_at	FACL3	D89053	fatty-acid-Coenzyme A ligase, long-chain 3	Acyl-CoA synthetase 3
676	33881_at	FACL3	AA977580	fatty-acid-Coenzyme A ligase, long-chain 3	
677	33360_at	FBXL11	AB023221	F-box and leucine-rich repeat protein 11	KIAA1004 protein
678	37205_at	FBXL7	AB020647	F-box and leucine-rich repeat protein 7	KIAA0840 protein
679	32854_at	FBXW1B	AB014596	F-box and WD-40 domain protein 1B	KIAA0696 protein
680	32169_at	FBXO21	AB020682	F-box only protein 21	KIAA0875 protein
681	35337_at	FBXO7	AL050254	F-box only protein 7	hypothetical protein
682	33817_at	D10S102	S63912	FBRNP; heterogeneous ribonucleoprotein homolog; This sequence comes from Fig. 3; D10S102=FBRNP [human, fetal brain, mRNA, 3043 nt].	
683	1877_g_at	nilH	HG1103-HT1103	Fe protein	FBRNP
684	34678_at	FER1L3	AL096713	fer-1-like 3, myoferlin (C. elegans)	dinitrogenase reductase
685	32148_at	FARP1	A1701049	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	hypothetical protein

Fig 21

	A	B	C	D	E
686	33943_at	FTH1	L20941	ferritin, heavy polypeptide 1	ferritin heavy chain
687	41091_at	FALZ	U05237	fetal Alzheimer antigen	fetal Alzheimer antigen
688	32535_at	FBN1	X63556	fibrillin 1 (Marfan syndrome)	fibrillin
689	39945_at	FAP	U09278	fibroblast activation protein, alpha	fibroblast activation protein
690	1380_at	FGF7	M60828	fibroblast growth factor 7 (keratinocyte growth factor)	keratinocyte growth factor
691	2057_g_at	FGFR1	M34641	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)	fibroblast growth factor receptor 1, isoform 1 precursor; fibroblast growth factor receptor 1, isoform 2 precursor; fibroblast growth factor receptor 1, isoform 3 precursor; fibroblast growth factor receptor 1, isoform 4 precursor; fibroblast growth factor receptor 1, isoform 5 precursor; fibroblast growth factor receptor 1, isoform 6 precursor; fibroblast growth factor receptor 1, isoform 7 precursor; fibroblast growth factor receptor 1, isoform 8 precursor; fibroblast growth factor receptor 1, isoform 9 precursor
692	31720_s_at	FN1	M10905		fibronectin 1, isoform 1 preproprotein; fibronectin 1, isoform 2 preproprotein
693	31719_at	FN1	X02761		fibronectin precursor
694	34853_at	FLRT2	AB007865		fibronectin leucine rich transmembrane protein 2
695	38026_at	FBLN1	U01244	fibulin 1	fibulin-1D
696	39038_at	FBLN5	AF093118	fibulin 5	UF50
697	38078_at	FLNB	AF042166	filamin B, beta (actin binding protein 278)	beta-filamin
698	38761_s_at	FKBP9	AA487755	FK506 binding protein 9 (63 kD)	
699	40665_at	FMO3	M83772	flavin containing monooxygenase 3	flavoprotein
700	35254_at	FLN29	AB007447	FLN29 gene product	FLN29
701	38356_at	FST	M19481	follicle stimulating precursor; Human follistatin gene, exon 6.	follicle stimulating precursor; FST317 precursor; follistatin isoform FST344 precursor

Fig 21

	A	B	C	D	E
				forkhead (Drosophila)-like 7; FREAC3; Homo sapiens forkhead/winged helix-like transcription factor 7 (FKHL7) gene, complete cds.	forkhead/winged helix-like transcription factor 7
702	41027_at	FKHL7	AF078096		
703	36319_at	FOXF2	U13220	forkhead box F2	forkhead protein FREAC-2
704	40570_at	FOXO1A	AF032885	forkhead box O1A (rhabdomyosarcoma)	forkhead protein
705	34740_at	FOXO3A	AF032886	forkhead box O3A	forkhead protein
706	32542_at	FHL1	AF063002	four and a half LIM domains 1	LIM protein SLIMMER
707	38422_s_at	FHL2	U29332	four and a half LIM domains 2	heart protein
708	41649_at	FHX	AF038177	FOXJ2 forkhead factor	
709	34997_r_at	FZD5	U43318	frizzled homolog 5 (Drosophila)	transmembrane receptor
710	34472_at	FZD6	AB012911	frizzled homolog 6 (Drosophila)	Frizzled-6
711	33222_at	FZD7	AB017365	frizzled homolog 7 (Drosophila)	frizzled-7
712	38923_at	FRG1	L76159	FSDH region gene 1	FSDH region gene 1
713	38139_at	FPGT	AF017445	fructose-1-phosphate guanylyltransferase	GDP-L-fucose pyrophosphorylase
714	41814_at	FUCA1	M29877	fructosidase, alpha-L-1, tissue	fructosidase, alpha-L-1, tissue
715	40022_at	FCMD	AB008226	Fukuyama type congenital muscular dystrophy (fukutin)	fukutin
716	32546_at	FH	U59309	fumarate hydratase	fumarase precursor
717	36145_at	SIAHBP1	U51586	fuse-binding protein-interacting repressor	siah binding protein 1
718	40480_s_at	FYN	M14333	FYN oncogene related to SRC, FGR, YES	FYN oncogene related to SRC, FGR, YES
719	2039_s_at	FYN	M14333	FYN oncogene related to SRC, FGR, YES	FYN oncogene related to SRC, FGR, YES
720	34288_at	RDC1	U67784	G protein-coupled receptor	orphan G protein-coupled receptor
721	37308_at	GPR107	AI888084	G protein-coupled receptor 107	
722	37298_at	GABARAP	AF044671	GABA(A) receptor-associated protein	MM46
723	35785_at	GABARAPL1	W28281	GABA(A) receptor-associated protein like 1	
724	35767_at	GABARAPL2	AI565760	GABA(A) receptor-associated protein-like 2	
725	37825_at	GALK2	M84443	galactokinase 2	galactokinase
726	37742_at	GLB1	M34423	galactosidase, beta 1	galactosidase, beta 1

Fig 21

	A	B	C	D	E
727	37263_at	GGH	U55206	gamma-glutamyl hydrolase (conjugase, polygamma-glutamyl hydrolase)	human gamma-glutamyl hydrolase
728	32531_at	GJA1	X52947	gap junction protein, alpha 1, 43kD (connexin 43)	connexin 43
729	36603_at	GCN1L1	D86973	GCN1 general control of amino-acid synthesis 1-like 1 (yeast)	
730	35307_at	GDI2	Y13286	GDP dissociation inhibitor 2	GDP dissociation inhibitor beta
731	39386_at	KIAA0110	D14811	gene predicted from cDNA with a complete coding sequence	gene predicted from cDNA with a complete coding sequence
732	32180_s_at	RES4-22	AB000461	gene with multiple splice variants near HD locus on 4p16.3	gene with multiple splice variants near HD locus on 4p16.3
733	466_at	GTF2I	U77948	general transcription factor II, i	Bruton's tyrosine kinase-associated protein-135
734	35450_s_at	GTF2I	AF015553	general transcription factor II, i	TFII-I protein
735	37010_at	GTF2A2	AI203737	general transcription factor IIA, 2 (12kD subunit)	
736	869_at	GTF2A2	U14193	general transcription factor IIA, 2 (12kD subunit)	transcription factor IIA small 12 kDa subunit
737	37882_at	GTF2E1	X63468	general transcription factor IIE, polypeptide 1 (alpha subunit, 56kD)	TFII-E-alpha
738	37295_at	GTF2E2	X63469	general transcription factor IIE, polypeptide 2 (beta subunit, 34kD)	TFII-E-beta
739	38782_at	GTF2H1	M95809	general transcription factor IIH, polypeptide 1 (62kD subunit)	basic transcription factor 62kD subunit
740	40754_at	GTF2H3	Z30093	general transcription factor IIH, polypeptide 3 (34kD subunit)	basic transcription factor 2, 35 kD subunit
741	36188_at	GTF3A	D32257	general transcription factor IIIA	Xenopus transcription factor IIIA homologue
742	35296_at	GGPS1	AB019036	geranylgeranyl diphosphate synthase 1	geranylgeranyl pyrophosphate synthase
743	763_at	GMFB	AB001106	glia maturation factor, beta	glia maturation factor
744	39793_at	GBAS	AF029786	glioblastoma amplified sequence	GBAS
				glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV)	
745	32643_at	GBE1	L07956		1,4-alpha-glucan branching enzyme
746	34332_at	GNPI	D31766	glucosamine-6-phosphate isomerase	glucosamine-6-phosphate isomerase

Fig 21

	A	B	C	D	E
747	38218_at	GCNT1	M97347	glucosaminyl (N-acetyl) transferase 1, core 2 (beta-1,6-N-acetylglucosaminyltransferase)	beta-1,6-N-acetylglucosaminyltransferase
748	39122_at	GPI	K03515	glucose phosphate isomerase	neuroleukin
749	38986_at	GRP58	Z49835	glucose regulated protein, 58kD	protein disulfide isomerase
750	38042_at	G6PD	X03674	glucose-6-phosphate dehydrogenase	glucose-6-phosphate dehydrogenase
751	33308_at	GUSB	M15182	glucuronidase, beta	glucuronidase, beta
752	37341_at	GLUD1	M20867	glutamate dehydrogenase 1	glutamate dehydrogenase 1
753	35485_at	GRM4	X80818	glutamate receptor, metabotropic 4	metabotropic glutamate receptor type 4
754	40522_at	GLUL	X59834	glutamate-ammonia ligase (glutamine synthase)	glutamate--ammonia ligase
755	31850_at	GCLC	M90656	glutamate-cysteine ligase, catalytic subunit	gamma-glutamylcysteine synthetase
756	33163_r_at	GCLM	L35546	glutamate-cysteine ligase, modifier subunit	gamma-glutamylcysteine synthetase light subunit
757	35343_at	GOT1	M37400	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)	aspartate aminotransferase 1
758	40764_at	GOT2	M22632	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)	aspartate aminotransferase 2 precursor
759	34719_at	GLS	AB020645	glutaminase	KIAA0838 protein
760	32626_at	GFPT1	M90516	glutamine-fructose-6-phosphate transaminase 1	glutamine:fructose-6-phosphate amidotransferase
761	39640_at	GFPT2	AB016789	glutamine-fructose-6-phosphate transaminase 2	Glutamine:fructose-6-phosphate amidotransferase
762	35300_at	EPRS	X54326	glutamyl-prolyl-tRNA synthetase	glutamyl-tRNA synthetase
763	34311_at	GLRX	X76648	glutaredoxin (thioltransferase)	glutaredoxin
764	37033_s_at	GPX1	X13710	glutathione peroxidase 1	
765	40508_at	GSTA4	AF025887	glutathione S-transferase A4	glutathione S-transferase A4-4
766	38386_r_at	GSS	U34683	glutathione synthetase	glutathione synthetase
767	824_at	GSTTLp28	U90313	glutathione-S-transferase like; glutathione transferase omega	glutathione-S-transferase homolog
768	AFFX-HUMGAP	GAPD	M33197	glyceraldehyde-3-phosphate dehydrogenase	glyceraldehyde-3-phosphate dehydrogenase
769	35905_s_at	GAPD	U34995	glyceraldehyde-3-phosphate dehydrogenase	

Fig 21

	A	B	C	D	E
770	AFEX-HUMGAP1	GAPD	M33197	glyceraldehyde-3-phosphate dehydrogenase	glyceraldehyde-3-phosphate dehydrogenase
771	39392_at	GNPAT	AJ002190	glyceronephosphate O-acyltransferase	dihydroxyacetone phosphate acyltransferase
772	37357_at	GCSH	D00723	glycine cleavage system protein H (aminomethyl carrier)	glycine cleavage system protein H (aminomethyl carrier)
773	39665_at	GLRB	U33267	glycine receptor, beta	glycine receptor beta subunit
774	40645_at	GSK3B	L33801	glycogen synthase kinase 3 beta	protein kinase
775	40876_at	GYG	U31525	glycogenin	glycogenin
776	35334_at	GYG2	U94362	glycogenin 2	glycogenin-2 alpha
777	38379_at	GPNMB	X76534	glycoprotein (transmembrane) nmb	glycoprotein (transmembrane) nmb
778	37251_s_at	GPM6B	AF016004	glycoprotein M6B	
779	33126_at	AD-017	L13435	glycosyltransferase AD-017	
780	36582_g_at	GARS	U09510	glycyl-tRNA synthetase	glycyl-tRNA synthetase
781	36581_at	GARS	U09510	glycyl-tRNA synthetase	glycyl-tRNA synthetase
782	36201_at	GLO1	D13315	glyoxalase I	lactoyl glutathione lyase
783	40133_s_at	GRHPR	W28944	glyoxylate reductase/hydroxypyruvate reductase	
784	37449_i_at	GNAS	X04409		guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1, isoform alpha-s-2; neuroendocrine secretory protein 55; guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1, isoform XL-alpha-s; guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1, isoform alpha-s-1
785	37448_s_at	GNAS	X56009	GNAS complex locus GNAS complex locus	alpha subunit of GsGTP binding protein

Fig 21

	A	B	C	D	E
786	37450_r_at	GNAS	X04409	GNAS complex locus	guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1, isoform alpha-s-2; neuroendocrine secretory protein 55; guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1, isoform XL-alpha-s; guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1, isoform
787	37959_at	GGA3	D63876	golgi associated, gamma adaptin ear containing, ARF binding protein 3	ADP-ribosylation factor binding protein 3, isoform short; ADP-ribosylation factor binding protein 3, isoform long
788	32713_at	GOLGA1	U51587	golgi autoantigen, golgin subfamily a, 1	Golgi complex autoantigen golgin-97
789	32150_at	GOLGA4	X82834	golgi autoantigen, golgin subfamily a, 4	256 kD golgin
790	36827_at	GOLPH1	AF020762	golgi phosphoprotein 1	unknown protein
791	38620_at	GOSR2	AA905543	golgi SNAP receptor complex member 2	
792	34737_at	GOLTC1	AF058718	golgi transport complex 1 (90 kD subunit)	putative 13 S Golgi transport complex 90kD subunit brain-specific isoform
793	41767_r_at	KIAA0855	AB020662	golgin-67	KIAA0855 protein
794	36950_at	HSGP25L2G	X90872	gp25L2 protein	
795	36035_at	GPAA1	AB002135	GPAA1P anchor attachment protein 1 homolog (yeast)	glycosylphosphatidylinositol anchor attachment 1 (GPAA1)
796	32595_at	GRSF1	U07231	G-rich RNA sequence binding factor 1	G-rich sequence factor-1
797	39822_s_at	GADD45B	AF078077	growth arrest and DNA-damage-inducible, beta	growth arrest and DNA-damage-inducible protein GADD45beta
798	39821_s_at	GADD45B	N95168	growth arrest and DNA-damage-inducible, beta	
799	661_at	GAS1	L13698	growth arrest-specific 1	growth arrest-specific 1
800	41839_at	GAS1	L13698	growth arrest-specific 1	growth arrest-specific 1
801	37658_at	GAS6	L13720	growth arrest-specific 6	growth-arrest-specific protein
802	1598_g_at	GAS6	L13720	growth arrest-specific 6	growth-arrest-specific protein
803	37615_at	GRB10	D86962	growth factor receptor-bound protein 10	growth factor receptor-bound protein 10
804	41752_at	GHITM	W28190	growth hormone inducible transmembrane protein	

Fig 21



	A	B	C	D	E
805	160030_at	GHR	X06562	growth hormone receptor	growth hormone receptor
806	40113_at	GS3955	D87119	GS3955 protein	GS3955
807	37279_at	GEM	U10550	GTP binding protein overexpressed in skeletal muscle	Gem
808	33809_at	GNAI1	AL049933	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1	hypothetical protein
809	37307_at	GNAI2	X04828	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2
810	34608_at	GNB2L1	M24194	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	MHC B complex protein 12.3
811	35272_at	NGG5	AI541042	guanine nucleotide binding protein (G protein), gamma 5	
812	37735_at	NGG10	U31383	guanine nucleotide binding protein 10	G protein gamma-10 subunit
813	35735_at	GBP1	M55542	guanylate binding protein 1, interferon-inducible, 67kD	guanylate binding protein isoform I
814	905_at	GUK1	L76200	guanylate kinase 1	guanylate kinase
815	32249_at	HFL1	M65292	H factor (complement)-like 1	factor H homologue
816	32250_at	HF1	X07523	H factor 1 (complement)	complement factor H
817	420_at	ACTH-R	X65633	H.sapiens ACTH-R gene for adrenocorticotrophic hormone receptor.	candidate adrenocorticotrophic hormone receptor
818	31673_s_at	cell adhesion regul	X65784	H.sapiens CAR gene.	cell matrix adhesion regulator
819	37003_at	CD63; MLA1; ME4	X62654	H.sapiens gene for Me491/CD63 antigen.	ME491 /CD63 antigen
820	38076_at	P1 gene for c subu	X69907	H.sapiens gene for mitochondrial ATP synthase c subunit (P1 form).	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1
821	35125_at	hrp S6	X67309	H.sapiens gene for ribosomal protein S6.	ribosomal protein S6
822	34646_at	rpS7	Z25749	H.sapiens gene for ribosomal protein S7.	ribosomal protein S7
823	31510_s_at	hH3.3B	Z48950	H.sapiens hH3.3B gene for histone H3.3.	histone H3.3

Fig 21

203/303

	A	B	C	D	E
824	33820_g_at	ldhB	X13794	H.sapiens lactate dehydrogenase B gene exon 1 and 2 (EC 1.1.1.27) (and joined CDS).	lactate dehydrogenase B
825	33819_at	ldhB	X13794	H.sapiens lactate dehydrogenase B gene exon 1 and 2 (EC 1.1.1.27) (and joined CDS).	lactate dehydrogenase B
826	34787_at	ORF1	X93209	H.sapiens mRNA for NRD1 convertase.	NRD1 convertase
827	36012_at	PIBF1	Y09631	H.sapiens mRNA for PIBF1 protein, complete.	PIBF1 protein
828	31526_f_at	tre	X63547	H.sapiens mRNA for tre oncogene (clone 213).	oncogene
829	40471_at	PxF	Y09048	H.sapiens PxF gene.	PxF protein
830	37038_at	PXMP1	X83467	H.sapiens PXMP1 gene, exon 1 (and joined CDS).	70kD peroxisomal integral membrane protein
831	31583_at	rpS8	X67247	H.sapiens rpS8 gene for ribosomal protein S8.	ribosomal protein S8
832	1685_at	SPHAR	X82554	H.sapiens SPHAR gene for cyclin-related protein.	S-phase response (cyclin-related)
833	38127_at	syndecan-1	Z48199	H.sapiens syndecan-1 gene (exons 2-5).	syndecan 1
834	37310_at	uPA	X02419	H.sapiens uPA gene.	urokinase-plasminogen activator
835	34308_at	H2AFL	U90551	H2A histone family, member L	histone 2A-like protein
836	39337_at	H2AFZ	M37583	H2A histone family, member Z	H2A histone family, member Z
837	33458_r_at	H2BFL	A168098	H2B histone family, member L	
838	40818_at	LOC51580	D14041	H-2K binding factor-2	H-2K binding factor-2
839	254_at	H3F3A	M11353	H3 histone family, member 3A	H3 histone, family 3A
840	39969_at	H4FG	AA255502	H4 histone family, member G	
841	32591_at	HCDI	A1494623	HCDI protein	
842	35215_at	HDCMA18P	ALO49996	HDCMA18P protein	hypothetical protein
843	39353_at	HSPE1	A1912041	heat shock 10kD protein 1 (chaperonin 10)	
844	37720_at	HSPD1	M22382	heat shock 60kD protein 1 (chaperonin)	mitochondrial matrix protein
845	36614_at	HSPA5	X87949	heat shock 70kD protein 5 (glucose-regulated protein, 78kD)	heat shock 70kD protein 5 (glucose-regulated protein, 78kD)
846	41510_s_at	HSPA9B	L15189	heat shock 70kD protein 9B (mortalin-2)	MTHSP75

Fig 21

	A	B	C	D	E
847	32316_s_at	HSPCA	X15183	heat shock 90kD protein 1, alpha	heat shock 90kD protein 1, alpha
848	33984_at	HSPCB	M16660	heat shock 90kD protein 1, beta	heat shock 90kD protein 1, beta
849	31906_at	HSBP1	AF088754	heat shock factor binding protein 1	heat shock factor binding protein 1 HSBP1
850	1468_at	TRAP1	U12595	heat shock protein 75	tumor necrosis factor type 1 receptor associated protein
851	38054_at	HBXIP	AF029890	hepatitis B virus x interacting protein	hepatitis B virus X interacting protein
852	38779_r_at	HDGF	D16431	hepatoma-derived growth factor (high-mobility group protein 1-like)	hepatoma-derived GF
853	35644_at	HEPH	AB014598	hephaestin	KIAA0698 protein
854	38094_at	HNRPA0	M65028	heterogeneous nuclear ribonucleoprotein A/B	hnRNP type A/B protein
855	37334_at	HNRPA0	U23803	heterogeneous nuclear ribonucleoprotein A0	heterogeneous ribonucleoprotein A0
856	34987_s_at	HNRPA1	X79536	heterogeneous nuclear ribonucleoprotein A1	hnRNP core protein A1
857	36654_s_at	HNRPA2B1	M29065	heterogeneous nuclear ribonucleoprotein A2/B1	heterogeneous nuclear ribonucleoprotein A2/B1, isoform A2; heterogeneous nuclear ribonucleoprotein A2/B1, isoform B1
858	33666_at	HNRPC	M16342	heterogeneous nuclear ribonucleoprotein C (C1/C2)	heterogeneous nuclear ribonucleoprotein C, isoform b; heterogeneous nuclear ribonucleoprotein C, isoform a
859	38016_at	HNRPD	M94630	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kD)	DNA-binding protein
860	33845_at	HNRPH1	W28483	heterogeneous nuclear ribonucleoprotein H1 (H)	
861	41132_r_at	HNRPH2	U01923	heterogeneous nuclear ribonucleoprotein H2 (H')	heterogeneous nuclear ribonucleoprotein H2
862	41283_at	HNRPH3	AF052131	heterogeneous nuclear ribonucleoprotein H3 (2H9)	heterogeneous nuclear ribonucleoprotein H3, isoform a; heterogeneous nuclear ribonucleoprotein H3, isoform b
863	40836_s_at	HNRPH3	W26677	heterogeneous nuclear ribonucleoprotein H3 (2H9)	

Fig 21

	A	B	C	D	E
864	39415_at	HNRPK	X72727	heterogeneous nuclear ribonucleoprotein K	transformation upregulated nuclear protein
865	35201_at	HNRPL	X16135	heterogeneous nuclear ribonucleoprotein L	heterogeneous nuclear ribonucleoprotein L
866	37717_at	HNRPM	L03532	heterogeneous nuclear ribonucleoprotein M	M4 protein
867	39792_at	HNRPR	AF000364	heterogeneous nuclear ribonucleoprotein R	heterogeneous nuclear ribonucleoprotein R
868	38654_at	HNRPU	X65488	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	hnRNP U protein
869	32818_at	HXB	X78565	hexabrachion (tenascin C, cytolaclin)	human tenascin-C
870	39827_at	RTP801	AA522530	HIF-1 responsive RTP801	
871	31504_at	HDLBP	M64098	high density lipoprotein binding protein (vigilin)	high density lipoprotein binding protein
872	32220_at	HMG1	D63874	high-mobility group (nonhistone chromosomal) protein 1	HMG-1
873	306_s_at	HMG14	J02621	high-mobility group (nonhistone chromosomal) protein 14	high-mobility group (nonhistone chromosomal) protein 14
874	35738_at	HMG17L3	A1347088	high-mobility group (nonhistone chromosomal) protein 17-like 3	
875	38065_at	HMG2	X62534	high-mobility group (nonhistone chromosomal) protein 2	high-mobility group (nonhistone chromosomal) protein 2
876	38843_at	HMG2L1	AL079310	high-mobility group (nonhistone chromosomal) protein 2-like 1	hypothetical protein
877	35693_at	HPCAL1	AF070616	hippocalcin-like 1	BDP-1 protein
878	1009_at	HINT1	U51004	histidine triad nucleotide binding protein 1	protein kinase C inhibitor
879	34231_at	HBOA	AF074606	histone acetyltransferase	histone acetyltransferase
880	41855_at	HAT1	AF030424	histone acetyltransferase 1	histone acetyltransferase 1
881	38771_at	HDAC1	D50405	histone deacetylase 1	RPD3 protein
882	34368_at	HDAC2	U31814	histone deacetylase 2	transcriptional regulator homolog RPD3
883	38271_at	HDAC4	AB006626	histone deacetylase 4	KIAA0288 protein
884	39046_at	H2AV	AL049324	histone H2A.F/Z variant	
885	39092_at	H2AV	AW007731	histone H2A.F/Z variant	
886	38824_at	HTATIP2	AF039103	HIV-1 Tat interactive protein 2, 30 kD	Tat-interacting protein TIP30
887	40220_at	HIS1	AB021179	HMBA-inducible	HEXIM1 protein

Fig 21

	A	B	C	D	E
888	39809_at	HBP1	AF019214	HMG-box containing protein 1	HMG box containing protein 1
				HMG-domain containing protein which is the 57 kd subunit within SWI/SNF-related BAF complexes; contains a proline-rich N-terminus, a kinesin-like coiled-coil region, and a highly acidic c-terminus; Homo sapiens BAF57 (BAF57) gene, complete cds.	BAF57
889	33828_at	BAF57	AF035262	HMT1 hnRNP methyltransferase-like 1 (S. cerevisiae)	arginine methyltransferase
890	39348_at	HRMT1L1	X99209	HMT1 hnRNP methyltransferase-like 2 (S. cerevisiae)	arginine methyltransferase
891	32825_at	HRMT1L2	Y10805	HNRNP Core Protein A1 LIKE pseudogene; match: proteins P04256 Q28521 P49312 P09651 P51991 P51992 P51968 P17130 P22626	
892	31463_s_at	dJ256G22.1	AL022097	holocytochrome c synthase (cytochrome c heme-lyase)	holocytochrome c-type synthetase
893	38943_at	HCCS	U36787	homeo box B2	homeo box B2
894	39610_at	HOXB2	X16665	homeo box C6	homeo box C6
895	40674_s_at	HOXC6	S82986		
896	38233_at	HOMER-3	AF093265	Homer, neuronal immediate early gene, 3	homer-3
				Homo sapiens (clone f17252) ubiquinol cytochrome c reductase Rieske iron-sulphur protein (UQCRCF1) gene, exon 2.	Rieske Fe-S protein
897	34401_at	UQCRCF1	L32977	Homo sapiens (clone FFE-7) type II inosine monophosphate dehydrogenase (IMPDH2) gene, exons 1-13, complete cds.	inosine monophosphate dehydrogenase type II
898	36624_at	IMPDH2	L33842		
				Homo sapiens aldehyde oxidase (AOX1) gene, exon 35 and complete cds.	aldehyde oxidase
899	37599_at	AOX1	AF017060	Homo sapiens alpha NAC mRNA, complete cds.	alpha NAC
900	39740_g_at	NACA	AF054187		

Fig 21

	A	B	C	D	E
901	39739_at	NACA	AF054187	Homo sapiens alpha NAC mRNA, complete cds.	alpha NAC
902	41154_r_at	CTNNA1	AF102803	Homo sapiens alphaE-catenin (CTNNA1) gene, exon 18 and complete cds.	alphaE-catenin
903	41153_f_at	CTNNA1	AF102803	Homo sapiens alphaE-catenin (CTNNA1) gene, exon 18 and complete cds.	alphaE-catenin
904	39324_at		AL050078	Homo sapiens cDNA FLJ10784 f1s, clone NT2RP4000448, highly similar to Homo sapiens mRNA; cDNA DKFZp566G0746	
905	35310_at		D45288	Homo sapiens cDNA FLJ13267 f1s, clone OVARC1000964	
906	35754_at		L40391	Homo sapiens cDNA FLJ13553 f1s, clone PLACE1007454	
907	33325_at		W26667	Homo sapiens cDNA FLJ14821 f1s, clone OVARC1000556, highly similar to RIBOSOMAL PROTEIN S6 KINASE II ALPHA 2 (EC 2.7.1.-)	
908	38102_at		W28575	Homo sapiens cDNA FLJ25016 f1s, clone CBL01574	
909	41253_s_at		AI983043	Homo sapiens cDNA FLJ30436 f1s, clone BRACE2009037	
910	39162_at		AA156987	Homo sapiens cDNA FLJ30544 f1s, clone BRAWH2001412	
911	41807_at		AL040137	Homo sapiens cDNA FLJ31959 f1s, clone NT2RP7007422	
912	38643_at		W87466	Homo sapiens cDNA FLJ33151 f1s, clone UTERU2000263	
913	34246_at		AA418437	Homo sapiens cDNA: FLJ21175 f1s, clone CAS11071	
914	40813_at		AI768188	Homo sapiens cDNA: FLJ21243 f1s, clone COL01164	

Fig 21

	A	B	C	D	E
				Homo sapiens cDNA: FLJ21449 f1s, clone COL04483, highly similar to AF010235	
915	40923_at		AA290994	Homo sapiens mRNA from chromosome 5q31-33 region	
916	38993_r_at		W27522	Homo sapiens cDNA: FLJ21904 f1s, clone HEP03585	
				Homo sapiens cDNA: FLJ21927 f1s, clone HEP04178, highly similar to HSU90909	
917	38093_at		U90909	Human clone 23722 mRNA sequence	
918	34840_at		AI700633	Homo sapiens cDNA: FLJ22642 f1s, clone HSI06970	
				Homo sapiens cDNA: FLJ23324 f1s, clone HEP12482, highly similar to HUMMYOHC B Human nonmuscle myosin heavy chain-B (MYH10) mRNA	smooth muscle myosin heavy chain isoform SMemb
919	32838_at	smooth muscle m	S67247	Homo sapiens cervical cancer suppressor-1 mRNA, complete cds	
920	33737_f_at		AI871359	Homo sapiens clone 23570 mRNA sequence	
921	41663_at		AF038202	Homo sapiens clone 23700 mRNA sequence	
922	36815_at		AF038185	Homo sapiens clone 23718 mRNA sequence	
923	41841_at		AF052138	Homo sapiens clone 23903 mRNA sequence	
924	37794_at		AF035281	Homo sapiens clone 23938 mRNA sequence	
925	38764_at		AF007142	Homo sapiens clone 24416 mRNA sequence	
926	35342_at		AF052159	Homo sapiens clone 24630 mRNA sequence	
927	31867_at		AF052174	Homo sapiens clone 24674 mRNA sequence	
928	36758_at		AF070578	Homo sapiens clone 24790 mRNA sequence	
929	41864_at		AF052181		

Fig 21

	A	B	C	D	E
930	38070_at		AL080234	Homo sapiens clone FBD3 Cri-du-chat critical region mRNA	
931	34773_at	TBCA	AF038952	Homo sapiens cofactor A protein mRNA, complete cds.	cofactor A protein
932	39027_at	COX4	AF017115	Homo sapiens cytochrome c oxidase subunit IV precursor (COX4) gene, nuclear gene encoding mitochondrial protein, complete cds.	cytochrome c oxidase subunit IV precursor
933	40878_f_at	D15F37	AF041081	Homo sapiens D15F37 pseudogene, S4 allele, mRNA sequence.	
934	631_g_at	DCTD	L39874	Homo sapiens deoxycytidylate deaminase gene, complete cds.	deoxycytidylate deaminase
935	630_at	DCTD	L39874	Homo sapiens deoxycytidylate deaminase gene, complete cds.	deoxycytidylate deaminase
936	33936_at	GALC	D86181	Homo sapiens DNA for galactocerebrosidase, exon 17 and complete cds.	galactocerebrosidase
937	40134_at	ATP5J2; ATP5JL	AF047436	Homo sapiens F1Fo-ATPase synthase f subunit mRNA, complete cds.	F1Fo-ATPase synthase f subunit
938	36103_at	SCYA3; LD78ALP	D90144	Homo sapiens gene for LD78 alpha precursor, complete cds.	LD78 alpha precursor
939	40725_at	GOSR1; P28; GS	AF047438	Homo sapiens GOS28/P28 protein mRNA, complete cds.	GOS28/P28 protein
940	38708_at	RAN; TC4; ARA24	AF054183	Homo sapiens GTP binding protein mRNA, complete cds.	GTP binding protein
941	35790_at	VPS26; HB58; HB	AF054179	Homo sapiens H beta 58 homolog mRNA, complete cds.	H beta 58 homolog
942	36576_at	H2AFY; H2A.y; H2	AF054174	Homo sapiens histone macroH2A1.2 mRNA, complete cds.	histone macroH2A1.2
943	35303_at	INSIG1	U96876	Homo sapiens insulin induced protein 1 (INSIG1) gene, complete cds.	insulin induced protein 1
944	1038_s_at	interferon-gamma	U19247	Homo sapiens interferon-gamma receptor alpha chain gene, exon 7 and complete cds.	interferon-gamma receptor alpha chain

Fig 21



	A	B	C	D	E
945	895_at	MIF	L19686	Homo sapiens macrophage migration inhibitory factor (MIF) gene, complete cds.	macrophage migration inhibitory factor
946	38967_at	C14orf2; MP68; P1AF054175		Homo sapiens mitochondrial proteolipid 68MP homolog cds.	mitochondrial proteolipid 68MP homolog
947	31881_at		Y14155	Homo sapiens mRNA for Hmob33 protein, 3' untranslated region	
948	34677_f_at	tl132	AJ012755	Homo sapiens mRNA for TL132	TL132 protein
949	38786_at		AL079279	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 248114	
950	33418_at		AL096752	Homo sapiens mRNA; cDNA DKFZp434A012 (from clone DKFZp434A012)	
951	38630_at		AL080192	Homo sapiens mRNA; cDNA DKFZp434B102 (from clone DKFZp434B102)	
952	41529_g_at		W72239	Homo sapiens mRNA; cDNA DKFZp434M162 (from clone DKFZp434M162)	
953	36451_at		A1743299	Homo sapiens mRNA; cDNA DKFZp434M245 (from clone DKFZp434M245)	
954	36821_at	DKFZp564A026	AL050367	Homo sapiens mRNA; cDNA DKFZp564A026 (from clone DKFZp564A026)	hypothetical protein
955	37366_at		AL049969	Homo sapiens mRNA; cDNA DKFZp564A072 (from clone DKFZp564A072)	
956	39506_at		AA933984	Homo sapiens mRNA; cDNA DKFZp564B222 (from clone DKFZp564B222)	
957	39748_at		AL050021	Homo sapiens mRNA; cDNA DKFZp564D016 (from clone DKFZp564D016)	

Fig 21

	A	B	C	D	E
958	38357_at		AL049321	Homo sapiens mRNA; cDNA DKFZp564D156 (from clone DKFZp564D156)	
959	33716_at		N95443	Homo sapiens mRNA; cDNA DKFZp564E122 (from clone DKFZp564E122)	
960	35301_at		AL049941	Homo sapiens mRNA; cDNA DKFZp564E2222 (from clone DKFZp564E2222)	
961	35842_at		AL049265	Homo sapiens mRNA; cDNA DKFZp564F053 (from clone DKFZp564F053)	
962	40552_s_at		AL049987	Homo sapiens mRNA; cDNA DKFZp564F112 (from clone DKFZp564F112)	
963	39170_at		AL049957	Homo sapiens mRNA; cDNA DKFZp564J0323 (from clone DKFZp564J0323)	
964	34303_at		AL049949	Homo sapiens mRNA; cDNA DKFZp564L0822 (from clone DKFZp564L0822)	
965	36509_at		AL049998	Homo sapiens mRNA; cDNA DKFZp564L222 (from clone DKFZp564L222)	
966	40353_at		AL049962	Homo sapiens mRNA; cDNA DKFZp564P0823 (from clone DKFZp564P0823)	
967	35290_at		AL050081	Homo sapiens mRNA; cDNA DKFZp566J2146 (from clone DKFZp566J2146)	
968	38079_at		AL049367	Homo sapiens mRNA; cDNA DKFZp586B0918 (from clone DKFZp586B0918)	
969	32195_at		AL049450	Homo sapiens mRNA; cDNA DKFZp586B1922 (from clone DKFZp586B1922)	

Fig 21

212/303

	A	B	C	D	E
970	39379_at		AL049397	Homo sapiens mRNA; cDNA DKFZp586C1019 (from clone DKFZp586C1019)	
971	37575_at		AL050192	Homo sapiens mRNA; cDNA DKFZp586C1723 (from clone DKFZp586C1723)	
972	34283_at		AL050125	Homo sapiens mRNA; cDNA DKFZp586F071 (from clone DKFZp586F071)	
973	39600_at		AL080110	Homo sapiens mRNA; cDNA DKFZp586G1922 (from clone DKFZp586G1922)	
974	34752_at		AL080111	Homo sapiens mRNA; cDNA DKFZp586G2222 (from clone DKFZp586G2222)	
975	39103_s_at		H98552	Homo sapiens mRNA; cDNA DKFZp586I0523 (from clone DKFZp586I0523)	
976	36092_at		AL080213	Homo sapiens mRNA; cDNA DKFZp586I1823 (from clone DKFZp586I1823)	
977	35187_at		AL080216	Homo sapiens mRNA; cDNA DKFZp586K1123 (from clone DKFZp586K1123)	
978	35363_at	DDX17	AL080113	Homo sapiens mRNA; cDNA DKFZp586K2322 (from clone DKFZp586K2322)	
979	41013_at		AL080114	Homo sapiens mRNA; cDNA DKFZp586M2022 (from clone DKFZp586M2022)	
980	41690_at		AL049471	Homo sapiens mRNA; cDNA DKFZp586N012 (from clone DKFZp586N012)	
981	40349_at		AL049442	Homo sapiens mRNA; cDNA DKFZp586N1720 (from clone DKFZp586N1720)	

Fig 21

	A	B	C	D	E
982	32672_at		AL049387	Homo sapiens mRNA; cDNA DKFZp586N1918 (from clone DKFZp586N1918)	
983	36668_at	DIA1	M28713	Homo sapiens NADH-cytochrome b5 reductase (b5R) gene, exon 9.	NADH-cytochrome b5 reductase
984	38542_at		U89322	Homo sapiens nucleophosmin phosphoprotein (NPM) gene, 3' flanking sequence.	
985	40587_s_at	EEF1E1; P18	AF054186	Homo sapiens p18 protein mRNA, complete cds.	p18 protein
986	41448_at	HOXA4	AC004080	Homo sapiens PAC clone RP1-170O19 from 7p15-p21, complete sequence.	even-skipped homeo box 1 (homolog of Drosophila)
987	36159_s_at	PrP	U29185	Homo sapiens prion protein (PrP) gene, complete cds.	prion protein
988	32756_at	ECH1	AF030249	Homo sapiens putative dienoyl-CoA isomerase (ECH1) gene, exons 7-10, and complete cds.	putative dienoyl-CoA isomerase
989	35824_at	RP58	AJ223321	Homo sapiens RP58 gene, complete CDS.	RP58 protein
990	39169_at	SEC61G	AF054184	Homo sapiens Sec61 gamma mRNA, complete cds.	Sec61 gamma
991	41222_at	STAT6	AF067575	Homo sapiens signal transducer and activator of transcription 6 (STAT6) gene, exons 15 through 23 and complete cds.	signal transducer and activator of transcription 6
992	38817_at	SPAG7; ACRP; F3	AF047437	Homo sapiens sperm acrosomal protein mRNA, complete cds.	sperm acrosomal protein
993	36033_at		AL049309	Homo sapiens splicing factor, arginine/serine-rich 12 (SFRS12) mRNA, complete cds	
994	31481_s_at	TMSB10	M92383	Homo sapiens thymosin beta-10 gene, 3'end.	thymosin beta-10
995	1693_s_at	TIMP	D11139	Homo sapiens TIMP gene for tissue inhibitor of metalloproteinases, partial cds.	tissue inhibitor of metalloproteinases

Fig 21

	A	B	C	D	E
996	37311_at	TALDO1; TAL-H;	AF010400	Homo sapiens transaldolase-related protein gene, exons 3-8 and complete cds.	transaldolase-related protein
997	32229_at	EIF4EL3; 4EHP; 4	AF038957	Homo sapiens translation initiation factor 4e mRNA, complete cds.	translation initiation factor 4e
998	1323_at	UBB	X04803	Homo sapiens ubiquitin gene.	ubiquitin
999	32153_s_at	UBB	U49869	Homo sapiens ubiquitin gene.	ubiquitin
1000	38372_at		U66042	Homo sapiens unknown mRNA	
1001	38814_at	ATP6V1G1; ATP6	AF038954	Homo sapiens vacuolar H(+)-ATPase subunit mRNA, complete cds.	vacuolar H(+)-ATPase subunit
1002	41597_s_at	SEC22L1; SEC22	AF047442	Homo sapiens vesicle trafficking protein sec22b mRNA, complete cds.	vesicle trafficking protein sec22b
1003	34957_at	X5L	Y18504	Homo sapiens X5L gene.	XAP-5-like protein
1004	38662_at		AL047596	Homo sapiens, clone IMAGE:3028427, mRNA, partial cds	
1005	38312_at		AL050002	Homo sapiens, clone IMAGE:3140802, mRNA	
1006	33388_at		AL080223	Homo sapiens, clone IMAGE:3855224, mRNA, partial cds	
1007	38676_at		AA059408	Homo sapiens, clone IMAGE:4132509, mRNA	
1008	40238_at		AI674208	Homo sapiens, clone IMAGE:4150198, mRNA, partial cds	
1009	32119_at		AL049423	Homo sapiens, clone IMAGE:4182947, mRNA	
1010	38650_at	IGFBP5	L27560	Homo sapiens, clone IMAGE:4183312, mRNA, partial cds	
1011	1396_at	IGFBP5	L27560	Homo sapiens, clone IMAGE:4183312, mRNA, partial cds	
1012	40432_at		AA522891	Homo sapiens, clone IMAGE:4391536, mRNA	
1013	36130_f_at	MT1E	R92331	Homo sapiens, Similar to RNA helicase-related protein, clone MGC:9246 IMAGE:3892441, mRNA, complete cds	

Fig 21

	A	B	C	D	E
				Homo sapiens, Similar to serine (or cysteine) proteinase inhibitor, clade E (nexin), plasminogen activator inhibitor type 1, member 2, clone MGC:23129 IMAGE:4578406, mRNA, complete cds	
1014	41246_at		A1743134	Homo sapiens, similar to unknown, clone MGC:39325 IMAGE:5440447, mRNA, complete cds	
1015	41533_at		U79298	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1
1016	39733_at	HERPUD1	AF055001	homolog of yeast mutL gene; Human homolog of yeast mutL (hPMS1) gene, complete cds.	postmeiotic segregation 1
1017	525_g_at	hPMS1	U13695	homologous to mouse Rsu-1; putative; Human RSU-1/RSP-1 mRNA, complete cds.	ras suppressor protein 1
1018	32545_r_at	RSU-1	L12535	homologous to mouse Rsu-1; putative; Human RSU-1/RSP-1 mRNA, complete cds.	ras suppressor protein 1
1019	32544_s_at	RSU-1	L12535	HS1 binding protein	HAX-1
1020	39800_s_at	HAX1	U68566	Human 2,4-dienyl-CoA reductase gene, exon 10 and complete cds.	2,4-dienyl-CoA reductase
1021	38104_at	DECR1; NADPH	U78302	Human alcohol dehydrogenase chi polypeptide (ADH5) gene exons 8-9, complete cds.	alcohol dehydrogenase
1022	37708_r_at	ADH5	M81118	Human alcohol dehydrogenase chi polypeptide (ADH5) gene exons 8-9, complete cds.	alcohol dehydrogenase
1023	37707_i_at	ADH5	M81118	Human alpha-1 collagen type IV gene, exon 52.	alpha-1 type IV collagen
1024	39333_at	COL4A1	M26576	Human AMP deaminase (AMPD2) mRNA.	AMP deaminase isoform L splicing variant
1025	38417_at	AMPD2	M91029	Human annexin V (ANX5) gene, exon 13.	annexin V
1026	37747_at	ANX5	U05770		

Fig 21

	A	B	C	D	E
1027	41143_at	CALM1	U12022	Human calmodulin (CALM1) gene, exons 2, 3, 4, 5 and 6, and complete cds.	calmodulin
1028	239_at	CTSD	M63138	Human cathepsin D (catD) gene, exons 7, 8, and 9.	cathepsin D
1029	1916_s_at	c-fos	V01512	Human cellular oncogene c-fos (complete sequence).	v-fos FBJ murine osteosarcoma viral oncogene homolog
1030	1915_s_at	c-fos	V01512	Human cellular oncogene c-fos (complete sequence).	v-fos FBJ murine osteosarcoma viral oncogene homolog
1031	32563_at	JUN	J04111	Human c-jun proto oncogene (JUN), complete cds, clone hCJ-1.	v-jun avian sarcoma virus 17 oncogene homolog
1032	1895_at	JUN	J04111	Human c-jun proto oncogene (JUN), complete cds, clone hCJ-1.	v-jun avian sarcoma virus 17 oncogene homolog
1033	41604_at		U79297	Human clone 23589 mRNA sequence	
1034	32185_at		U00946	Human clone A9A2BRB5 (CAC)n/(GTG)n repeat-containing mRNA	
1035	33667_at	PPIA	X52851	Human cyclophilin gene for cyclophilin (EC 5.2.1.8).	peptidylprolyl isomerase
1036	38459_g_at	CYB5	L39945	Human cytochrome b5 (CYB5) gene, exon 6 and complete cds.	cytochrome b5
1037	38458_at	CYB5	L39945	Human cytochrome b5 (CYB5) gene, exon 6 and complete cds.	cytochrome b5
1038	36163_at	DLD; E3; LAD; DL	L13761	Human dihydrolipoamide dehydrogenase gene, exon 14.	dihydrolipoamide dehydrogenase
1039	1424_s_at	YWHAH; YWHA1	D78577	Human DNA for 14-3-3 protein eta chain, exon2 and complete cds.	14-3-3 protein eta chain
1040	31797_at	dJ73H22.1	AL035699	Human DNA sequence from clone 73H22 on chromosome 6q23, complete sequence.	dJ73H22.1 (TBP-like protein)
1041	40193_at	ENO2	X51956	Human ENO2 gene for neuron specific (gamma) enolase.	human gamma enolase
1042	38326_at	GOS2	M69199	Human GOS2 protein gene, complete cds.	GOS2 protein.
1043	40567_at	TUBA3; FLJ25113	X01703	Human gene for alpha-tubulin (b alpha 1).	alpha-tubulin

Fig 21

	A	B	C	D	E
1044	39775_at	SERP1G1; C1IN	X54486	Human gene for C1-inhibitor.	C1 inhibitor
1045	40862_i_at	CKB; CKBB	X15334	Human gene for creatine kinase B (EC 2.7.3.2).	creatine kinase B
1046	37641_at	IFI44; p44; MTAP	D28915	Human gene for hepatitis C-associated microtubular aggregate protein p44, exon 9 and complete cds.	hepatitis C-associated microtubular aggregate protein p44
1047	40211_at	HNRPA1; HNRNP	X12671	Human gene for heterogeneous nuclear ribonucleoprotein (hnRNP) core protein A1.	hnmp a1 protein
1048	408_at	MGSA	X54489	Human gene for melanoma growth stimulatory activity (MGSA).	melanoma growth stimulatory activity preprotein
1049	36203_at	ODC1	X16277	Human gene for ornithine decarboxylase ODC (EC 4.1.1.17).	ornithine decarboxylase (ODC)
1050	36873_at	VLDLR	D16532	Human gene for very low density lipoprotein receptor, exon 19.	very low density lipoprotein receptor
1051	34759_at		U68494	Human hbc647 mRNA sequence	
1052	32805_at	AKR1C1; DD1; DI	U05861	Human hepatic dihydrodiol dehydrogenase gene, exon 9.	hepatic dihydrodiol dehydrogenase
1053	41231_f_at	HMG17; MGC562	X13546	Human HMG-17 gene for non-histone chromosomal protein HMG-17.	put. HMG-17 protein
1054	38294_at	HOXD4; HOX4; H	X17360	Human HOX 5.1 gene for HOX 5.1 protein.	hox 5.1 protein
1055	40637_at	HSP73 HSC70 HS	Y00371	Human hsc70 gene for 71 kd heat shock cognate protein.	71 Kd heat shock cognate protein
1056	232_at	LAMB2	M55210	Human laminin B2 chain gene, exon 28.	laminin B2 chain
1057	40767_at	TFPI	M59499	Human lipoprotein-associated coagulation inhibitor (LACI) gene, exon 9 and complete cds.	lipoprotein-associated coagulation inhibitor
1058	38637_at	LOX	L16895	Human lysyl oxidase (LOX) gene, exon 7.	lysyl oxidase
1059	37532_at	MCAD	M91432	Human medium-chain acyl-CoA dehydrogenase (MCAD) gene, exon 12.	medium-chain acyl-CoA dehydrogenase
1060	870_f_at	MT3; GIF; GIFB	M93311	Human metallothionein-III gene, complete cds.	metallothionein-III

Fig 21



	A	B	C	D	E
1061	40890_at	MTX	U46920	Human metaxin (MTX) gene, complete cds.	metaxin
1062	32145_at	ADD1	X58141	Human mRNA for erythrocyte adducin alpha subunit.	erythrocyte alpha adducin
1063	37381_g_at	TF2B	X59268	Human mRNA for general transcription factor IIB.	IIB protein
1064	33683_at	TI-227H	D50525	Human mRNA for TI-227H.	
				Human myocyte-specific enhancer factor 2A (MEF2A) gene, last coding exon, and complete cds.	myocyte-specific enhancer factor 2A, C9 form; myocyte-specific enhancer factor 2A, C4 form
1065	41747_s_at	MEF2A	U49020	Human NAD(P)H:quinone oxidoreductase gene, exon 6.	NAD(P)H:quinone oxidoreductase
1066	38066_at	NQO1	M81600	Human natural killer cell enhancing factor (NKEFB) mRNA, complete cds.	enhancer protein
1067	39729_at	NKEFB	L19185		
				Human nonmuscle/smooth muscle alkali myosin light chain gene, complete cds.	non-muscle myosin light chain; smooth muscle myosin light chain
1068	33994_g_at	MLC	M22919	Human nucleic acid binding protein gene, complete cds.	nucleic acid binding protein
1069	32841_at	ZNF9; DM2; CNB1	U19765	Human nucleolin gene, complete cds.	nucleolin
1070	32590_at	NCL	M60858	Human oncoprotein 18 (Op18) gene, complete cds.	oncoprotein 18
1071	1782_s_at	Op18	M31303	Human prostaglandin D2 synthase gene, exon 7.	prostaglandin D2 synthase (21kD, brain)
1072	216_at	PTGDS	M98539		
				Human protein phosphatase 2A catalytic subunit-alpha gene, complete cds.	protein phosphatase-2A catalytic subunit-alpha
1073	237_s_at	PPP2CA	M60483	Human protein phosphatase inhibitor 2 (PPP1R2) gene, exon 6 and complete cds.	protein phosphatase inhibitor 2
1074	812_at	PPP1R2	U68111	Human protein phosphatase inhibitor 2 (PPP1R2) gene, exon 6 and complete cds.	protein phosphatase inhibitor 2
1075	33180_at	PPP1R2	U68111	Human putative ribosomal protein S1 mRNA	protein phosphatase inhibitor 2
1076	35356_at		W21884		

Fig 21

	A	B	C	D	E
1077	491_at	PTPRG	U46116	Human receptor tyrosine phosphatase gamma (PTPRG) gene, exon 30 and complete cds.	receptor tyrosine phosphatase gamma
1078	492_g_at	PTPRG	U46116	Human receptor tyrosine phosphatase gamma (PTPRG) gene, exon 30 and complete cds.	receptor tyrosine phosphatase gamma
1079	36611_at	ACP1	U25849	Human red cell-type low molecular weight acid phosphatase (ACP1) gene, exon 6 and 7, complete cds.	red cell-type low molecular weight acid phosphatase
1080	174_s_at	SH3P18	U61167	Human SH3 domain-containing protein SH3P18 mRNA, complete cds	SH3 domain-containing protein SH3P18
1081	241_g_at	SRM	M64231	Human spermidine synthase gene, complete cds.	spermidine synthase
1082	36688_at	SCP-X/SCP-2	U11313	Human sterol carrier protein-X/sterol carrier protein-2 (SCP-X/SCP-2) gene, exon 16, and complete cds.	sterol carrier protein-X/sterol carrier protein-2
1083	32587_at	ZFP36L2; BRF2;	U07802	Human Tis11d gene, complete cds.	Tis11d
1084	31680_at	TOP1P2	M55630	Human topoisomerase I pseudogene 2.	
1085	36446_s_at	HMG1L2	L24521	Human transformation-related protein mRNA, 3' end	transformation-related protein
1086	39351_at	CD59	M84349	Human transmembrane protein (CD59) gene, exon 4.	CD59 protein
1087	38727_at	THE1	M23161	Human transposon-like element mRNA	
1088	41433_at	VCAM1	M73255	Human vascular cell adhesion molecule-1 (VCAM1) gene, complete CDS.	vascular cell adhesion molecule-1
1089	40121_at	HIP2	U58522	huntingtin interacting protein 2	huntingtin interacting protein
1090	35973_at	HYPH	AB023163	Huntingtin interacting protein H	KIAA0946 protein
1091	40196_at	HYA22	D88153	HYA22 protein	HYA22
1092	36952_at	HADHA	D16480	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase alpha-subunit of trifunctional protein

Fig 21

	A	B	C	D	E
1093	39741_at	HADHB	D16481	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	3-ketoacyl-CoA thiolase beta-subunit of trifunctional protein
1094	36626_at	HSD17B4	X87176	hydroxysteroid (17-beta) dehydrogenase 4	17beta-hydroxysteroid dehydrogenase
1095	41583_at	FEN1	AC004770	<p>Hypothetical protein of unknown function; Hypothetical 52 kDa protein; Hypothetical protein exhibits similarity to motifs found in (U79010) delta 6 desaturase, a hypothetical cytochrome b5 containing fusion protein, and hypothetical proteins encoded by (Z81122) T13F2.1 [Caenorhabditis elegans] and (Z70271) W08D2.4 [Caenorhabditis elegans]; DNA structure-specific endonuclease FEN1; FLAP ENDONUCLEASE-1; MATURATION FACTOR 1 (MF1); DNase IV; RAD2_HUMAN; Hypothetical human Best's macular dystrophy related protein; Simulated translation extends ORF of previously reported partial coding sequence for Best's macular dystrophy related protein (AF038536); Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.</p>	<p>BC269730_1; BC269730_2; FEN1_HUMAN; BC269730_4</p>

Fig 21

A	B	C	D	E
			<p>Hypothetical protein of unknown function; Hypothetical 52 kDa protein; Hypothetical protein exhibits similarity to motifs found in (U79010) delta 6 desaturase, a hypothetical cytochrome b5 containing fusion protein, and hypothetical proteins encoded by (Z81122) T13F2.1 [Caenorhabditis elegans] and (Z70271) W08D2.4 [Caenorhabditis elegans]; DNA structure-specific endonuclease FEN1; FLAP ENDONUCLEASE-1; MATURATION FACTOR 1 (MF1); DNase IV; RAD2_HUMAN; Hypothetical human Best's macular dystrophy related protein; Simulated translation extends ORF of previously reported partial coding sequence for Best's macular dystrophy related protein (AF038536); Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.</p>	
1096 34224_at	FEN1	AC004770		BC269730_1; BC269730_2; FEN1_HUMAN;
1097 1527_s_at	CG018	U50527	hypothetical gene CG018	BC269730_4 hypothetical protein CG018
1098 33466_at	LOC90355	AF038182	hypothetical gene supported by AF038182; BC009203	hypothetical protein AF038182

Fig 21

222/303

A	B	C	D	E
1099 35983_at	MGC2436	AC004528	<p>Hypothetical human protein (partial CDS); CDS constructed from combination of BLASTX, EST matches and Xgrail predictions. N-terminus of protein likely encoded in flanking cosmid R29942. Predicted protein exhibits weak similarity to hypothetical protein PIDle1226191 (AL021106) from <i>Drosophila melanogaster</i>; Hypothetical human protein most similar to Rat ionotropic glutamate receptor (L34938); CDS constructed primarily from XGRAIL predictions and BLASTX similarity to (L34938) ionotropic glutamate receptor [Rattus norvegicus] and gil2160125 (U29873) NMDAR-L [Rattus norvegicus]. Also exhibits similarity to PIDle258718 (Z78413) T01C3.10 [Caenorhabditis elegans]. C-terminus of hypothetical protein is ill-defined at this point; definition will require identification and characterization of appropriate cDNAs; Hypothetical 59.8 kDa human protein; CDS constructed from EST matches and Xgrail predictions. C-terminus of predicted protein not fully confirmed by EST or cDNA coverage. Hypothetical protein exhibits no significant database similarities when queried against R32184_1; R32184_2; R32184_3</p>	
1100 38440_s_at	FLJ20811	AA015605		hypothetical protein, similar to (AC007017) putative RNA helicase A [Arabidopsis thaliana]
1101 39140_at	LOC54505	AL079292		
1102 37819_at	LOC54104	AF007130		
1103 39517_at	LOC56007	AF035313		
1104 41561_s_at	LOC55977	A1651368		

Fig 21

223/303

	A	B	C	D	E
1105	41128_at	LOC92703	AF070537	hypothetical protein BC013073	
1106	38972_at	LOC115207	AF052169	hypothetical protein BC013764	
1107	34864_at	CGI-57	AF070638	hypothetical protein CGI-57	hypothetical protein CGI-57
1108	39960_at	CL640	AF091086	hypothetical protein CL640	hypothetical protein CL640
1109	38837_at	DJ971N18.2	W26226	hypothetical protein DJ971N18.2	
1110	35142_at	DKFZP564D172	AF070617	hypothetical protein DKFZp564D172	
1111	34830_at	DKFZP564K0822	W25986	hypothetical protein DKFZp564K0822	
1112	31852_at	DKFZP564O043	AL050390	hypothetical protein DKFZp564O043	
1113	33895_at	DKFZP586F1318	AL050373	hypothetical protein DKFZP586F1318	hypothetical protein
1114	39692_at	DKFZP586F2423	AL080209	hypothetical protein DKFZp586F2423	
1115	35682_at	FLB6421	A1133727	hypothetical protein FLB6421	
1116	36647_at	FLJ10326	AA526812	hypothetical protein FLJ10326	
1117	34804_at	FLJ10618	AL049246	hypothetical protein FLJ10618	
1118	36840_at	FLJ10737	AF052158	hypothetical protein FLJ10737	
1119	35283_at	FLJ10738	H05692	hypothetical protein FLJ10738	
1120	37610_at	FLJ10803	A1765280	hypothetical protein FLJ10803	
1121	33173_g_at	FLJ10849	T75292	hypothetical protein FLJ10849	
1122	39923_at	FLJ10971	A1935420	hypothetical protein FLJ10971	
1123	38105_at	FLJ11021	W26521	hypothetical protein FLJ11021 similar to splicing factor, arginine/serine-rich 4	
1124	33394_at	FLJ11126	AA034074	hypothetical protein FLJ11126	
1125	35709_at	FLJ11149	AF038172	hypothetical protein FLJ11149	
1126	38141_at	FLJ11193	AF038176	hypothetical protein FLJ11193	
1127	40859_at	FLJ11806	A1561196	hypothetical protein FLJ11806	
1128	41177_at	FLJ12443	AW024285	hypothetical protein FLJ12443	
1129	41434_at	FLJ12552	AF070557	hypothetical protein FLJ12552	hypothetical protein FLJ12552
1130	36580_at	FLJ13910	AL050139	hypothetical protein FLJ13910	hypothetical protein FLJ13910
1131	32222_at	FLJ14639	AA152202	hypothetical protein FLJ14639	
1132	38710_at	FLJ20113	AL096714	hypothetical protein FLJ20113	
1133	38652_at	FLJ20154	AF070644	hypothetical protein FLJ20154	
1134	40868_at	FLJ20274	AA442799	hypothetical protein FLJ20274	
1135	34739_at	FLJ20275	W26023	hypothetical protein FLJ20275	
1136	34857_at	FLJ20986	Z24724	hypothetical protein FLJ20986	
1137	32251_at	FLJ21174	AA149307	hypothetical protein FLJ21174	
1138	40615_at	FLJ21439	AA780049	hypothetical protein FLJ21439	
1139	33915_at	FLJ23027	W22655	hypothetical protein FLJ23027	

Fig 21

A	B	C	D	E
1140 35198_at	LOC57146	AF070596	hypothetical protein from clone 24796	hypothetical protein from clone 24796
1141 38483_at	HSA011916	AJ011916	hypothetical protein HSA011916	hypothetical protein
1142 41236_at	HSU79252	U79252	hypothetical protein HSU79252	hypothetical protein HSU79252
1143 38443_at	MGC14433	U79291	hypothetical protein MGC14433	
1144 39811_at	MGC2749	AA402538	hypothetical protein MGC2749	
1145 32051_at	MGC2840	AJ224875	hypothetical protein MGC2840 similar to a putative glucosyltransferase	glucosyltransferase
1146 35219_at	MGC3047	AL050202	hypothetical protein MGC3047	
1147 41696_at	MGC3077	AI620381	hypothetical protein MGC3077	
1148 41147_at	MGC4276	AF038186	hypothetical protein MGC4276 similar to CG8198	hypothetical protein MGC4276 similar to CG8198
1149 37242_at	MGC5149	U79260	hypothetical protein MGC5149	
1150 36975_at	MGC8721	W26659	hypothetical protein MGC8721	
1151 35677_at	MGC9084	AL035369	hypothetical protein MGC9084	hypothetical protein
1152 32504_at	MY014	AW024812	hypothetical protein My014	
1153 38106_at	YR-29	AJ012409	hypothetical protein YR-29	hypothetical protein
1154 37640_at	HPRT1	M31642	hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)	hypoxanthine phosphoribosyltransferase 1
1155 1039_s_at	HIF1A	U22431	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	hypoxia-inducible factor 1 alpha
1156 39781_at	IGFBP4	U20982	IGF binding protein-4; Human insulin-like growth factor binding protein-4 (IGFBP4) gene, promoter and complete cds.	insulin-like growth factor binding protein-4
1157 38046_at	IK	AJ005579	IK cytokine, down-regulator of HLA II	Prer protein
1158 218_at	IK	S74221	IK cytokine, down-regulator of HLA II	IK factor
1159 37690_at	ILVBL	U61263	ilvB (bacterial acetolactate synthase)-like	acetolactate synthase homolog
1160 36097_at	ETR101	M62831	immediate early protein	immediate early protein
1161 1237_at	IER3	S81914	immediate early response 3	immediate early response 3, isoform short; immediate early response 3, isoform long
1162 34391_at	IGBP1	Y08915	immunoglobulin (CD79A) binding protein 1	alpha 4 protein

Fig 21

	A	B	C	D	E
1163	38636_at	ISLR	AB003184	immunoglobulin superfamily containing leucine-rich repeat	ISLR
1164	40695_at	IMPDH1		IMP (inosine monophosphate)	IMP (inosine monophosphate)
1165	36875_at	IBTK	J05272	dehydrogenase 1	dehydrogenase 1
1166	36617_at	ID1	AL050018	inhibitor of Bruton's tyrosine kinase	hypothetical protein
			X77956	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein
1167	41215_s_at	ID2	D13891	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	Id-2H
				inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein	
1168	34344_at	IKBKAP	AF044195	inner membrane protein, mitochondrial (mitofilin)	IkappaB kinase complex associated protein
1169	37659_at	IMMT	L42572		transmembrane protein
			D26070	inositol 1,4,5-triphosphate receptor, type 1	human type 1 inositol 1,4,5-trisphosphate receptor
1170	755_at	ITPR1		inositol 1,4,5-triphosphate receptor, type 1	human type 1 inositol 1,4,5-trisphosphate receptor
1171	32778_at	ITPR1	D26070	inositol 1,4,5-triphosphate kinase 1	KIAA0263 protein
1172	36154_at	IHPK1	D87452	inositol(myo)-1(or 4)-monophosphatase 1	lithium-sensitive myo-inositol monophosphatase A1
1173	32697_at	IMPA1	AF042729	inositol(myo)-1(or 4)-monophosphatase 2	myo-inositol monophosphatase 2
1174	36496_at	IMPA2	AF014398	insulin induced protein 2	
1175	35833_at	LOC51141	AL080184	insulin receptor substrate 1	insulin receptor substrate-1
1176	41049_at	IRS1	S62539	insulin receptor substrate 1	insulin receptor substrate-1
1177	851_s_at	IRS1	S62539	insulin-like growth factor 1 (somatomedin C)	insulin-like growth factor 1
1178	38737_at	IGF1	X57025	insulin-like growth factor 1 (somatomedin C)	insulin-like growth factor 1
1179	1501_at	IGF1	X57025	insulin-like growth factor 2 receptor	insulin-like growth factor 2 receptor
1180	160027_s_at	IGF2R	Y00285	insulin-like growth factor binding protein 2 (36kD)	insulin-like growth factor binding protein 2 (36kD)
1181	40422_at	IGFBP2	X16302	insulin-like growth factor binding protein 4	insulin-like growth factor binding protein 4
1182	1737_s_at	IGFBP4	M62403		

Fig 21



A	B	C	D	E
1183 2062_at	IGFBP7	L19182	insulin-like growth factor binding protein 7	
1184 37991_at	ITM1	L38961	integral membrane protein 1	integral membrane protein 1
1185 37326_at	A4	U93305	integral membrane protein; swiss-prot accession: O04901; may play role in cell differentiation in intestinal epithelium	LIM domain only 6
1186 41163_at	P24B	AL109672	integral type I protein	p24B protein
1187 32808_at	ITGB1; CD29; FN	X07979	integrin beta 1 subunit precursor; Human mRNA for integrin beta 1 subunit.	integrin beta 1 isoform 1A precursor; integrin beta 1 isoform 1B precursor; integrin beta 1 isoform 1C-1 precursor; integrin beta 1 isoform 1D precursor
1188 1195_s_at	ICAP-1A	AF012024	integrin cytoplasmic domain-associated protein 1	integrin cytoplasmic domain associated protein
1189 120_at	ITGA1	X68742	integrin, alpha 1	
1190 37484_at	ITGA1	X68742	integrin, alpha 1	
1191 36892_at	ITGA7	AF032108	integrin, alpha 7	integrin alpha-7
1192 39071_at	ITGAV	M14648	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)
1193 39754_at	ITGB5	X53002	integrin, beta 5	
1194 2058_s_at	ITGB5	M35011	integrin, beta 5	integrin, beta 5
1195 40681_at	ITGBL1	AB008375	integrin, beta-like 1 (with EGF-like repeat domains)	osteoblast specific cysteine-rich protein
1196 35365_at	ILK	U40282	integrin-linked kinase	integrin-linked kinase
1197 41743_i_at	OPTN; NRP; FIP2	AF061034	interacts with adenovirus E3-14.7KDa, a TNF-alpha cytolysis antagonist; leucine zipper protein; alternatively translated; long form; interacts with adenovirus E3-14.7KDa, a TNF-alpha cytolysis antagonist; leucine zipper protein; alternatively translated; short form; Homo sapiens FIP2 alternatively translated mRNA, complete cds.	FIP2

Fig 21

A	B	C	D	E
1198 41742_s_at	OPTN; NRP; FIP2; AF061034		interacts with adenovirus E3-14.7kDa, a TNF-alpha cytolysis antagonist; leucine zipper protein; alternatively translated; long form; interacts with adenovirus E3-14.7kDa, a TNF-alpha cytolysis antagonist; leucine zipper protein; alternatively translated; short form; Homo sapiens FIP2 alternatively translated mRNA, complete cds.	FIP2
1199 676_g_at	IFITM1	J04164	interferon induced transmembrane protein 1 (9-27)	interferon induced transmembrane protein 1 (9-27)
1200 675_at	IFITM1	J04164	interferon induced transmembrane protein 1 (9-27)	interferon induced transmembrane protein 1 (9-27)
1201 41745_at	IFITM3	X57352	interferon induced transmembrane protein 3 (1-8U)	interferon induced transmembrane protein 3 (1-8U)
1202 1456_s_at	IFI16	M63838	interferon, gamma-inducible protein 16	interferon-gamma induced protein
1203 925_at	IFI30	J03909	interferon, gamma-inducible protein 30	interferon, gamma-inducible protein 30
1204 39728_at	IFI30	J03909	interferon, gamma-inducible protein 30	interferon, gamma-inducible protein 30
1205 32814_at	IFIT1	M24594	interferon-induced protein with tetratricopeptide repeats 1	interferon-induced protein with tetratricopeptide repeats 1
1206 37679_at	IFRD1	Y10313	interferon-related developmental regulator 1	PC4 protein
1207 1368_at	IL1R1	M27492	interleukin 1 receptor, type I	interleukin 1 receptor, type I
1208 33228_g_at	IL10RB	A1984234	interleukin 10 receptor, beta	
1209 33227_at	IL10RB	A1984234	interleukin 10 receptor, beta	
1210 38969_at	IL27	A1828168	interleukin 27	
1211 38299_at	IL6	X04430	interleukin 6 (interferon, beta 2)	interleukin 6 (interferon, beta 2)
1212 35372_r_at	IL8	M17017	interleukin 8	interleukin 8
1213 36189_at	ILF2	U10323	interleukin enhancer binding factor 2, 45kD	NF45 protein
1214 36030_at	DKFZP586I2223	AL080214	intermediate filament-like MGC:2625	hypothetical protein
1215 35776_at	ITSN1	AF064243	intersectin 1 (SH3 domain protein)	intersectin short form
1216 41431_at	ICK	AB023153	intestinal cell kinase	KIAA0936 protein
1217 1825_at	IQGAP1	L33075	IQ motif containing GTPase activating protein 1	ras GTPase-activating-like protein

Fig 21

A	B	C	D	E
1218 39023_at	IDH1	AF020038	isocitrate dehydrogenase 1 (NADP+), soluble	NADP-dependent isocitrate dehydrogenase
1219 40112_at	IDH3B	AA522698	isocitrate dehydrogenase 3 (NAD+) beta	NAD+-specific isocitrate dehydrogenase
1220 40111_g_at	IDH3B	U49283	isocitrate dehydrogenase 3 (NAD+) beta	beta precursor
1221 40478_at	KIAA1162	AL021396	isoform 1 match: protein Tr:Q9UJA1	hypothetical protein
1222 32695_at	dJ196E23.1	Z97632	isoform 2 match: protein Q99991	bombesin-like receptor 3
1223 40827_at	IARS	U04953	isoleucine-tRNA synthetase	isoleucyl-tRNA synthetase
1224 36985_at	IDH1	X17025	isopentenyl-diphosphate delta isomerase	isopentenyl-diphosphate delta isomerase
1225 41775_at	ICMT	AF064084	isoprenylcysteine carboxyl methyltransferase	prenylcysteine carboxyl methyltransferase
1226 34877_at	JAK1	AL039831	Janus kinase 1 (a protein tyrosine kinase)	
1227 34318_at	JM4	AJ005896	JM4 protein	JM4 protein
1228 40957_at	JJAZ1	D63881	joined to JAZF1	joined to JAZF1
1229 41250_at	JTV1	U24169	JTV1 gene	JTV-1
1230 41483_s_at	JUND	X56681	jun D proto-oncogene	junD protein
1231 1612_s_at	JUND	X56681	jun D proto-oncogene	junD protein
1232 40464_g_at	KPNB2	U70322	karyopherin (importin) beta 2	transportin
1233 39028_at	KPNB3	Y08890	karyopherin (importin) beta 3	Ran_GTP binding protein 5
1234 35725_at	KPNA3	D89618	karyopherin alpha 3 (importin alpha 4)	karyopherin alph 3
1235 32487_s_at	KPNA4	AB002533	karyopherin alpha 4 (importin alpha 3)	Qip1
1236 32708_g_at	KATNA1	A191768	katanin p60 (ATPase-containing) subunit A 1	
1237 37386_i_at	KDEL1	X55885	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1	KDEL receptor
1238 39080_at	KDEL2	M88458	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	KDEL receptor 2
1239 33402_at	KDEL3	AL035081	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	hypothetical protein
1240 37150_at	AB026190	AB026190	Kelch motif containing protein	Kelch motif containing protein
1241 32329_at	KRTHB6	X99142	keratin, hair, basic, 6 (monilethrix)	type II intermediate filament of hair keratin
1242 39346_at	KHDRBS1	M88108	KH domain containing, RNA binding, signal transduction associated 1	p62

Fig 21

	A	B	C	D	E
1243	32679_at	KIAA0009	D13634	KIAA0009 gene product	KIAA0009 gene product
1244	34760_at	KIAA0022	D14664	KIAA0022 gene product	KIAA0022 gene product
1245	41129_at	KIAA0033	D26067	KIAA0033 protein	
1246	38797_at	KIAA0062	D31887	KIAA0062 protein	
1247	36978_at	KIAA0077	D38521	KIAA0077 protein	
1248	37718_at	KIAA0096	D43636	KIAA0096 protein	
1249	37293_at	KIAA0097	D43948	KIAA0097 gene product	KIAA0097 protein
				KIAA0098 is a human counterpart of mouse chaperonin containing TCP-1 gene. Start codon is not identified. ha01413 cDNA clone for KIAA0098 has a 2-bp insertion between 736-737 of the sequence of KIAA0098.; Homo sapiens mRNA for KIAA0098 protein, partial cds.	
1250	40417_at	KIAA0098	D43950	KIAA0100 gene product	KIAA0098 protein
1251	39783_at	KIAA0100	D43947	KIAA0102 gene product	KIAA0100 protein
1252	37359_at	KIAA0102	D14658	KIAA0102 gene product	KIAA0102 gene product
1253	38031_at	KIAA0111	D21853	KIAA0111 gene product	KIAA0111 gene product
1254	40279_at	KIAA0121	D50911	KIAA0121 gene product	KIAA0121 protein
1255	36845_at	KIAA0136	D50926	KIAA0136 protein	
1256	32099_at	KIAA0138	D50928	KIAA0138 gene product	KIAA0138 gene product
1257	38472_at	KIAA0143	D63477	KIAA0143 protein	
1258	41728_at	KIAA0152	D63486	KIAA0152 gene product	KIAA0152 gene product
1259	37642_at	KIAA0157	D63877	KIAA0157 protein	KIAA0157 protein
1260	32661_s_at	KIAA0170	D79992	KIAA0170 gene product	KIAA0170 gene product
1261	37225_at	KIAA0172	D79994	KIAA0172 protein	
1262	36942_at	KIAA0174	D79996	KIAA0174 gene product	KIAA0174 gene product
1263	31863_at	KIAA0179	D80001	KIAA0179 protein	
1264	37734_at	KIAA0184	D80006	KIAA0184 protein	
1265	41669_at	KIAA0191	D83776	KIAA0191 protein	
1266	36192_at	KIAA0193	D83777	KIAA0193 gene product	KIAA0193 gene product
1267	38056_at	KIAA0195	D83779	KIAA0195 gene product	KIAA0195 gene product
1268	38419_at	KIAA0196	D83780	KIAA0196 gene product	KIAA0196 gene product
1269	38067_at	KIAA0202	D86957	KIAA0202 protein	
1270	32586_at	KIAA0217	D86971	KIAA0217 protein	
1271	38728_at	KIAA0225	D86978	KIAA0225 protein	

Fig 21

	A	B	C	D	E
1272	40971_at	KIAA0229	D86982	KIAA0229 protein	
1273	37748_at	KIAA0232	D86985	KIAA0232 gene product	KIAA0232 protein
1274	38892_at	KIAA0240	D87077	KIAA0240 protein	
1275	40765_at	KIAA0251	D87438	KIAA0251 protein	
1276	41634_at	KIAA0256	D87445	KIAA0256 gene product	KIAA0256 protein
1277	36971_at	KIAA0257	D87446	KIAA0257 protein	
1278	32237_at	KIAA0265	D87454	KIAA0265 protein	
1279	39405_at	KIAA0266	D87455	KIAA0266 gene product	KIAA0266 gene product
1280	35039_at	KIAA0276	D87466	KIAA0276 protein	
1281	38592_s_at	KIAA0284	A1828210	KIAA0284 protein	
1282	41381_at	KIAA0308	AB002306	KIAA0308 protein	
1283	37943_at	KIAA0321	AB002319	KIAA0321 protein	
1284	32592_at	KIAA0323	AB002321	KIAA0323 protein	
1285	39797_at	KIAA0349	AB002347	KIAA0349 protein	
1286	34661_at	KIAA0350	AB002348	KIAA0350 protein	KIAA0350 protein
1287	32208_at	KIAA0355	AB002353	KIAA0355 gene product	KIAA0355 gene product
1288	32223_at	KIAA0365	AB002363	KIAA0365 gene product	
1289	33442_at	KIAA0367	AB002365	KIAA0367 protein	
1290	35830_at	KIAA0370	AB002368	KIAA0370 protein	
1291	40517_at	KIAA0372	AB002370	KIAA0372 gene product	KIAA0372 gene product
1292	34837_at	KIAA0376	AB002374	KIAA0376 protein	
1293	41457_at	KIAA0423	AB007883	KIAA0423 protein	
1294	35167_at	KIAA0433	AB007893	KIAA0433 protein	KIAA0433 protein
1295	33340_at	KIAA0438	AB007898	KIAA0438 gene product	KIAA0438 gene product
1296	40805_at	KIAA0440	AB007900	KIAA0440 protein	KIAA0440 protein
1297	32091_at	KIAA0446	AB007915	KIAA0446 gene product	KIAA0446 protein
1298	41243_at	KIAA0447	AB007916	KIAA0447 gene product	KIAA0447 protein
1299	32206_at	KIAA0451	AB007920	KIAA0451 gene product	KIAA0451 protein
1300	36069_at	SRGAP2	AB007925	KIAA0456 protein	KIAA0456 protein
1301	37230_at	KIAA0469	AB007938	KIAA0469 gene product	KIAA0469 protein
1302	33893_r_at	KIAA0470	AB007939	KIAA0470 gene product	KIAA0470 protein
1303	34445_at	KIAA0471	AB007940	KIAA0471 gene product	KIAA0471 protein
1304	35318_at	KIAA0475	AB007944	KIAA0475 gene product	KIAA0475 protein
1305	35786_at	KIAA0476	AB007945	KIAA0476 gene product	KIAA0476 protein
1306	35762_at	KIAA0483	AB007952	KIAA0483 protein	KIAA0483 protein
1307	41830_at	KIAA0494	AB007963	KIAA0494 gene product	KIAA0494 protein

5-21

	A	B	C	D	E
1308	35534_at	KIAA0514	AB011086	KIAA0514 gene product	KIAA0514 protein
1309	38724_at	KIAA0515	AB011087	KIAA0515 protein	KIAA0515 protein
1310	34192_at	KIAA0532	AB011104	KIAA0532 protein	KIAA0532 protein
1311	33787_at	KIAA0537	AB011109	KIAA0537 gene product	KIAA0537 protein
1312	35184_at	KIAA0546	AB011118	KIAA0546 protein	KIAA0546 protein
1313	31849_at	KIAA0564	AB011136	KIAA0564 protein	KIAA0564 protein
1314	39434_at	KIAA0592	AB011164	KIAA0592 protein	KIAA0592 protein
1315	41379_at	KIAA0594	AB011166	KIAA0594 protein	KIAA0594 protein
1316	32866_at	KIAA0605	AB011177	KIAA0605 gene product	KIAA0605 protein
1317	39852_at	KIAA0610	AB011182	KIAA0610 protein	KIAA0610 protein
1318	40160_at	KIAA0618	AL080109	KIAA0618 gene product	hypothetical protein
1319	40083_at	KIAA0625	AB014525	KIAA0625 protein	KIAA0625 protein
1320	33241_at	KIAA0626	AB014526	KIAA0626 gene product	KIAA0626 protein
1321	39376_at	KIAA0630	AB014530	KIAA0630 protein	KIAA0630 protein
1322	34353_at	KIAA0648	AB014548	KIAA0648 protein	KIAA0648 protein
1323	38082_at	KIAA0650	AB014550	KIAA0650 protein	KIAA0650 protein
1324	39117_at	KIAA0662	AB014562	KIAA0662 gene product	KIAA0662 protein
1325	41170_at	KIAA0663	AB014563	KIAA0663 gene product	KIAA0663 protein
1326	31826_at	KIAA0674	AB014574	KIAA0674 protein	KIAA0674 protein
1327	39403_at	KIAA0678	AB014578	KIAA0678 protein	KIAA0678 protein
1328	39519_at	KIAA0692	AB014592	KIAA0692 protein	KIAA0692 protein
1329	39380_at	KIAA0697	AB014597	KIAA0697 protein	KIAA0697 protein
1330	39705_at	KIAA0700	AB014600	KIAA0700 protein	KIAA0700 protein
1331	41620_at	KIAA0716	AB018259	KIAA0716 gene product	KIAA0716 protein
1332	33835_at	KIAA0721	AB018264	KIAA0721 protein	KIAA0721 protein
1333	35177_at	KIAA0725	AB018268	KIAA0725 protein	KIAA0725 protein
1334	41218_at	KIAA0729	AB018272	KIAA0729 protein	KIAA0729 protein
1335	38694_at	KIAA0738	AB018281	KIAA0738 gene product	KIAA0738 protein
1336	39771_at	KIAA0740	AB018283	KIAA0740 gene product	KIAA0740 protein
1337	41585_at	KIAA0746	AB018289	KIAA0746 protein	KIAA0746 protein
1338	38424_at	KIAA0747	AB018290	KIAA0747 protein	KIAA0747 protein
1339	40848_g_at	KIAA0750	AB018293	KIAA0750 gene product	KIAA0750 protein
1340	32224_at	KIAA0769	AB018312	KIAA0769 gene product	KIAA0769 protein
1341	36474_at	KIAA0776	AB018319	KIAA0776 protein	KIAA0776 protein
1342	33251_at	KIAA0779	AB018322	KIAA0779 protein	KIAA0779 protein
1343	35999_r_at	KIAA0781	AB018324	KIAA0781 protein	KIAA0781 protein

Gis 21

	A	B	C	D	E
1344	41224_at	KIAA0788	AB018331	KIAA0788 protein	KIAA0788 protein
1345	34285_at	KIAA0795	AB018338	KIAA0795 protein	KIAA0795 protein
1346	39614_at	KIAA0802	AB018345	KIAA0802 protein	KIAA0802 protein
1347	36588_at	KIAA0810	AB018353	KIAA0810 protein	KIAA0810 protein
1348	40492_at	KIAA0826	AB020633	KIAA0826 protein	KIAA0826 protein
1349	40455_at	KIAA0830	AB020637	KIAA0830 protein	KIAA0830 protein
1350	41372_at	KIAA0831	AB020638	KIAA0831 protein	KIAA0831 protein
1351	36888_at	KIAA0841	AB020648	KIAA0841 protein	KIAA0841 protein
1352	39597_at	KIAA0843	AB020650	KIAA0843 protein	KIAA0843 protein
1353	41503_at	KIAA0854	AB020661	KIAA0854 protein	KIAA0854 protein
1354	38730_at	KIAA0864	AB020671	KIAA0864 protein	KIAA0864 protein
1355	39021_at	KIAA0877	AB020684	KIAA0877 protein	KIAA0877 protein
1356	32215_i_at	KIAA0878	AB020685	KIAA0878 protein	KIAA0878 protein
1357	38254_at	KIAA0882	AB020689	KIAA0882 protein	KIAA0882 protein
1358	35720_at	KIAA0893	AB020700	KIAA0893 protein	KIAA0893 protein
1359	40423_at	KIAA0903	AB020710	KIAA0903 protein	KIAA0903 protein
1360	41421_at	KIAA0909	AB020716	KIAA0909 protein	KIAA0909 protein
1361	41498_at	KIAA0911	AB020718	KIAA0911 protein	KIAA0911 protein
1362	39777_at	KIAA0916	AF075587	KIAA0916 protein	protein associated with Myc
1363	32735_at	KIAA0931	AB023148	KIAA0931 protein	KIAA0931 protein
1364	33408_at	KIAA0934	AB023151	KIAA0934 protein	KIAA0934 protein
1365	35369_at	KIAA0937	AB023154	KIAA0937 protein	KIAA0937 protein
1366	33235_at	KIAA0938	AB023155	KIAA0938 protein	KIAA0938 protein
1367	32740_at	Rab11-FIP2	AB023158	KIAA0941 protein	KIAA0941 protein
1368	35794_at	KIAA0942	AB023159	KIAA0942 protein	KIAA0942 protein
1369	41595_at	KIAA0947	AB023164	KIAA0947 protein	KIAA0947 protein
1370	38649_at	KIAA0970	AB023187	KIAA0970 protein	KIAA0970 protein
1371	34396_at	KIAA0978	AB023195	KIAA0978 protein	KIAA0978 protein
1372	32085_at	KIAA0981	AB023198	KIAA0981 protein	KIAA0981 protein
1373	35199_at	KIAA0982	AB023199	KIAA0982 protein	KIAA0982 protein
1374	32769_at	KIAA0993	AB023210	KIAA0993 protein	KIAA0993 protein
1375	34751_at	KIAA0997	AI970189	KIAA0997 protein	KIAA0997 protein
1376	34808_at	KIAA0999	AB023216	KIAA0999 protein	KIAA0999 protein
1377	33193_at	KIAA1001	AW052084	KIAA1001 protein	KIAA1001 protein
1378	36002_at	KIAA1012	AB023229	KIAA1012 protein	KIAA1012 protein
1379	35802_at	KIAA1014	AB023231	KIAA1014 protein	KIAA1014 protein

Fig 21

	A	B	C	D	E
1380	39615_at	KIAA1026	AB028949	KIAA1026 protein	KIAA1026 protein
1381	34089_at	KIAA1030	AB028953	KIAA1030 protein	KIAA1030 protein
1382	41651_at	KIAA1033	AB028956	KIAA1033 protein	KIAA1033 protein
1383	41708_at	KIAA1034	AB028957	KIAA1034 protein	KIAA1034 protein
1384	35163_at	KIAA1041	AB028964	KIAA1041 protein	KIAA1041 protein
1385	38778_at	KIAA1046	AB028969	KIAA1046 protein	KIAA1046 protein
1386	41268_g_at	KIAA1049	AB028972	KIAA1049 protein	KIAA1049 protein
1387	40855_at	KIAA1053	AB028976	KIAA1053 protein	KIAA1053 protein
1388	39400_at	KIAA1055	AB028978	KIAA1055 protein	KIAA1055 protein
1389	33877_s_at	KIAA1067	AB028990	KIAA1067 protein	KIAA1067 protein
1390	34688_at	KIAA1078	AB029001	KIAA1078 protein	KIAA1078 protein
1391	33924_at	KIAA1091	AB029014	KIAA1091 protein	KIAA1091 protein
1392	32508_at	KIAA1096	AL096857	KIAA1096 protein	hypothetical protein
1393	41179_at	KIAA1100	AB029023	KIAA1100 protein	KIAA1100 protein
1394	34839_at	KIAA1104	AB029027	KIAA1104 protein	KIAA1104 protein
1395	33457_at	RAP140	AB029028	KIAA1105 protein	KIAA1105 protein
1396	36814_at	KIAA1109	AB029032	KIAA1109 protein	KIAA1109 protein
1397	34274_at	KIAA1116	AB029039	KIAA1116 protein	KIAA1116 protein
1398	37617_at	KIAA1128	U90912	KIAA1128 protein	
1399	33358_at	KIAA1157	W29087	KIAA1157 protein	
1400	40308_at	KIAA1240	AI830496	KIAA1240 protein	
1401	33811_at	KIAA1254	AI761567	KIAA1254 protein	
1402	38674_at	KIAA1354	AA115140	KIAA1354 protein	
1403	32730_at	KIAA1750	AL080059	KIAA1750 protein	
1404	32171_at	KIAA1856	AL080102	KIAA1856 protein	hypothetical protein
1405	39897_at	KIAA1966	N36997	KIAA1966 protein	
1406	32846_s_at	KTN1	D13629	kineclin 1 (kinesin receptor)	kineclin 1
1407	39057_at	KNS2	L04733	kinesin 2 (60-70kD)	kinesin light chain
1408	32079_at	KIF13B	AB014539	kinesin family member 13B	KIAA0639 protein
1409	33345_at	KIF3C	AF035621	kinesin family member 3C	kinesin-related protein
1410	34294_at	KIFC3	AL041493	kinesin family member C3	
1411	41474_at	KIF2	Y08319	kinesin heavy chain member 2	kinesin-2
1412	40779_at	KIFAP3	U59919	kinesin-associated protein 3	SMAP
1413	34216_at	KLF7	AA478904	Kruppel-like factor 7 (ubiquitous)	
1414	38768_at	HADHSC	X96752	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain	3-hydroxyacyl-CoA dehydrogenase

Cis 21



	A	B	C	D	E
1415	41485_at	LDHA	X02152	lactate dehydrogenase A	lactate dehydrogenase A
1416	288_s_at	LBR	L25931	lamin B receptor	lamin B receptor
1417	256_s_at	LAMR1	M14199	laminin receptor 1 (67kD, ribosomal protein SA)	laminin receptor 1
1418	37671_at	LAMA4	S78569	laminin, alpha 4	laminin alpha 4 chain
1419	581_at	LAMB1	M61916	laminin, beta 1	laminin B1
1420	39441_at	LANCL1	Y11395	LanC lantibiotic synthetase component C-like 1 (bacterial)	lantionine synthetase C-like protein 1
1421	1495_at	LTBP1	M34057	latent transforming growth factor beta binding protein 1	latent transforming growth factor beta binding protein 1 precursor
1422	37906_at	LTBP2	Z37976	latent transforming growth factor beta binding protein 2	LTBP-2 precursor
1423	33412_at	LGALS1	AI535946	lectin, galactoside-binding, soluble, 1 (galectin 1)	
1424	35367_at	LGALS3	AB006780	lectin, galactoside-binding, soluble, 3 (galectin 3)	galectin-3
1425	37754_at	LGALS3BP	L13210	lectin, galactoside-binding, soluble, 3 binding protein	Mac-2 binding protein
1426	1846_at	LGALS8	L78132	lectin, galactoside-binding, soluble, 8 (galectin 8)	prostate carcinoma tumor antigen
1427	34267_r_at	LEPR	U50748	leptin receptor	leptin receptor
1428	33830_at	HSOBRGRP	AW026535	leptin receptor gene-related protein	
1429	33829_at	HSOBRGRP	Y12670	leptin receptor gene-related protein	leptin receptor gene-related protein
1430	38985_at	LEPROTL1	AF063605	leptin receptor overlapping transcript-like 1	brain my047 protein
1431	41320_s_at	LRRFIP1	U69609	leucine rich repeat (in FLII) interacting protein 1	transcription repressor
1432	39967_at	LDLC1	AB019527	leucine zipper, down-regulated in cancer 1	LDLC1 protein
1433	41754_at	LRPPRC	M92439	leucine-rich PPR-motif containing	leucine-rich PPR-motif containing protein
1434	37470_at	LAIR1	AF013249	leukocyte-associated Ig-like receptor 1	leukocyte-associated Ig-like receptor-1
1435	38081_at	LT44H	J03459	leukotriene A4 hydrolase	leukotriene A4 hydrolase
1436	36062_at	LPXN	AF062075	leupaxin	leupaxin
1437	35278_at	RPS29	AI541542	libtest16.A02.r.bvnorm Homo sapiens cDNA 5' mRNA sequence.	
1438	39687_at	E46L	AI524873	like mouse brain protein E46	

Gis 21

A	B	C	D	E
1439 39686_g_at	E46L	AL050282	like mouse brain protein E46	hypothetical protein
1440 39685_at	E46L	AL050282	like mouse brain protein E46	hypothetical protein
1441 39163_at	KIDINS220	W27233	likely homolog of rat kinase D-interacting substance of 220 kDa	
1442 32669_at	SOC55	AB014571	likely ortholog of mouse suppressors of cytokine signalling 5	KIAA0671 protein
1443 40555_at	TC10	AL043108	likely ortholog of mouse TC10-alpha	
1444 40844_at	TSBP	D63875	likely ortholog of mouse TPR-containing, SH2-binding phosphoprotein	KIAA0155 gene product
1445 41248_at	CSTF2T	AB014589	likely ortholog of mouse variant polyadenylation protein CSTF-64	KIAA0689 protein
1446 35805_at	GRASP55	AA447263	likely ortholog of rat golgi stacking protein homolog GRASP55	
1447 39232_at	LIMS1	U09284	LIM and senescent cell antigen-like domains 1	PINCH protein
1448 36181_at	LASP1	X82456	LIM and SH3 protein 1	LIM and SH3 domain protein
1449 38617_at	LIMK2	D45906	LIM domain kinase 2	LIMK-2
1450 1452_at	LMO4	U24576	LIM domain only 4	breast tumor autoantigen
1451 31936_s_at	LKAP	AB007890	limkain b1	KIAA0430 protein
1452 38745_at	LIPA	X76488	lipase A, lysosomal acid, cholesterol esterase (Wolman disease)	lysosomal acid lipase
1453 38098_at	LPIN1	D80010	lipin 1	
1454 37542_at	LHFPL2	D86961	lipoma HMGIC fusion partner-like 2	
1455 41209_at	LPL	M15856	lipoprotein lipase	lipoprotein lipase precursor
1456 1798_at	LIV-1	U41060	LIV-1 protein, estrogen regulated liver form; Homo sapiens glycogen phosphorylase (PYGL) gene, exon 20 and complete cds.	estrogen regulated LIV-1 protein
1457 37215_at	PYGL	AF046798		glycogen phosphorylase

Fig 21

	A	B	C	D	E
1458	40493_at	CD44	L05424	long tailed isoform; individual exons 6-14 are alternative exons any of which can be spliced out of the mRNA.; putative; long tailed isoform; putative; long tailed isoform; hemopoietic variant; putative; long tailed isoform; epithelial form; putative; Human cell surface glycoprotein CD44 (CD44) gene, 3' end of long tailed isoform.	cell surface glycoprotein CD44
1459	36194_at	LRPAP1	M63959	low density lipoprotein-related protein-associated protein 1 (alpha-2-macroglobulin receptor-associated protein 1)	alpha-2-macroglobulin receptor-associated protein
1460	34400_at	QP-C	A1540957	low molecular mass ubiquinone-binding protein (9.5kD)	
1461	37025_at	PIG7	AL120815	LPS-induced TNF-alpha factor	
1462	39017_at	LSM1	AJ238094	Lsm1 protein	Lsm1 protein
1463	38038_at	LUM	U21128	lumican	lumican
1464	38115_at	FUS1	AF055479	lung cancer candidate	lung cancer candidate FUS1
1465	39428_at	LNK	AF055581	lymphocyte adaptor protein	adaptor protein Lnk
1466	39396_at	LYPLA1	AF081281	lysophospholipase I	lysophospholipase
1467	33788_at	LYSAL1	AB002390	lysosomal apyrase-like 1	lysosomal apyrase-like 1
1468	39758_f_at	LAMP1	J04182	lysosomal-associated membrane protein 1	lysosomal membrane glycoprotein-1
1469	38403_at	LAMP2	X77196	lysosomal-associated membrane protein 2	lysosome-associated membrane protein-2
1470	38402_at	LAMP2	U36336	lysosomal-associated membrane protein 2	lysosome-associated membrane protein-2b
1471	39019_at	LAPTM4A	D14696	lysosomal-associated protein	lysosomal-associated protein
1472	33127_at	LOXL2	U89942	transmembrane 4 alpha	transmembrane 4 alpha
1473	34336_at	KARS	D32053	lysyl oxidase-like 2	lysyl oxidase-related protein
1474	32832_at	MAEA	AF084928	lysyl-tRNA synthetase	Lysyl tRNA Synthetase
1475	36174_at	MACMARCKS	X70326	macrophage erythroblast attacher	erythroblast macrophage protein EMP
				macrophage myristoylated alanine-rich C kinase substrate	macrophage myristoylated alanine-rich C kinase substrate

Fig 21

	A	B	C	D	E
1476	1453_at	MADH2	U68018	MAD, mothers against decapentaplegic homolog 2 (Drosophila)	mad protein homolog
1477	38944_at	MADH3	U68019	MAD, mothers against decapentaplegic homolog 3 (Drosophila)	mad protein homolog
1478	1433_g_at	MADH3	U68019	MAD, mothers against decapentaplegic homolog 3 (Drosophila)	mad protein homolog
1479	36953_at	MADH4	U44378	MAD, mothers against decapentaplegic homolog 4 (Drosophila)	Dpc4
1480	1013_at	MADH5	U59913	MAD, mothers against decapentaplegic homolog 5 (Drosophila)	Smad5
1481	1955_s_at	MADH6	AF035528	MAD, mothers against decapentaplegic homolog 6 (Drosophila)	Smad6
1482	1857_at	MADH7	AF010193	MAD, mothers against decapentaplegic homolog 7 (Drosophila)	MAD-related gene SMAD7
1483	41237_at	HLA-A	D32129	major histocompatibility complex, class I, A	HLA-A26
1484	41609_at	HLA-DMB	U15085	major histocompatibility complex, class II, DM beta	HLA-DMB
1485	38096_f_at	HLA-DPB1	M83664	major histocompatibility complex, class II, DP beta 1	HLA-DPB1
1486	38095_i_at	HLA-DPB1	M83664	major histocompatibility complex, class II, DP beta 1	HLA-DPB1
1487	37039_at	HLA-DRA	J00194	major histocompatibility complex, class II, DR alpha	major histocompatibility complex, class II, DR alpha precursor
1488	33261_at	HLA-DRB1	M16941	major histocompatibility complex, class II, DR beta 1	
1489	34425_at	HLA-ALS	AF031469	major histocompatibility complex, class I-like sequence	MHC class I-related protein 1 isoform D
1490	34003_at	CD4	U47924	major receptor for HIV-1; member of immunoglobulin supergene family; T cell surface glycoprotein T4	protein 'A', isoform 1
1491	36608_at	MDH1	D55654	malate dehydrogenase 1, NAD (soluble)	cytosolic malate dehydrogenase
1492	837_s_at	ME1	U43944	malic enzyme 1, NADP(+)-dependent, cytosolic	cytosolic NADP(+)-dependent malic enzyme

Fig 21

	A	B	C	D	E
1493	36599_at	ME2	M55905	malic enzyme 2, NAD(+)-dependent, mitochondrial	mitochondrial NAD(P)+ -dependent malic enzyme
1494	36673_at	MPI	X76057	mannose phosphate isomerase	phosphomannose isomerase
1495	35299_at	MKNK1	AB000409	MAP kinase-interacting serine/threonine kinase 1	MNK1
1496	40826_at	MARK3	M80359	MAP/microtubule affinity-regulating kinase 3	protein p78
1497	41506_at	MAPKAPK5; PRA	AF032437	MAPK-activated protein kinase; PRK; Homo sapiens mitogen activated protein kinase activated protein kinase gene, complete cds.	mitogen activated protein kinase activated protein kinase
1498	37009_at	CAT	AL035079	match proteins: Sw:P04040 Sw:P04762 Sw:P24270 Tr:O62839 Sw:P00432 Sw:P17336 Tr:P90682 Tr:Q27487 Sw:O61235 Tr:O18193 Tr:O77229 Tr:Q49133 Sw:P26901 Sw:P55306 Sw:P30263 Tr:P95631 Sw:P44390 Tr:Q27710 Sw:Q96528 Sw:O13289 Sw:P07820 Sw:P30265 Sw:P77872 Tr:Q59602 Tr:P77924 Sw:Q59170 Sw:P15202 Tr:Q59296 Tr:O33613 Sw:Q92405 Sw:Q59635 Sw:P81138 match ESTs: W94164 N28621	dJ53C18.1 (Catalase)
1499	40297_at	WUGSC:H_RG04	AC005053	match to ESTs AA316181 (NID:g3165221), AA032221 (NID:g1502183), and AI167942 (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from 7q21, complete sequence.	six transmembrane epithelial antigen of the prostate

Cis 21

A	B	C	D	E
1500 34860_g_at	BCG1	Z98046	match: cDNAs X67055 X14690 D89287 X70393 S82800 X16260 M18192 Y11283 D38535 D38595 match: proteins Q06033 P97280 O54882 O35802 Q61704 Q14624 P79263 Q63416 O42141 P19823 O02668 Q61703 P97279 Q29052 match: cDNAs: Em:AL050345 match: ESTs: Em:AA304885 Em:AA447346 Em:AA314213 Em:AA209368 Em:AA209372 Em:T84723 Em:H23039 Em:AA542125 Em:W41686 Em:AA394854 Em:AA492678	hepatocellular carcinoma associated protein; breast cancer associated gene 1
1501 35336_at	HS508I15A	AL021707	match: protein O15214	chromosome 22 open reading frame 2
1502 32658_at	dJ1033B10.1	AL031228	match: protein O15214	BING4
1503 31545_at	dJ1033B10.1	AL031228	match: protein O15214	BING4
1504 36986_at	dJ886K2.1	AL031295	match: protein SPTREMBL: Q14241	UDP-galactose-4-epimerase
1505 38072_at	dJ465N24.1	AL031432	match: proteins CE02000 O59733 CE01999; supported by FGENSES and GENSCAN	hypothetical protein dJ465N24.2.1
1506 32478_f_at	dJ281H8.1	AL031133	match: proteins O15037 CE16881 supported by GENSCAN possibly this partial gene and dJ281H8.1 are part of one gene	dJ281H8.2 (PUTATIVE novel protein similar to KIAA0323 and worm C30F12.1)

Fig 21

240/303

A	B	C	D	E
1507 39759_at	dJ51J12.1	AL031781	<p>match: proteins O42476 Q94539; match: protein O88972; match: cDNA AF091047; owing to a different in-frame ORF, the translation of the last coding exon (8 C-terminal amino-acids) differs from that in mouse and is terminated more upstream; match: protein Q61110; Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.</p>	<p>dJ51J12.1 (human ortholog of zebrafish Quaking protein homolog ZKQ-1 (isoform 1)); dJ51J12.1.2 (human ortholog of mouse KH Domain RNA Binding protein QKI-7B (isoform 2)); dJ51J12.1.3 (human ortholog of mouse KH Domain RNA Binding protein QKI-7 (isoform 3))</p>
1508 39760_at	dJ51J12.1	AL031781	<p>match: proteins O42476 Q94539; match: protein O88972; match: cDNA AF091047; owing to a different in-frame ORF, the translation of the last coding exon (8 C-terminal amino-acids) differs from that in mouse and is terminated more upstream; match: protein Q61110; Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.</p>	<p>dJ51J12.1 (human ortholog of zebrafish Quaking protein homolog ZKQ-1 (isoform 1)); dJ51J12.1.2 (human ortholog of mouse KH Domain RNA Binding protein QKI-7B (isoform 2)); dJ51J12.1.3 (human ortholog of mouse KH Domain RNA Binding protein QKI-7 (isoform 3))</p>
1509 32573_at	COX6A	AL021546	<p>match: proteins P13182 P12074 P10818 P43024 Q02221 P07471 P10817 P43023 P13182 O13085 O13082</p>	<p>cytochrome c oxidase subunit VIa polypeptide 1</p>

Fig 21

	A	B	C	D	E
1510 33443_at		HSF2	Z99129	match: proteins P38533 Q03933 P38530 P41154 Q00613 P38529 P38531 Q63717 P38532 Q99472	heat shock transcription factor 2
1511 36133_at		dJ512B11.1	AL031058	match: proteins Q14189 P15924 Q03001 P97395 P97396 P97394; Human DNA sequence from clone 512B11 on chromosome 6p24-25. Contains the Desmoplakin I (DPI) gene, ESTs, STSs and GSSs, complete sequence.	dJ512B11.1 (Desmoplakin I (DPI))
1512 37043_at		E2F-2	AL021154	match: proteins Q14209 Q16254 Q35261 Q00716 Q61501 Q90977 Q01094 Q27368	E2F transcription factor 2
1513 41227_at		OCRL1	AL022162	match: proteins Q15774; match: protein Q01968 P32019; Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.	dJ454M7.1.2 (Lowe Oculocerebrorenal Syndrome protein OCRL-1) (isoform 2); dJ454M7.1.1 (Lowe Oculocerebrorenal Syndrome protein OCRL-1) (isoform 1)
1514 38990_at		dJ341E18.1	AL031178	match: proteins Q62726 P20793 Q04859 Q39423 P43294 Q49669	dJ341E18.1 (Serine/Threonine Protein Kinase (presumptive isolog of Rat protein Q62726))

Fig 21



A	B	C	D	E
1515 34782_at	JUMONJI	AL021938	<p>match: proteins Q92833 Q62315; protein Q92833 has a different stop codon 19 aa further downstream because it jumps frame twice, circumventing the stopcodon in this entry. This could be due to a sequence error in the cDNA sequence; Homo sapiens DNA sequence from PAC 232K4 on chromosome 6p22.3. Contains the JUMONJI gene for a hypothetical 141.7 kD protein. Contains ESTs, STSs, a CA repeat polymorphism and genomic marker D6S260', complete sequence.</p>	dJ232K4.1 (hypothetical 141.7 kD protein JUMONJI)
1516 37350_at	dJ889N15.1	AL031177	<p>match: proteins Q99795 Q91665 Q91664 O09052 P78310 P97792 Q91667 O60939 P54900 Q62861 Q61148 O00426 P06907 P25189 Q92677 P20938 P27573 P10522 P37301 match: patented sequence I80040 supported by GENSCAN and FGENES</p>	dJ889N15.1 (novel protein similar to X. laevis Cortical Thymocyte Marker CTX)
1517 39738_at	APOL2	Z82215	match: proteins: Sw:O14791	apolipoprotein L
1518 31824_at	ME1	AL049699	<p>match: proteins: Sw:P06801 Sw:P28227 Sw:Q29558 Sw:P13697 Sw:P40927 Sw:Q16798 Tr:Q16797 Sw:P48163</p>	dJ747H23.1 (malic enzyme 1, soluble (NADP-dependent malic enzyme, malate oxidoreductase, EC 1.1.1.40))
1519 32766_at	OTK27 SSFA1	Z83840	match: proteins: Sw:P12956	non-histone chromosome protein 2 (S. cerevisiae)-like 1
1520 39756_g_at	XBP1	Z93930	<p>match: proteins: Sw:P17861 Tr:O35426; Human DNA sequence from clone CTA-292E10 on chromosome 22q11-12 Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs, GSSs and a putative CpG island, complete sequence.</p>	bK292E10.1 (X-box binding protein 1 (TREB5))

Fig 21

	A	B	C	D	E
1521	39755_at	XBP1	Z93930	match: proteins: Sw:P17861 Tr:O35426; Human DNA sequence from clone CTA- 292E10 on chromosome 22q11-12 Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs, GSSs and a putative CpG island, complete sequence. match: proteins: Sw:P26038 Tr:Q35763 Sw:P26041 Sw:P26042 Sw:P26044 Sw:P35241 Sw:P26043 Sw:P15311 Sw:P31976 Sw:P26040 Tr:Q26520 Tr:Q24788 Tr:Q24796 Tr:Q94815; Human DNA sequence from clone 376D21 on chromosome Xq11.1-12 Contains the MSN gene for Moesin (Membrane- organizing Extension Spike protein), ESTs, STSs, GSSs, genomic marker DXS8029 and a putative CpG island, complete sequence.	bK292E10.1 (X-box binding protein 1 (TREB5))
1522	40771_at	MSN	Z98946	match: proteins: Sw:P39023 Sw:O16797 Sw:P21531 Sw:P39872 Sw:P27659 Sw:Q92901 Sw:P49149 Sw:P22738 Sw:P35684 Sw:P17094 Wp:CE05598 match: proteins: Sw:P50550 Sw:O09181 Tr:O62622 Sw:P40984 Sw:P50623 Tr:Q42551 Tr:O24240 Tr:Q42973 Sw:P52478 Sw:Q02159 Sw:P15732 Sw:O00102 Tr:O76542 Sw:P27949 Sw:P49427 Tr:O17424 Sw:P25867 Sw:P52490	dJ376D21.1 (Moesin (Membrane-organizing Extension Spike protein))  ribosomal protein L3
1523	31722_at	RPL3	AL022326	match: proteins: Sw:P12772 Sw:Q60429 Sw:P36956 Sw:Q60416 Tr:O15352 match: proteins: Sw:Q28038 Sw:Q16674 Tr:P97591 Sw:Q61865	C358B7.1 (ubiquitin-conjugating enzyme E2) (homologous to yeast UBC9))
1524	33136_at	UBE21	AL031714	match: proteins: Sw:Q12772 Sw:Q60429 Sw:P36956 Sw:Q60416 Tr:O15352 match: proteins: Sw:Q28038 Sw:Q16674 Tr:P97591 Sw:Q61865	seplin 3
1525	36607_at	bK250D10.3	Z99716	match: proteins: Sw:Q28038 Sw:Q16674 Tr:P97591 Sw:Q61865	small nuclear ribonucleoprotein polypeptide B"
1526	38399_at	SNRNP2	AL034428		

Fig 21

A	B	C	D	E
1527 36711_at			match: proteins: Tr:O54791 Sw:Q90595 Sw:Q61827 Sw:Q90596 Tr:O54790 Tr:O15525 Sw:Q90889 Tr:O73679 Tr:O75444 Sw:P54844 Sw:P54843 Sw:Q00056 Sw:Q10060 Sw:Q15427	chromosome 22 open reading frame 5
1528 39561_at	HS506A DKFZP5 DNAL4	AL021977 AL008583	match: proteins: Tr:O54793 Tr:O44229 match: proteins: Tr:O75354 Tr:O75356 Tr:Q9QYC8 Tr:Q9WUZ9 Tr:O70214 Tr:Q9QYC9	chromobox homolog 6
1529 39876_at	dJ738P15.1	AL035252	match: proteins: Tr:O94136 Sw:Q99798 Sw:P49609 Sw:P20004 Sw:P16276 Tr:O75809 Tr:O74699 Wp:CE00516 Sw:P19414 Tr:O75944 Sw:O13966	dJ738P15.2 (CD39-like 2 (a nucleoside phosphatase))
1530 37189_at	ACO2	AL023553	match: proteins: Tr:P70386 Sw:Q02527 Sw:Q10470 Sw:Q09327	dJ347H13.1 (aconitase 2, mitochondrial (Aconitate Hydratase, EC 4.2.1.3, Citrate Hydrolase))
1531 41235_at	TAXREB67 TXRE	AL022312	match: proteins: Tr:Q00425 Sw:Q13671 Tr:O15010 Tr:P97680	activating transcription factor 4 dJ117516.1 (Ras inhibitor JC265 (Ras association (RalGDS/AF-6) domain containing protein))
1532 36550_at	dJ117516.1	AL049538	match: proteins: Tr:Q14621 Tr:Q64012 Sw:P07910 Sw:P19600 Tr:O60812 Sw:Q14011 Sw:P26686	RNA-binding protein (autoantigenic) long isoform
1533 39368_at	P542	AL031668	match: proteins: Tr:Q9Y3M0 Tr:Q9WU14 Sw:P39540 Tr:Q9Y396 maternal G10 transcript	dJ483K16.1.1 (novel protein (isoform 1)) maternal G10 transcript
1534 33821_at	dJ483K16.1	AL034374	MAX binding protein	ROX protein
1535 39029_at	G10	U11861	MAX interacting protein 1	MAX interacting protein 1, isoform a; MAX interacting protein 1, isoform b
1536 35145_at	MNT	X96401	MAX interacting protein 1	MAX interacting protein 1, isoform a; MAX interacting protein 1, isoform b
1537 39072_at	MX11	L07648	MAX interacting protein 1	
1538 654_at	MX11	L07648	MAX interacting protein 1	
1539 35312_at	MCM2	D21063	MCM2 minichromosome maintenance deficient 2, mitotin (S. cerevisiae)	
1540 40469_at	MCM3AP	AB011144	MCM3 minichromosome maintenance deficient 3 (S. cerevisiae) associated protein	KIAA0572 protein

Fig 21

	A	B	C	D	E
1541	40117_at	MCM6	D84557	MCM6 minichromosome maintenance deficient 6 (MIS5 homolog, <i>S. pombe</i> ) ( <i>S. cerevisiae</i> )	HsMcm6
1542	41388_at	MEIS2	AF017418	Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse)	homeobox protein MEIS2
1543	37486_f_at	MEIS3	U68385	Meis1, myeloid ecotropic viral integration site 1 homolog 3 (mouse)	Meis1-related protein 2
1544	35340_at	MEL	A1819948	mel transforming oncogene (derived from cell line NK14)- RAB8 homolog	
1545	36500_at	MAGEA2A	AF027974	melanoma antigen, family A, 2, copy a; similar to GenBank Accession Number L18920	melanoma antigen family A2a
1546	41139_at	MAGED1	W26633	melanoma antigen, family D, 1	
1547	39327_at	D2S448	D86983	Melanoma associated gene	
1548	38441_s_at	MCP	X59408	membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen)	membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen)
1549	39471_at	M11S1	Z48042	membrane component, chromosome 11, surface marker 1	GPI-anchored protein p137
1550	33444_at	M17S2	D30756	membrane component, chromosome 17, surface marker 2 (ovarian carcinoma antigen CA125)	membrane component, chromosome 17, surface marker 2
1551	1389_at	MME	J03779	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)	membrane metallo-endopeptidase
1552	40399_r_at	MEOX2	A1743406	mesenchyme homeo box 2 (growth arrest-specific homeo box)	
1553	37697_s_at	por	L08666	Met at bp 326 also used as initiation codon in vitro; Homo sapiens initiation codon in vitro; Homo sapiens porin (por) mRNA, complete cds and truncated cds.	porin
1554	40244_s_at	MPPE1	A1743654	metallo phosphoesterase	

Fig 21

A	B	C	D	E
			metallothionein (MT)-like gene; H.sapiens pseudogene for metallothionein and AG/CT repetitive element.	metallothionein
1555 31975_at		X55503	metallothionein 2A	
1556 39081_at	MT2A	AI547258	metal-regulatory transcription factor 1	metal-regulatory transcription factor
1557 38945_at	MTF1	X78710	metastasis associated 1	metastasis associated protein
1558 1643_g_at	MTA1	U35113	metaxin 2	metaxin 2
1559 35642_at	MTX2	AF053551		
1560 39342_at	MARS	X94754	methionine-tRNA synthetase	yeast methionyl-tRNA synthetase homolog
1561 37619_at	METAP1	D42084	methionyl aminopeptidase 1	
1562 41828_at	MBD1	Y10746	methyl-CpG binding domain protein 1	methyl-CpG binding protein
1563 33905_at	MBD2	AF072242	methyl-CpG binding domain protein 2	methyl-CpG binding protein MBD2
1564 34386_at	MBD4	AF072250	methyl-CpG binding domain protein 4	methyl-CpG binding protein MBD4
			methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase	methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase, precursor
1565 40074_at	MTHFD2	X16396		
			methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase	methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase
1566 674_g_at	MTHFD1	J04031		
1567 40105_at	MUT	M65131	methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase	methylmalonyl-CoA mutase
			MHC class I chain-related gene B; cDNA sequence deposited under GenBank Accession Number X91625; Human MHC class I molecule (MICB) gene, complete cds.	
1568 35937_at	MICB	U65416		MHC class I molecule
1569 36535_at	MFAP1	U04209	microfibrillar-associated protein 1	associated microfibrillar protein
			microphthalmia-associated transcription factor	A-type microphthalmia associated transcription factor
1570 38228_g_at	MITF	AB006909		
1571 820_at	MGST2	U77604	microsomal glutathione S-transferase 2	microsomal glutathione S-transferase 2
1572 38704_at	MACF1	AB007934	microtubule-actin crosslinking factor 1	KIAA0465 protein
1573 35917_at	MAP1A	W26631	microtubule-associated protein 1A	
1574 33850_at	MAP4	W28892	microtubule-associated protein 4	

21

	A	B	C	D	E
1575	33456_at	MAPRE1	U24166	microtubule-associated protein, RP/EB family, member 1	EB1
1576	39370_at	MAP1A/1BLC3	W28807	microtubule-associated proteins 1A/1B light chain 3	
1577	34296_at	MID1	AF041210	midline 1 (Opitz/BBB syndrome)	midline 1 fetal kidney isoform 3
1578	34403_at	MFGE8	U58516	milk fat globule-EGF factor 8 protein	BA46
1579	40027_at	ATPW	W52999	mitochondrial ATP synthase regulatory component factor B	
1580	37174_at	MRPL19	D14660	mitochondrial ribosomal protein L19	mitochondrial ribosomal protein L19
1581	37726_at	MRPL3	X06323	mitochondrial ribosomal protein L3	mitochondrial ribosomal protein L3
1582	39717_g_at	MRPL33	AI597616	mitochondrial ribosomal protein L33	
1583	32221_at	MRPS18B	AL050361	mitochondrial ribosomal protein S18B	mitochondrial ribosomal protein S18B
1584	38899_s_at	MFN1	U95822	mitofusin 1	putative transmembrane GTPase
1585	34369_at	MFN2	D86987	mitofusin 2	KIAA0214 protein
1586	36577_at	MIG2	Z24725	mitogen inducible 2	mitogen inducible gene mig-2
1587	37733_at	MAPK14	L35263	mitogen-activated protein kinase 14	CSAids binding protein
1588	36926_at	MAPK6	X80692	mitogen-activated protein kinase 6	p97mapk
1589	38431_at	MAPK9	U09759	mitogen-activated protein kinase 9	protein kinase
1590	1238_at	MAPK9	U09759	mitogen-activated protein kinase 9	protein kinase
1591	1130_at	MAP2K1	L11284	mitogen-activated protein kinase kinase 1	mitogen-activated protein kinase kinase 1
1592	1327_s_at	MAP3K5	U67156	mitogen-activated protein kinase kinase kinase 5	mitogen-activated kinase kinase kinase 5
1593	36905_at	MAP3K7	AB009356	mitogen-activated protein kinase kinase kinase 7	TGF-beta activated kinase 1a
1594	38980_at	MAP3K7IP2	AB018276	mitogen-activated protein kinase kinase kinase 7 interacting protein 2	KIAA0733 protein
1595	35694_at	MAP4K4	AB014587	mitogen-activated protein kinase kinase kinase kinase 4	KIAA0687 protein
1596	36179_at	MAPKAPK2	U12779	mitogen-activated protein kinase-activated protein kinase 2	MAP kinase activated protein kinase 2
1597	1637_at	MAPKAPK3	U09578	mitogen-activated protein kinase-activated protein kinase 3	MAPKAP kinase
1598	41220_at	MSF	AB023208	MLL septin-like fusion	KIAA0991 protein
1599	38437_at	MLN51	X80199	MLN51 protein	MLN51 protein

G's 21

	A	B	C	D	E
1600	35273_at	MMS19L	AF007151	MMS19-like (MET18 homolog, S. cerevisiae)	MMS19 (MET18 S. cerevisiae)-like
1601	34767_at	MAP-1	A1670788	modulator of apoptosis 1	
1602	41771_g_at	MAOA	AA420624	monoamine oxidase A	monoamine oxidase A
1603	41772_at	MAOA	M68840	monoamine oxidase A	
1604	41770_at	MAOA	AA420624	monoamine oxidase A	
1605	37628_at	MAOB	M69177	monoamine oxidase B	monoamine oxidase B
1606	37565_at	MMD	X85750	monocyte to macrophage differentiation-associated	monocyte to macrophage differentiation-associated, precursor
1607	40861_at	MRGX	D14812	MORF-related gene X	MORF-related gene X
1608	33797_at	MPHOSPH10	X98494	M-phase phosphoprotein 10 (U3 small nuclear ribonucleoprotein)	M phase phosphoprotein 10
1609	34306_at	MBNL	AB007888	muscleblind-like (Drosophila)	muscleblind (Drosophila)-like
1610	35992_at	MSC	AF087036	musculin (activated B-cell factor-1)	musculin
1611	31884_at	MLH3	L40399	mutL homolog 3 (E. coli)	mutL homolog 3
1612	860_at	MSH2	U03911	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)	mutS homolog 2
1613	2003_s_at	MSH6	U28946	mutS homolog 6 (E. coli)	G/T mismatch binding protein
1614	33769_at	MPZL1	AF087020	myelin protein zero-like 1	protein zero related protein
1615	33146_at	MCL1	L08246	myeloid cell leukemia sequence 1 (BCL2-related)	myeloid cell leukemia sequence 1 (BCL2-related)
1616	277_at	MCL1	L08246	myeloid cell leukemia sequence 1 (BCL2-related)	myeloid cell leukemia sequence 1 (BCL2-related)
1617	39037_at	MLLT2	L13773	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 2	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 2
1618	41637_at	MYLE	AF108145	MYLE protein	DEXI
1619	41439_at	MYO1B	AJ001381	myosin IB	myh-1c
1620	35729_at	MYO1D	AB018270	myosin ID	KIAA0727 protein
1621	37631_at	MYO1E	U14391	myosin IE	myosin-IC
1622	38251_at	MLC1SA	A1127424	myosin light chain 1 slow a	myosin regulatory light chain
1623	41187_at	MLC-B	U26162	myosin regulatory light chain	KIAA0799 protein
1624	35362_at	MYO10	AB018342	myosin X	myosin, light polypeptide, regulatory, non-sarcomeric (20kD)
1625	33447_at	MLCB	X54304	myosin, light polypeptide, regulatory, non-sarcomeric (20kD)	myosin, light polypeptide, regulatory, non-sarcomeric (20kD)
1626	35739_at	MTMR3	AB002369	myotubularin related protein 3	myotubularin related protein 3

Fig 21

A	B	C	D	E
1627 39707_at	MTMR4	AB014547	myotubularin related protein 4	KIAA0647 protein
1628 38035_at	MTMR6	AF072928	myotubularin related protein 6	myotubularin related protein 6
1629 39607_at	MTMR8	AL080178	myotubularin related protein 8	hypothetical protein
1630 36692_at	MTMR8	AF052099	myotubularin related protein 8	
1631 32434_at	MARCKS	D10522	myristoylated alanine-rich protein kinase C substrate	80K-L protein
1632 39267_at	AGM1	AF102265	N-acetylglucosamine-phosphate mutase	N-acetylglucosamine-phosphate mutase
1633 36938_at	ASAH	U70063	N-acylsphingosine amidohydrolase (acid ceramidase)	acid ceramidase
1634 461_at	ASAH	U70063	N-acylsphingosine amidohydrolase (acid ceramidase)	acid ceramidase
1635 36169_at	NDUFA1	N47307	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1 (7.5kD, MWFE)	
1636 40546_s_at	NDUFA2	AF047185	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (8kD, B8)	NADH-ubiquinone oxidoreductase subunit C1
1637 38462_at	NDUFA5	U64028	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 (13kD, B13)	B8
1638 32752_at	NDUFA7	W72440	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (14.5kD, B14.5a)	NADPH:ubiquinone oxidoreductase subunit B13
1639 38605_at	NDUFB1	AI345944	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1 (7kD, MNLL)	
1640 38981_at	NDUFB3	AA203354	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3 (12kD, B12)	
1641 32232_at	NDUFB5	AF047181	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5 (16kD, SGDH)	NADH-ubiquinone oxidoreductase subunit C1
1642 32774_at	NDUFB8	AI541050	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASH1)	SGDH
1643 38485_at	NDUFC1	AA760866	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1 (6kD, KFYI)	
1644 38395_at	NDUFS1	X61100	NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase)	75 kDa subunit NADH dehydrogenase precursor
1645 38695_at	NDUFS4	AA203303	NADH dehydrogenase (ubiquinone) Fe-S protein 4 (18kD) (NADH-coenzyme Q reductase)	

6's 21



A	B	C	D	E
1646 38060_at	NDUFS5	A1541336	NADH dehydrogenase (ubiquinone) Fe-S protein 5 (15kD) (NADH-coenzyme Q reductase)	
1647 34893_at	NDUFV2	A1557064	NADH dehydrogenase (ubiquinone) flavoprotein 2 (24kD)	
1648 34519_at	NPR3	M59305	natriuretic peptide receptor C/guanylate cyclase C (atrial natriuretic peptide receptor C)	atrial natriuretic peptide clearance receptor
1649 34234_l_at	NKTR	A1688640	natural killer-tumor recognition sequence	
1650 41795_at	NCK1	X17576	NCK adaptor protein 1	NCK adaptor protein 1
1651 33357_at	NCKAP1	AB011159	NCK-associated protein 1	KIAA0587 protein
1652 36073_at	NDN	U35139	necdin homolog (mouse)	NECDIN related protein
1653 34202_at	DKFZP566B0846	AL050071	nectin 3	hypothetical protein
1654 34264_at	NESCA	AB026894	nesca protein	NESCA
1655 38719_at	NSF	U03985	N-ethylmaleimide-sensitive factor	N-ethylmaleimide-sensitive factor
1656 39356_at	NEDD4L	AB007899	neural precursor cell expressed, developmentally down-regulated 4-like	ubiquitin-protein ligase NEDD4-like
1657 40281_at	NEDD5	D63878	neural precursor cell expressed, developmentally down-regulated 5	neural precursor cell expressed, developmentally down-regulated 5
1658 1695_at	NEDD8	D23662	neural precursor cell expressed, developmentally down-regulated 8	ubiquitin-like protein
1659 37005_at	NBL1	D28124	neuroblastoma, suppression of tumorigenicity 1	neuroblastoma, suppression of tumorigenicity 1
1660 31896_at	NAG	AL050281	neuroblastoma-amplified protein	hypothetical protein
1661 37286_at	NRCAM	AB002341	neuronal cell adhesion molecule	neuronal cell adhesion molecule
1662 37673_at	NSMAF	X96586	neural sphingomyelinase (N-SMase) activation associated factor	FAN protein
1663 38692_at	NAB1	AF045451	NGF1-A binding protein 1 (EGR1 binding protein 1)	transcriptional regulatory protein p54
1664 34835_at	NCSTN	D87442	nicastatin	
1665 37032_at	NNMT	U08021	nicotinamide N-methyltransferase	nicotinamide N-methyltransferase
1666 41722_at	NNT	U40490	nicotinamide nucleotide transhydrogenase	nicotinamide nucleotide transhydrogenase
1667 35366_at	NID	M30269	nidogen (enactin)	nidogen
1668 753_at	NID2	D86425	nidogen 2	osteonidogen

Gig 21

	A	B	C	D	E
1669	37047_at	NPC1	AF002020	Niemann-Pick disease, type C1	Niemann-Pick C disease protein
1670	980_at	NPC1	AF002020	Niemann-Pick disease, type C1	Niemann-Pick C disease protein
1671	39345_at	NPC2	AI525834	Niemann-Pick disease, type C2	
1672	35153_at	NBS1	AF058696	Nijmegen breakage syndrome 1 (nibrin)	cell cycle regulatory protein p95
1673	36047_at	NEK1	AL050385	NIMA (never in mitosis gene a)-related kinase 1	
1674	35843_at	Nek8	L40402	NIMA-related kinase Nek8	
1675	40866_at	NIPSNAP1	AJ001258	nipsnap homolog 1 (C. elegans)	NIPSNAP1 protein
1676	33916_at	NISCH	AB023192	nischarin	KIAA0975 protein
1677	39165_at	NIFU	U47101	nitrogen fixation cluster-like	NifU-like protein
1678	36472_at	NMI	U32849	N-myc (and STAT) interactor	Nmi
1679	36933_at	NDRG1	D87953	N-myc downstream regulated gene 1	RTP
1680	41656_at	NMT2	AF043325	N-myristoyltransferase 2	N-myristoyltransferase 2
1681	39040_at	NCUBE1	W28360	non-canonical ubiquitin conjugating enzyme 1	
1682	39039_s_at	NCUBE1	AI557497	non-canonical ubiquitin conjugating enzyme 1	
1683	1521_at	NME1	X17620	non-metastatic cells 1, protein (NM23A) expressed in	Nm23 protein
1684	33415_at	NME2	X58965	non-metastatic cells 2, protein (NM23B) expressed in	NM23-H2 protein
1685	1980_s_at	NME2	X58965	non-metastatic cells 2, protein (NM23B) expressed in	NM23-H2 protein
1686	38527_at	NONO	U02493	non-POU domain containing, octamer-binding	54 kDa protein
1687	38750_at	NOTCH3	U97669	Notch homolog 3 (Drosophila)	Notch3
1688	34781_at	WS-3	D84145	novel RGD-containing protein	novel RGD-containing protein
1689	40122_at	NSAP1	AF037448	NS1-associated protein 1	Gry-rbp
1690	33752_at	NS1-BP	AB020657	NS1-binding protein	KIAA0850 protein
1691	35626_at	SGSH	U30894	N-sulfolucosamine sulfolucosylase (sulfamidase)	N-sulfolucosamine sulfolucosylase
1692	37352_at	SP100	M60618	nuclear antigen Sp100	nuclear autoantigen
1693	37353_g_at	SP100	M60618	nuclear antigen Sp100	nuclear autoantigen
1694	40901_at	GS2NA	U17989	nuclear autoantigen	GS2NA
1695	32789_at	NCBP2	AA149428	nuclear cap binding protein subunit 2, 20kD	

fig 21

A	B	C	D	E
1696 35836_at	NUDC	AB019408	nuclear distribution gene C homolog (A. nidulans)	nuclear distribution gene C (A. nidulans) homolog
1697 39782_at	C1D	X95592	nuclear DNA-binding protein	C1D protein
1698 40063_at	NDP52	U22897	nuclear domain 10 protein	NDP52
1699 853_at	NFE2L2	S74017	nuclear factor (erythroid-derived 2)-like 2	Nrf2
1700 38354_at	CEBPB; LAP; CRI	X52560	nuclear factor NF-IL6 (AA 1-345); Human gene for nuclear factor NF-IL6.	CCAAT/enhancer binding protein (C/EBP), beta
1701 40822_at	NFATC3	L41067	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3
1702 38438_at	NFKB1	M58603	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	nuclear factor kappa-B DNA binding subunit
1703 1377_at	NFKB1	M58603	gene enhancer in B-cells 1 (p105)	nuclear factor kappa-B DNA binding subunit
1704 1461_at	NFKBIA	M69043	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha
1705 37544_at	NFIL3	X64318	nuclear factor, interleukin 3 regulated	nuclear factor, interleukin 3 regulated
1706 38648_at	CI2	U80760	nuclear matrix transcription factor 4	CAGH1 alternate open reading frame
1707 40816_at	PWP1	L07758	nuclear phosphoprotein similar to S. cerevisiae PWP1	IEF SSP 9502
1708 34312_at	NCOA2	A1040324	nuclear receptor coactivator 2	Amplified in Breast Cancer
1709 33381_at	NCOA3	AF012108	nuclear receptor coactivator 3	Ret fused gene
1710 39174_at	NCOA4	X77548	nuclear receptor coactivator 4	nuclear factor RIP140
1711 40088_at	NRIP1	X84373	nuclear receptor interacting protein 1	
1712 39397_at	NR2F2	M64497	nuclear receptor subfamily 2, group F, member 2	apolipoprotein AI regulatory protein-1
1713 36690_at	NR3C1	M10901	nuclear receptor subfamily 3, group C, member 1	nuclear receptor subfamily 3, group C, member 1
1714 35302_at	NXF1	AJ132712	nuclear RNA export factor 1	nuclear RNA export factor 1
1715 37928_at	NFYB	AA621555	nuclear transcription factor Y, beta	
1716 34667_at	NFX1	U15306	nuclear transcription factor, X-box binding 1	NFX1
1717 33413_at	PRL-1	AF051160	nuclear; Homo sapiens tyrosine phosphatase (PRL-1) gene, complete cds.	tyrosine phosphatase

fig. 21

A	B	C	D	E
1718 32340_s_at	NSEP1	M85234	nuclease sensitive element binding protein 1	nuclease sensitive element binding protein-1
1719 35643_at	NUCB2	X76732	nucleobindin 2	NEFA protein
1720 36597_at	NOLC1	D21262	nucleolar and coiled-body phosphoprotein 1	ORF
1721 37520_at	HSA6591	AJ006591	nucleolar cysteine-rich protein	cysteine-rich protein
1722 36930_at	HUMAUANTIG	L05425	nucleolar GTPase	nucleolar GTPase
1723 39390_at	NUP133	AF052123	nucleoporin 133kD	
1724 32850_at	NUP153	Z25535	nucleoporin 153kD	
1725 39024_at	NUP98	AF042357	nucleoporin 98kD	nuclear pore complex protein hnup153
1726 571_at	NAP1L1	M86667	nucleosome assembly protein 1-like 1	nucleosome assembly protein 1-like 1
1727 743_at	NAP1L3	D50370	nucleosome assembly protein 1-like 3	nucleosome assembly protein
1728 32575_at	NAP1L4	U77456	nucleosome assembly protein 1-like 4	nucleosome assembly protein 2
1729 36127_g_at	NBP	U18919	nucleotide binding protein	nucleotide binding protein
1730 41584_at	NUDT3	AF062529	nudix (nucleoside diphosphate linked moiety X)-type motif 3	diphosphoinositol polyphosphate phosphohydrolase
1731 37693_at	NUMB	L40393	numb homolog (Drosophila)	numb homolog
			ob15e02.s1 NCL CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1323770 3' similar to SW:ROA3_HUMAN P51991 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A3 ; mRNA sequence.	
1732 35916_s_at	INHBC	AA877215	oculocerebrorenal syndrome of Lowe	ocr1
1733 34169_s_at	OCRL	U57627	olfactory receptor; Human olfactory receptor (OLF3) gene, complete cds.	HsOLF3
1734 31921_at	OLF3	U56421	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	hypothetical protein
1735 39507_at	OGT	AL050366	opioid growth factor receptor	Jul-60
1736 40332_at	OGFR	AF109134	optic atrophy 1 (autosomal dominant)	KIAA0567 protein
1737 39745_at	OPA1	AB011139	optineurin	optineurin
1738 41744_at	OPTN	AF070533	OR11-3; olfactory receptor; Homo sapiens OR7E12P pseudogene, complete sequence.	
1739 34539_at	OR7E12P	AF065854		

Fig-21

A	B	C	D	E
1740 AFFX-BioC-3_at bioA		J04423	ORF 1	7,8-diamino-pelargonic acid aminotransferase
1741 AFFX-BioB-M_at bioA		J04423	ORF 1	7,8-diamino-pelargonic acid aminotransferase
1742 AFFX-BioDn-5_a bioA		J04423	ORF 1	7,8-diamino-pelargonic acid aminotransferase
1743 AFFX-BioDn-3_a bioA		J04423	ORF 1	7,8-diamino-pelargonic acid aminotransferase
1744 AFFX-BioC-5_at bioA		J04423	ORF 1	7,8-diamino-pelargonic acid aminotransferase
1745 32412_at	RPS14	M13934	ORF; putative; Human ribosomal protein S14 gene, complete cds.	unknown protein; ribosomal protein S14
1746 1315_at	OAZ1	D78361	ORF1; ORF 2; no start codon; Human mRNA for ornithine decarboxylase antizyme, ORF 1 and ORF 2.	ornithine decarboxylase antizyme 1
1747 32800_at	RXRA; NR2B1	U66306	ORF-2; ORF-3; Human retinoid X receptor alpha mRNA, 3' UTR, partial sequence.	retinoid X receptor, alpha
1748 38155_at	ORC5L	U92538	origin recognition complex, subunit 5-like (yeast)	origin recognition complex subunit 5 homolog
1749 36636_at	OAT	M12267	ornithine aminotransferase (gyrate atrophy)	ornithine aminotransferase
1750 1959_at	OAZIN	D88674	ornithine decarboxylase antizyme inhibitor	antizyme inhibitor
1751 33367_s_at	OAZIN	D88674	ornithine decarboxylase antizyme inhibitor	antizyme inhibitor
1752 1081_at	ODC1	M33764	ornithine decarboxylase; Human ornithine decarboxylase gene, complete cds.	ornithine decarboxylase 1
1753 31700_at	GPR35	AF027957	orphan G protein-coupled receptor; Homo sapiens G protein-coupled receptor (GPR35) gene, complete cds.	G protein-coupled receptor
1754 1451_s_at	OSF-2	D13666	osteoblast specific factor 2 (fasciclin I-like)	osteoblast specific factor 2
1755 39774_at	OXA1L	X80695	oxidase (cytochrome c) assembly 1-like	oxidase (cytochrome c) assembly 1-like

Fig-21

	A	B	C	D	E
1756	39136_at	OSR1	AB017642	oxidative-stress responsive 1	oxidative-stress responsive 1
1757	41438_at	OSBPL8	AL049923	oxysterol binding protein-like 8	oxysterol-binding protein-like protein 8
1758	34329_at	PAK2	N25547	p21 (CDKN1A)-activated kinase 2	
1759	39710_at	P311	U30521	P311 protein	P311 HUM
1760	36136_at	PIG11	AF010315	p53-induced protein	Pig11
1761	40441_g_at	PAI-RBP1	AL080119	PAI-1 mRNA-binding protein	hypothetical protein
1762	40440_at	PAI-RBP1	AL080119	PAI-1 mRNA-binding protein	hypothetical protein
1763	32001_s_at	PACE4	M80482	paired basic amino acid cleaving system 4	subtilisin-like protease
					paired box gene 8, isoform PAX8A; paired box gene 8, isoform PAX8B; paired box gene 8, isoform PAX8C; paired box gene 8, isoform PAX8D; paired box gene 8, isoform PAX8E
1764	121_at	PAX8	X69699	paired box gene 8	homeobox protein
1765	40127_at	PMX1	M95929	paired mesoderm homeo box 1	KIAA0992 protein
1766	41191_at	KIAA0992	AB023209	palladin	paraoxonase
1767	40504_at	PON2	AF001601	paraoxonase 2	
				partially supported by FGGENES and GENSCAN	hypothetical protein
1768	36032_at	dJ167A19.1	AL031427	PC4 and SFRS1 interacting protein 2	DFS70
1769	39243_s_at	PSIP2	U94319	PCF11p homolog	KIAA0824 protein
1770	41665_at	PCF11	AB020631	PDGFA associated protein 1	
1771	38758_at	PDAP1	R98910	PDZ and LIM domain 1 (ellin)	carboxyl terminal LIM domain protein
1772	36937_s_at	PDLIM1	U90878	PDZ domain containing guanine nucleotide exchange factor(GEF)1	PDZ domain containing guanine nucleotide exchange factor(GEF)1
1773	32026_s_at	PDZ-GEF1	AB002311	PDZ domain containing guanine nucleotide exchange factor(GEF)1	
1774	34745_at	PDZ-GEF1	AF070570	PDZ domain containing guanine nucleotide exchange factor(GEF)1	
1775	40856_at	SERPINF1; PEDF	U29953	PEDF; Human pigment epithelium-derived factor gene, complete cds.	pigment epithelium-derived factor
1776	1491_at	PTX3	M31166	pentaxin-related gene, rapidly induced by IL-1 beta	tumor necrosis factor
1777	38465_at	PAM	M37721	peptidylglycine alpha-amidating monooxygenase	peptidylglycine alpha-amidating monooxygenase
1778	35823_at	PIPB	M63573	peptidylprolyl isomerase B (cyclophilin B)	secreted cyclophilin-like protein

fig-21

A	B	C	D	E
1779 37422_at	PPIC	S71018	peptidylprolyl isomerase C (cyclophilin C)	cyclophilin C
1780 37385_at	PPIG	U40763	peptidyl-prolyl isomerase G (cyclophilin G)	CARS-Cyp
1781 36829_at	PER1	AF022991	period homolog 1 (Drosophila)	Rigui
1782 35835_at	PDL-108	AB019409	periodontal ligament fibroblast protein	
			peripheral benzodiazepine receptor; Human peripheral benzodiazepine receptor (hpb) mRNA, complete cds.	peripheral benzodiazepine receptor; peripheral benzodiazepine receptor short form
1783 32806_at	BZRP; MBR; PBR	M36035		PMP-22(PAS-II/SR13/Gas-3)
1784 36653_at	PMP22	D11428	peripheral myelin protein 22	
1785 41213_at	PRDX1	X67951	peroxiredoxin 1	peroxiredoxin 1
1786 36631_at	PRDX3	D49396	peroxiredoxin 3	Aop1_Human, MER5(Aop1_Mouse)-like protein
1787 38435_at	PRDX4	U25182	peroxiredoxin 4	antioxidant enzyme AOE37-2
1788 37900_at	PEX11B	AF093670	peroxisomal biogenesis factor 11B	peroxisomal biogenesis factor
1789 36864_at	PEX3	AJ001625	peroxisomal biogenesis factor 3	Pex3 protein
			peroxisomal long-chain acyl-coA thioesterase	peroxisomal long-chain acyl-coA thioesterase
1790 36625_at	ZAP128	L40401		
			peroxisomal membrane protein 3 (35kD, Zellweger syndrome)	peroxisome assembly factor-1
1791 33265_at	PXMP3	M86852		KIAA0834 protein
1792 36502_at	PFTK1	AB020641	PFTAIRE protein kinase 1	
1793 37694_at	PHF3	D87685	PHD finger protein 3	PHD finger protein 3
				PHD zinc finger protein XAP135, isoform a; PHD zinc finger protein XAP135, isoform b
1794 39381_at	XAP135	AF055030	PHD zinc finger protein XAP135	
			phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	MMAC1
1795 1434_at	PTEN	U92436		type-2 phosphatidic acid phosphatase alpha- 1
1796 34797_at	PPAP2A	AF014402	phosphatidic acid phosphatase type 2A	
1797 33862_at	PPAP2B	AF017786	phosphatidic acid phosphatase type 2B	phosphatidic acid phosphohydrolase homolog
1798 40783_s_at	PIK4CA	L36151	phosphatidylinositol 4-kinase, catalytic, alpha polypeptide	phosphatidylinositol 4-kinase
1799 37685_at	PICALM	U45976	phosphatidylinositol binding clathrin assembly protein	CALM

Fig. 21

	A	B	C	D	E
1800	39993_at	PIGA	D11466	phosphatidylinositol glycan, class A (paroxysmal nocturnal hemoglobinuria)	PIG-A protein
1801	314_at	PIGB	D42138	phosphatidylinositol glycan, class B	PIG-B
1802	751_at	PIGC	D85418	phosphatidylinositol glycan, class C	phosphatidylinositol-glycan-class C (PIG-C)
1803	776_at	PIGF	D13435	phosphatidylinositol glycan, class F	PIG-F
1804	40629_at	PIGH	L19783	phosphatidylinositol glycan, class H	phosphatidylinositol glycan, class H
1805	38297_at	PITPNM	X98654	phosphatidylinositol transfer protein, membrane-associated	homologue of Drosophila retinal degeneration B gene
1806	35741_at	PIP5K2B	U85245	phosphatidylinositol-4-phosphate 5-kinase, type II, beta	phosphatidylinositol-4-phosphate 5-kinase type II beta
1807	37320_at	PTDSS1	D14694	phosphatidylserine synthase 1	phosphatidylserine synthase 1
1808	33705_at	PDE4B	L20971	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 duncce homolog, Drosophila)	phosphodiesterase
1809	39422_at	PDE4DIP	AB007923	phosphodiesterase 4D interacting protein (myomegalin)	KIAA0454 protein
1810	37676_at	PDE8A	AF056490	phosphodiesterase 8A	cAMP-specific phosphodiesterase 8A
1811	37188_at	PCK2	X92720	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	phosphoenolpyruvate carboxykinase (GTP)
1812	39175_at	PFKP	D25328	phosphofructokinase, platelet	platelet-type phosphofructokinase
1813	32210_at	PGM1	M83088	phosphoglucomutase 1	phosphoglucomutase 1
1814	36963_at	PGD	U30255	phosphogluconate dehydrogenase	phosphogluconate dehydrogenase
1815	37677_at	PGK1	V00572	phosphoglycerate kinase 1	phosphoglycerate kinase 1
1816	41221_at	PGAM1	J04173	phosphoglycerate mutase 1 (brain)	phosphoglycerate mutase 2
1817	35665_at	PIK3C3	Z46973	phosphoinositide-3-kinase, class 3	phosphatidylinositol 3-kinase
1818	1269_at	PIK3R1	M61906	phosphoinositide-3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)	
1819	37961_at	PIK3R3	U90907	phosphoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma)	
1820	32775_r_at	PLSCR1	AB006746	phospholipid scramblase 1	phospholipid scramblase 1
1821	32260_at	PEA15	X86809	phosphoprotein enriched in astrocytes 15	
1822	36489_at	PRPS1	D00860	phosphoribosyl pyrophosphate synthetase 1	phosphoribosyl pyrophosphate synthetase subunit I

Fig. 21



A	B	C	D	E
1823 37338_at	PRPSAP1	D61391	phosphoribosyl pyrophosphate synthetase-associated protein 1	phosphoribosyl pyrophosphate synthetase-associated protein 39
1824 39056_at			phosphoribosylaminimidazole carboxylase, phosphoribosylaminimidazole succinocarboxamide synthetase	phosphoribosylaminimidazole carboxylase, phosphoribosylaminoribosylaminimidazole succinocarboxamide synthetase
1825 37392_at	PAICS	X53793	phosphorylase kinase, beta	phosphorylase kinase
1826 36667_at	PHKB	X84908	phosphorylase kinase, brain	glycogen phosphorylase B
1827 32724_at	PYGB	U47025	phosphorylase, glycogen; brain	peroxisomal phytanoyl-CoA alpha-hydroxylase
1828 33543_s_at	PHYH	AF023462	phytanoyl-CoA hydroxylase (Refsum disease)	pinin
1829 39003_at	PNN	U77718	pinin, desmosome associated protein	pinin
1830 34793_s_at	PTTG1IP	Z50022	pituitary tumor-transforming 1 interacting protein	putative surface glycoprotein
1831 32569_at	PLS3	M22299	plasmin 3 (T isoform)	T-plasmin polypeptide
1832 1731_at	PAFAH1B1	L13385	platelet-activating factor acetylhydrolase, isoform 1b, alpha subunit (45kD)	Miller-Dieker lissencephaly protein
1833 38666_at	PDGFRA	M21574	platelet-derived growth factor receptor, alpha polypeptide	platelet-derived growth factor receptor A chain
1834 38741_at	PSCD1	M85169	pleckstrin homology, Sec7 and coiled/coiled domains 1 (cytohesin 1)	cytohesin 1, isoform 1; cytohesin 1, isoform 2
1835 36943_r_at	PSCD2	U70728	pleckstrin homology, Sec7 and coiled/coiled domains 2 (cytohesin-2)	cytohesin-2
1836 34780_at	PLXNB2	U81992	pleiomorphic adenoma gene-like 1	C2H2 zinc finger protein PLAGL1
1837 32193_at	PLXNC1	AB002313	plexin B2	plexin B2
1838 38270_at	PARG	AF030339	plexin C1	VESPR
1839 31951_s_at	PABPC1	AF005043	poly (ADP-ribose) glycohydrolase	poly (ADP-ribose) glycohydrolase
1840 31950_at	PABPC1	Z48501	poly (A) binding protein, cytoplasmic 1	polyadenylate binding protein II
1841 36003_at	PARN	Y00345	poly (A) binding protein, cytoplasmic 1	poly (A) binding protein, cytoplasmic 1
1842 34305_at	PCBP1	AJ005698	poly (A)-specific ribonuclease (deadenylation nuclease)	poly (A)-specific ribonuclease sub2.3
1843 35746_r_at	PCBP2	Z29505	poly (rC) binding protein 1	hnRNP-E2
1844 35745_l_at	PCBP2	X78136	poly (rC) binding protein 2	hnRNP-E2
1845 39868_at	PCBP3	X78136	poly (rC) binding protein 2	
		AL046394	poly (rC) binding protein 3	

fig-21

	A	B	C	D	E
1846	38120_at	PKD2	U50928	polycystic kidney disease 2 (autosomal dominant)	polycystin 2
1847	33380_at	POLS	AB005754	polymerase (DNA directed) sigma	LAK-1
1848	38702_at	POLE3	AF070640	polymerase (DNA directed), epsilon 3 (p17 subunit)	polymerase (DNA directed), epsilon 3 (p17 subunit)
1849	40791_at	POLR2A	X63564	polymerase (RNA) II (DNA directed) polypeptide A (220kD)	RNA polymerase II largest subunit
1850	39746_at	POLR2B	X63563	polymerase (RNA) II (DNA directed) polypeptide B (140kD)	RNA polymerase II 140 kDa subunit
1851	36027_at	POLR2F	AA418779	polymerase (RNA) II (DNA directed) polypeptide F	
1852	35631_at	POLR2H	U37689	polymerase (RNA) II (DNA directed) polypeptide H	RNA polymerase II subunit
1853	1248_at	POLR2H	U37689	polymerase (RNA) II (DNA directed) polypeptide H	RNA polymerase II subunit
1854	503_at	POLR2L	U37690	polymerase (RNA) II (DNA directed) polypeptide L (7.6kD)	RNA polymerase II subunit
1855	35841_at	POLR2L	N24355	polymerase (RNA) II (DNA directed) polypeptide L (7.6kD)	
1856	34320_at	PTRF	AL050224	polymerase I and transcript release factor	
1857	34005_at	PIGR	X73079	polymeric immunoglobulin receptor	Polymeric immunoglobulin receptor
1858	40593_at	PTBP1	X66975	polypyrimidine tract binding protein 1	nuclear ribonucleoprotein
1859	31600_s_at	PMS2L1	D38435	postmeiotic segregation increased 2-like 1	
1860	AFFX-CreX-5_at		X03453	pot. ORF1 (aa 1-73); ORF2, put. cre protein (aa 1-343); Bacteriophage P1 cre gene for recombinase protein.	
1861	AFFX-CreX-3_at		X03453	pot. ORF1 (aa 1-73); ORF2, put. cre protein (aa 1-343); Bacteriophage P1 cre gene for recombinase protein.	
1862	315_at	PRDM2	D45132	PR domain containing 2, with ZNF domain	zinc-finger DNA-binding protein
1863	32696_at	PBX3	X59841	pre-B-cell leukemia transcription factor 3	homeobox protein

Fig. 21

	A	B	C	D	E
1864	36666_at	P4HB	M22806	precursor; Human prolyl 4-hydroxylase beta-subunit and disulfide isomerase (P4HB) gene, exon 11, clones 6B-(1,3,5,6).	prolyl 4-hydroxylase beta-subunit
1865	34321_i_at	GS3786	D87120	predicted osteoblast protein	GS3786
1866	41003_at	PFDN4	U41816	prefoldin 4	C-1
1867	38698_at	PREI3	AL080070	preimplantation protein 3	hypothetical protein
1868	40269_at	PRP18	U51990	pre-mRNA processing factor 18	hPrp18
1869	38291_at	PENK	J00123	preproenkephalin (; Human enkephalin gene: exon 3 and 3'flank.	proenkephalin
1870	641_at	PSEN1	L76517	presenilin 1 (Alzheimer disease 3)	presenilin 1
1871	40621_at	PAWR	U63809	PRKC, apoptosis, WT1, regulator	prostate apoptosis response protein par-4
1872	41773_at	PCOLN3	U58048	procollagen (type III) N-endopeptidase	PRSM1
1873	31609_s_at	PCOLCE	L33799	procollagen C-endopeptidase enhancer	procollagen C-proteinase enhancer protein
1874	34795_at	PLOD2	U84573	procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2	lysyl hydroxylase isoform 2
1875	36184_at	PLOD	L06419	procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI)	lysyl hydroxylase
1876	37037_at	P4HA1	M24486	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I
1877	34390_at	P4HA2	U90441	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide II	prolyl 4-hydroxylase alpha (II) subunit
1878	691_g_at	P4HB	J02783	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55)	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55)
1879	38840_s_at	PFN2	L10678	profilin 2	profilin II
1880	38839_at	PFN2	AL096719	profilin 2	profilin 2 isoform b; profilin 2 isoform a
1881	38802_at	PGRMC1	Y12711	progesterone receptor membrane component 1	putative progesterone binding protein
1882	38821_at	PGRMC2	AJ002030	progesterone receptor membrane component 2	progesterone binding protein

Fig-21

A	B	C	D	E
1883 39035_at	DD5	AF006010	progesterone induced protein	progesterone induced protein
1884 39036_g_at	DD5	AF006010	progesterone induced protein	progesterone induced protein
1885 35218_at	PDCD10	AF022385	programmed cell death 10	TFAR15
1886 37569_at	PDCD6	AF035606	programmed cell death 6	calcium binding protein
1887 32212_at	PDCD8	AL049703	programmed cell death 8 (apoptosis-inducing factor)	hypothetical protein
1888 36592_at	PHB	S85655	prohibitin	prohibitin
1889 1884_s_at	PCNA	M15796	proliferating cell nuclear antigen	proliferating cell nuclear antigen
1890 41600_at	PA2G4	U59435	proliferation-associated 2G4, 38kD	cell cycle protein p38-2G4 homolog
1891 35978_at	PRRG1	AF009242	proline-rich Gla (G-carboxyglutamic acid) polypeptide 1	proline-rich Gla protein 1
1892 36023_at	PRH1	AI864120	proline-rich protein HaeIII subfamily 1	
1893 40803_at	PORIMIN	AL050161	pro-oncogene receptor inducing membrane injury gene	pro-oncogene receptor inducing membrane injury gene
1894 1348_s_at	PCCA	S79219	propionyl Coenzyme A carboxylase, alpha polypeptide	Propionyl-Coenzyme A carboxylase, alpha polypeptide precursor
1895 36561_at	PCCB	X73424	propionyl Coenzyme A carboxylase, beta polypeptide	propionyl-CoA carboxylase
1896 41032_at	PCSK5	U56387	proprotein convertase subtilisin/kexin type 5	protease PC6 isoform A
1897 36795_at	PSAP	J03077	prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)	prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)
1898 38406_f_at	PTGDS	AI207842	prostaglandin D2 synthase (21kD, brain)	
1899 828_at	PTGER2	U19487	prostaglandin E receptor 2 (subtype EP2), 53kD	prostaglandin E2 receptor
1900 1890_at	PLAB	AB000584	prostate differentiation factor	TGF-beta superfamily protein
1901 32611_at	PBP	X75252	prostatic binding protein	phosphatidylethanolamine binding protein
1902 719_g_at	PRSS11	D87258	protease, serine, 11 (IGF binding)	serin protease with IGF-binding motif
1903 718_at	PRSS11	D87258	protease, serine, 11 (IGF binding)	serin protease with IGF-binding motif
1904 33368_at	PRSS15	X76040	protease, serine, 15	Lon protease-like protein
1905 40078_at	SPUVE	AF015287	protease, serine, 23	serine protease
1906 39845_at	PRSS25	AF020760	protease, serine, 25	serine protease
1907 688_at	PSMC1	L02426	proteasome (prosome, macropain) 26S subunit, ATPase, 1	26S protease (S4) regulatory subunit

Fig. 21

262/303

A	B	C	D	E
1908 35353_at	PSMC2	D11094	proteasome (prosome, macropain) 26S subunit, ATPase, 2	MSS1 protein
1909 592_at	PSMC3	M34079	proteasome (prosome, macropain) 26S subunit, ATPase, 3	proteasome (prosome, macropain) 26S subunit, ATPase, 3
1910 37766_s_at	PSMC5	AF035309	proteasome (prosome, macropain) 26S subunit, ATPase, 5	
1911 949_s_at	PSMC6	D78275	proteasome (prosome, macropain) 26S subunit, ATPase, 6	proteasome subunit p42
1912 1314_at	PSMD1	D44466	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	proteasome subunit p112
1913 1192_at	PSMD12	AB003103	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	26S proteasome subunit p55
1914 32240_at	PSMD5	D31889	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5
1915 945_at	PSMD7	D50063	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog)	proteasome subunit p40 / Mov34 protein
1916 40276_at	PSMD7	D50063	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog)	proteasome subunit p40 / Mov34 protein
1917 32584_at	PSMD8	D38047	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	26S proteasome subunit p31
1918 36492_at	PSMD9	AI347155	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	
1919 41171_at	PSME2	D45248	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)	proteasome activator hPA28 suunit beta
1920 1184_at	PSME2	D45248	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)	proteasome activator hPA28 suunit beta
1921 36974_at	PSMF1	D88378	proteasome (prosome, macropain) inhibitor subunit 1 (Pl31)	proteasome inhibitor hPl31 subunit
1922 38371_at	PSMA1	M64992	proteasome (prosome, macropain) subunit, alpha type, 1	prosomeal protein P30-33K
1923 1446_at	PSMA2	D00760	proteasome (prosome, macropain) subunit, alpha type, 2	proteasome (prosome, macropain) subunit, alpha type, 2
1924 1448_at	PSMA3	D00762	proteasome (prosome, macropain) subunit, alpha type, 3	proteasome (prosome, macropain) subunit, alpha type, 3

Fig 21

	A	B	C	D	E
1925	1450_g_at	PSMA4	D00763	proteasome (prosome, macropain) subunit, alpha type, 4	proteasome (prosome, macropain) subunit, alpha type, 4
1926	1449_at	PSMA4	D00763	proteasome (prosome, macropain) subunit, alpha type, 4	proteasome (prosome, macropain) subunit, alpha type, 4
1927	37046_at	PSMA5	A1246726	proteasome (prosome, macropain) subunit, alpha type, 5	
1928	36122_at	PSMA6	X59417	proteasome (prosome, macropain) subunit, alpha type, 6	prosomeal P27K protein
1929	1447_at	PSMB1	D00761	proteasome (prosome, macropain) subunit, beta type, 1	proteasome (prosome, macropain) subunit, beta type, 1
1930	1310_at	PSMB2	D26599	proteasome (prosome, macropain) subunit, beta type, 2	proteasome subunit HsC7-l
1931	33154_at	PSMB4	D26600	proteasome (prosome, macropain) subunit, beta type, 4	proteasome subunit HsN3
1932	1311_at	PSMB4	D26600	proteasome (prosome, macropain) subunit, beta type, 4	proteasome subunit HsN3
1933	37666_at	PSMB5	D29011	proteasome (prosome, macropain) subunit, beta type, 5	proteasome subunit X
1934	941_at	PSMB6	D29012	proteasome (prosome, macropain) subunit, beta type, 6	proteasome subunit Y
1935	39060_at	PSMB7	D38048	proteasome (prosome, macropain) subunit, beta type, 7	proteasome subunit z
1936	1313_at	PSMB7	D38048	proteasome (prosome, macropain) subunit, beta type, 7	proteasome subunit z
1937	38287_at	PSMB9	AA808961	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protease 2)	
1938	41750_at	P5	D49489	protein disulfide isomerase-related protein	human P5
1939	32558_at	PIAS3	AB021868	protein inhibitor of activated STAT3	protein inhibitor of activated STAT3
1940	34376_at	PKIG	AB019517	protein kinase (cAMP-dependent, catalytic) inhibitor gamma	protein kinase inhibitor gamma
1941	36957_at	PRKCBP1	W22296	protein kinase C binding protein 1	
1942	1602_at	PRKCI	L33881	protein kinase C, iota	protein kinase C iota
1943	1603_g_at	PRKCI	L33881	protein kinase C, iota	protein kinase C iota
1944	36835_at	PRKCL2	U33052	protein kinase C-like 2	PRK2

fig. 21

	A	B	C	D	E
1945	41768_at	PRKAR1A	M33336	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	cAMP-dependent protein kinase type I-alpha subunit
1946	227_g_at	PRKAR1A	M33336	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	cAMP-dependent protein kinase type I-alpha subunit
1947	226_at	PRKAR1A	M33336	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	cAMP-dependent protein kinase type I-alpha subunit
1948	32205_at	PRKRA	AF072860	protein kinase, interferon-inducible double stranded RNA dependent activator	protein activator of the interferon-induced protein kinase
1949	37725_at	PPP1CC	X74008	protein phosphatase 1, catalytic subunit, gamma isoform	serine /threonine specific protein phosphatase
1950	40438_at	PPP1R12A	D87930	protein phosphatase 1, regulatory (inhibitor) subunit 12A	myosin phosphatase target subunit 1
1951	39366_at	PPP1R3C	N36638	protein phosphatase 1, regulatory (inhibitor) subunit 3C	
1952	41540_at	PPP1R7	Z50749	protein phosphatase 1, regulatory subunit 7	yeast sds22 homolog
1953	857_at	PPM1A	S87759	protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform	protein phosphatase 2C alpha
1954	36501_at	PPM1A	S87759	protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform	protein phosphatase 2C alpha
1955	37107_at	PPM1D	U78305	protein phosphatase 1D magnesium-dependent, delta isoform	Wip1
1956	924_s_at	PPP2CB	J03805	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	
1957	41167_at	PPP2R2A	M64929	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform	protein phosphatase-2A subunit-alpha
1958	1383_at	PPP2R2A	M64929	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform	protein phosphatase-2A subunit-alpha
1959	32734_at	PPP2R5E	L76703	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform	protein phosphatase B56-epsilon

Fig. 21

	A	B	C	D	E
1960	40786_at	PPP2R5C	U37352	protein phosphatase 2, regulatory subunit B (B56), gamma isoform	protein phosphatase 2A B'alpha1 regulatory subunit
1961	176_at	PPP2R5C	U37352	protein phosphatase 2, regulatory subunit B (B56), gamma isoform	protein phosphatase 2A B'alpha1 regulatory subunit
1962	39127_f_at	PPP2R4	X73478	protein phosphatase 2A, regulatory subunit B' (PR 53)	phosphotyrosyl phosphatase activator
1963	38277_at	PPP3CB	M29550	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform (calcineurin A beta)	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform (calcineurin A beta)
1964	32541_at	PPP3CC	S46622	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma)	calcineurin A catalytic subunit
1965	34371_at	PPP4R1	U79267	protein phosphatase 4, regulatory subunit 1	
1966	37581_at	PPP6C	X92972	protein phosphatase 6, catalytic subunit	protein phosphatase 6
1967	35752_s_at	PROS1	M15036	protein S (alpha)	protein S (alpha)
1968	32564_at	SEC61B	AA083129	protein translocation complex beta	
1969	1064_at	PTK9	U02680	protein tyrosine kinase 9	protein tyrosine kinase
1970	843_at	PTP4A1	U48296	protein tyrosine phosphatase type IVA, member 1	protein tyrosine phosphatase PTPCAAX1
1971	38415_at	PTP4A2	U14603	protein tyrosine phosphatase type IVA, member 2	protein-tyrosine phosphatase
1972	1241_at	PTP4A2	U14603	protein tyrosine phosphatase type IVA, member 2	protein-tyrosine phosphatase
1973	40137_at	PTPN1	M31724	protein tyrosine phosphatase, non-receptor type 1	protein tyrosine phosphatase, non-receptor type 1
1974	1463_at	PTPN12	M93425	protein tyrosine phosphatase, non-receptor type 12	protein tyrosine phosphatase
1975	34198_at	PTPN13	U12128	protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)	protein tyrosine phosphatase 1E
1976	1496_at	PTPRA	M34668	protein tyrosine phosphatase, receptor type, A	protein tyrosine phosphatase, receptor type, A, isoform 1 precursor; protein tyrosine phosphatase, receptor type, A, isoform 2 precursor

Fig. 21



	A	B	C	D	E
1977 36204_at		PTPRF	Y00815	protein tyrosine phosphatase, receptor type, F	put. LAR preprotein (AA -16 to 188i)
1978 41780_at		PPFIA1	U22816	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1	LAR-interacting protein 1b
1979 1488_at		PTPRK	L77886	protein tyrosine phosphatase, receptor type, K	protein tyrosine phosphatase
1980 995_g_at		PTPRM	X58288	protein tyrosine phosphatase, receptor type, M	protein-tyrosine phosphatase
1981 31892_at		PTPRM	X58288	protein tyrosine phosphatase, receptor type, M	protein-tyrosine phosphatase
1982 41141_at		PRKRI	AL049970	protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor)	hypothetical protein
1983 37737_at		PCMT1	D25547	protein-L-isoaspartate (D-aspartate) O-methyltransferase	PIMT isozyme I
1984 37736_at		PCMT1	D13892	protein-L-isoaspartate (D-aspartate) O-methyltransferase	carboxyl methyltransferase
1985 32227_at		PRG1	X17042	proteoglycan 1, secretory granule	proteoglycan 1, secretory granule
1986 38590_r_at		PTMA	M14630	prothymosin, alpha (gene sequence 28)	prothymosin, alpha (gene sequence 28)
1987 38589_i_at		PTMA	M14630	prothymosin, alpha (gene sequence 28)	prothymosin, alpha (gene sequence 28)
1988 37936_at		HPRP4P	A1184802	PRP4/STKWD splicing factor	
1989 31697_s_at		FTHP1	J04755	pseudoferritin H protein; Human ferritin H processed pseudogene, complete cds.	
1990 36117_at		PTK2	L13616	PTK2 protein tyrosine kinase 2	focal adhesion kinase
1991 40048_at		PUM1	D43951	pumilio homolog 1 (Drosophila)	KIAA0099 protein
1992 35359_at		PUM2	D87078	pumilio homolog 2 (Drosophila)	KIAA0235 protein
1993 35221_at		PURA	X91648	purine-rich element binding protein A	
				put. ORFX (AA 1-75); beta subunit (AA 1-340); Human liver mRNA for beta-subunit signal transducing proteins Gs/Gi (beta-G).	guanine nucleotide-binding protein, beta-1 subunit
1994 33341_at		GNB1	X04526	putative 28 kDa protein	
1995 33720_at		LOC56902	L48692	putative breast adenocarcinoma marker (32kD)	BC-2 protein
1996 39363_at		BC-2	AF042384		

Fig. 21

A		B	C	D	E
1997	39884_g_at	HSA9761	AF091078	putative dimethyladenosine transferase putative glioblastoma cell differentiation-related	putative dimethyladenosine transferase putative glioblastoma cell differentiation-related protein
1998	38841_at	GDBR1	AF068195		
1999	41188_at	LC27	W28186	putative integral membrane transporter	
2000	38984_at	KIAA0436	AB007896	putative L-type neutral amino acid transporter	
2001	39116_at	LOC54499	AF070626	putative membrane protein	
2002	35286_r_at	RY1	X76302	putative nucleic acid binding protein RY-1	nucleic acid binding protein
2003	36852_at	N33	U42349	Putative prostate cancer tumor suppressor	
2004	33710_at	C3F	U72515	putative protein similar to nessy (Drosophila)	C3f
2005	40203_at	SU11	AJ012375	putative translation initiation factor	putative translation initiation factor
2006	37678_at	NMA	U23070	putative transmembrane protein	putative transmembrane protein
				putative transmembrane protein; homolog of yeast Golgi membrane protein Ytl1p (Yip1p-interacting factor)	
2007	35326_at	54TM	AF004876	putative; Homo sapiens PTS gene, complete cds.	54TMp
2008	35697_at	PTS	L76259	putative; originally identified as an 'oncogene', product renamed by NCBI staff; Homo sapiens longation factor 1-alpha 1 (PTI-1) mRNA, complete cds.	6-pyruvoyltetrahydropterin synthase
2009	40887_g_at	PTI-1	L41498	putative; originally identified as an 'oncogene', product renamed by NCBI staff; Homo sapiens longation factor 1-alpha 1 (PTI-1) mRNA, complete cds.	longation factor 1-alpha 1
2010	40886_at	PTI-1	L41498	pVHL-interacting deubiquitinating enzyme 1	longation factor 1-alpha 1
2011	33219_at	VDU1	AB029020	Pyruvate dehydrogenase complex, lipoyl-containing component X; E3-binding protein	KIAA1097 protein
2012	36164_at	PDX1	U82328	pyruvate kinase, muscle	pyruvate dehydrogenase complex protein X subunit precursor
2013	32378_at	PKM2	M26252	quinoid dihydropteridine reductase	pyruvate kinase, muscle
2014	260_at	QDPR	M16447		quinoid dihydropteridine reductase

Fig. 21

	A	B	C	D	E
2015 36610_at	R3HDM		D21852	R3H domain (binds single-stranded nucleic acids) containing	KIAA0029 protein
2016 39030_at	RABAC1		AJ133534	Rab acceptor 1 (prenylated)	prenylated Rab acceptor 1 (PRA1)
2017 37703_at	RABGGTB		Y08201	Rab geranylgeranyltransferase, beta subunit	rab geranylgeranyl transferase
2018 38264_at	RABIF		U74324	RAB interacting factor	guanine nucleotide exchange factor mss4
2019 36660_at	RAB11A		AF000231	RAB11A, member RAS oncogene family	rab11a
2020 35325_at	RAB14		AF052113	RAB14, member RAS oncogene family	
2021 34393_r_at	RAB1A		AL050268	RAB1A, member RAS oncogene family	hypothetical protein
2022 34392_s_at	RAB1A		AL050268	RAB1A, member RAS oncogene family	hypothetical protein
2023 33326_at	RAB21		D42087	RAB21, member RAS oncogene family	RAB21, member RAS oncogene family
2024 809_at	RAB27A		U57094	RAB27A, member RAS oncogene family	Rab27a
2025 33371_s_at	RAB31		U59877	RAB31, member RAS oncogene family	low-Mr GTP-binding protein Rab31
2026 36110_at	RAB5A		M28215	RAB5A, member RAS oncogene family	GTP-binding protein
2027 35289_at	GAPCEN		AJ011679	rab6 GTPase activating protein (GAP and centrosome-associated)	Rab6 GTPase activating protein, GAPCenA
2028 35304_at	RAB6A		AF052130	RAB6A, member RAS oncogene family	
2029 39628_at	RAB9A		AI671547	RAB9A, member RAS oncogene family	
2030 41716_at	RC3		AB020663	rabconnectin-3	KIAA0856 protein
2031 37543_at	ARHGEF6		D25304	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	
2032 36857_at	RAD1		AF084513	RAD1 homolog (S. pombe)	DNA repair exonuclease
2033 38114_at	RAD21		D38551	RAD21 homolog (S. pombe)	RAD21 homolog
2034 1874_at	RAD23B		D21090	RAD23 homolog B (S. cerevisiae)	XP-C repair complementing protein (p58/HHR23B)
2035 32757_at	RAE1		U84720	RAE1 RNA export 1 homolog (S. pombe)	mRNA export protein
2036 1524_at			U46194	RAGE-4 ORF2; one of 2 possible coding regions; RAGE-4 ORF3; one of 2 possible coding regions; Human renal cell carcinoma antigen RAGE-4 mRNA, complete putative cds.	
2037 36628_at	RALBP1		L42542	ralA binding protein 1	RLIP76 protein
2038 37539_at	RGL		AB023176	RaIGDS-like gene	KIAA0959 protein

Fig. 21

	A	B	C	D	E
2039	41342_at	RANBP1	D38076	RAN binding protein 1	Ran-BP1 (Ran-binding protein 1)
2040	40824_at	RANBP16	AB018288	RAN binding protein 16	KIAA0745 protein
2041	41174_at	RANBP2L1	AF012086	RAN binding protein 2-like 1	Ran binding protein 2
2042	35255_at	RANBP7	AF098799	RAN binding protein 7	RanBP7/importin 7
2043	32602_at	RAP1GDS1	X63465	RAP1, GTP-GDP dissociation stimulator 1	smg GDS
2044	1848_at	RAP1A	M22995	RAP1A, member of RAS oncogene family	ras-related protein
2045	40146_at	RAP1B	AL080212	RAP1B, member of RAS oncogene family	hypothetical protein
2046	39601_at	RASSF1	AF061836	Ras association (RalGDS/AF-6) domain family 1	putative tumor suppressor protein
2047	37598_at	RASSF2	D79990	Ras association (RalGDS/AF-6) domain family 2	Ras association (RalGDS/AF-6) domain family 2
2048	1659_s_at	RHEB2	D78132	Ras homolog enriched in brain 2	ras-related GTP-binding protein
2049	37309_at	ARHA	L09159	ras homolog gene family, member A	multidrug resistance protein
2050	1394_at	ARHA	L25080	ras homolog gene family, member A	GTP-binding protein
2051	35803_at	ARHE	S82240	ras homolog gene family, member E	RhoE
2052	36935_at	RASA1	M23379	RAS p21 protein activator (GTPase activating protein) 1	GTPase-activating protein
2053	1675_at	RASA1	M23379	RAS p21 protein activator (GTPase activating protein) 1	GTPase-activating protein
2054	35793_at	G3BP2	AB014560	Ras-GTPase activating protein SH3 domain-binding protein 2	KIAA0660 protein
2055	40864_at	RAC1	D25274	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	
2056	2050_s_at	RAC1	M29870	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	ras-related C3 botulinum toxin substrate 1 isoform Rac1; ras-related C3 botulinum toxin substrate 1 isoform Rac1b
2057	35316_at	RAGA	U41654	Ras-related GTP-binding protein	adenovirus E3-14.7K interacting protein 1
2058	33234_at	BCAA	AA887480	RBP1-like protein	
2059	41407_at	RDBP	L03411	RD RNA-binding protein	RD protein
2060	34684_at	RECQL	L36140	RecQ protein-like (DNA helicase Q1-like)	DNA helicase

Fig. 21

A	B	C	D	E
2061 34685_at	RECQL	AI685944	RecQ protein-like (DNA helicase Q1-like) regulated at the translational level; contains l-mfa domain; utilizes unique GTG start codon; Homo sapiens HIC protein isoform p40 and HIC protein isoform p32 mRNAs, complete cds.	HIC protein isoform p40; HIC protein isoform p32
2062 37842_at	HIC	AF054589	regulator of G-protein signalling 19	RGS-GAIP interacting protein GIPC
2063 35756_at	RGS19IP1	AF089816	interacting protein 1	helix-loop-helix phosphoprotein
2064 37701_at	RGS2	L13463	regulator of G-protein signalling 2, 24kD	hypothetical protein
2065 35722_at	RENT2	AL080198	regulator of nonsense transcripts 2	
2066 32827_at	RRAS2	AI365215	related RAS viral (r-ras) oncogene homolog 2	
2067 34845_at	dJ796117.4	AL035398	remainder of gene in clone 549K18 (AL023654)	CGI-51 protein
2068 1055_g_at	RFC4	M87339	replication factor C (activator 1) 4 (37kD)	replication factor C, 37-kDa subunit
2069 38481_at	RPA1	M63488	replication protein A1 (70kD)	replication protein A, 70-kDa subunit
2070 652_g_at	RPA3	L07493	replication protein A3 (14kD)	replication protein A 14kDa subunit
2071 37651_at	RCOR	D31888	REST corepressor	REST corepressor
2072 34350_at	RSN	X64838	restin (Reed-Steinberg cell-expressed intermediate filament-associated protein)	restin
2073 31851_at	RFP2	AJ224819	ret finger protein 2	tumor suppressor
2074 40556_at	RCN1	D42073	reticulocalbin 1, EF-hand calcium binding domain	reticulocalbin
2075 37727_i_at	RCN2	X78669	reticulocalbin 2, EF-hand calcium binding domain	EF-hand protein
2076 37728_r_at	RCN2	X78669	reticulocalbin 2, EF-hand calcium binding domain	EF-hand protein
2077 31536_at	RTN4	AB020693	reticulocalbin 4	KIAA0886 protein
2078 39964_at	RP2	AJ007590	retinitis pigmentosa 2 (X-linked recessive)	XRP2 protein
2079 38164_at	RPGR	U57629	retinitis pigmentosa GTPase regulator	retinitis pigmentosa GTPase regulator
2080 2044_s_at	RB1	M15400	retinoblastoma 1 (including osteosarcoma)	retinoblastoma 1 (including osteosarcoma)

Fig. 21

A		B	C	D	E
2081	35227_at	RBBP8	U72066	retinoblastoma binding protein 8	CtBP interacting protein CtBP
2082	33860_at	RBAF600	AB007931	retinoblastoma-associated factor 600	KIAA0462 protein
2083	32597_at	RBL2	X76061	retinoblastoma-like 2 (p130)	130K protein
2084	35848_at	RAI17	AL049432	retinoic acid induced 17	
				retropseudogene; Human	
				retropseudogene MSSP-1 DNA, complete	MSSP-1
2085	31672_g_at	RBMS1P; MSSP1	D82351	cds.	
2086	38908_s_at	REV3L	AL096744	REV3-like, catalytic subunit of DNA polymerase zeta (yeast)	hypothetical protein
2087	35236_g_at	RECK	AA099265	reversion-inducing-cysteine-rich protein with kazal motifs	
2088	35235_at	RECK	AA099265	reversion-inducing-cysteine-rich protein with kazal motifs	
2089	35234_at	RECK	D50406	reversion-inducing-cysteine-rich protein with kazal motifs	RECK protein precursor
2090	553_g_at	ARHGAP1	U02570	Rho GTPase activating protein 1	CDC42 GTPase-activating protein
2091	39700_at	ARHGAP1	A1961929	Rho GTPase activating protein 1	
2092	34180_at	ARHGEF10	AB002292	Rho guanine nucleotide exchange factor (GEF) 10	Rho guanine nucleotide exchange factor 10
2093	40828_at	ARHGEF7	D63476	Rho guanine nucleotide exchange factor (GEF) 7	PAK-interacting exchange factor beta
2094	40100_at	ARHGEF2	U72206	rho/rac guanine nucleotide exchange factor (GEF) 2	guanine nucleotide regulatory factor
2095	36537_at	P114-RHO-GEF	AB011093	Rho-specific guanine nucleotide exchange factor p114	KIAA0521 protein
2096	41040_at	RPP38	U77664	ribonuclease P (38kD)	RNaseP protein P38
2097	32664_at	RNASE4	D37931	ribonuclease, RNase A family, 4	RNase 4
2098	36187_at	RNH	X13973	ribonuclease/angiogenin inhibitor	ribonuclease/angiogenin inhibitor
2099	34314_at	RRM1	X59543	ribonucleotide reductase M1 polypeptide	M1 subunit of ribonucleotide reductase
2100	2016_s_at	RPL10	M64241	ribosomal protein L10	Wilm's tumor-related protein
2101	41178_at	RPL11	X79234	ribosomal protein L11	ribosomal protein L11
2102	33668_at	RPL12	AF037643	ribosomal protein L12	ribosomal protein L13
2103	31509_at	RPL13	X64707	ribosomal protein L13	23 kD highly basic protein
2104	35119_at	RPL13A	X56932	ribosomal protein L13a	ribosomal protein L14
2105	31907_at	RPL14	D87735	ribosomal protein L14	

Fig. 21

	A	B	C	D	E
2106	32432_f_at	RPL15	L25899	ribosomal protein L15	ribosomal protein L10
2107	32440_at	RPL17	X53777	ribosomal protein L17	ribosomal protein L17
2108	31546_at	RPL18	L11566	ribosomal protein L18	ribosomal protein L18
2109	33614_at	RPL18A	X80822	ribosomal protein L18a	ribosomal protein L18a
2110	32435_at	RPL19	X63527	ribosomal protein L19	ribosomal protein L19
2111	32337_at	RPL21	U25789	ribosomal protein L21	ribosomal protein L21
2112	33451_s_at	RPL22	A1526079	ribosomal protein L22	
2113	32395_r_at	RPL23	X55954	ribosomal protein L23	HL23 ribosomal protein
2114	32394_s_at	RPL23	X55954	ribosomal protein L23	HL23 ribosomal protein
2115	32341_f_at	RPL23A	U37230	ribosomal protein L23a	ribosomal protein L23a
2116	33677_at	RPL24	M94314	ribosomal protein L24	ribosomal protein L30
2117	32444_at	RPL26	X69392	ribosomal protein L26	ribosomal protein L26
2118	39830_at	RPL27	AA044823	ribosomal protein L27	
2119	32436_at	RPL27A	U14968	ribosomal protein L27a	ribosomal protein L27a
2120	31708_at	RPL30	L05095	ribosomal protein L30	ribosomal protein L30
2121	33676_at	RPL31	X15940	ribosomal protein L31	ribosomal protein L31
2122	32276_at	RPL32	X03342	ribosomal protein L32	ribosomal protein L32
2123	33657_at	RPL34	L38941	ribosomal protein L34	ribosomal protein L34
2124	41765_at	RPL35	A1541285	ribosomal protein L35	
2125	41152_f_at	RPL36A	T89651	ribosomal protein L36a	
2126	33656_at	RPL37	D23661	ribosomal protein L37	ribosomal protein L37
2127	31962_at	RPL37A	L06499	ribosomal protein L37a	ribosomal protein L37a
2128	34085_at	RPL38	Z26876	ribosomal protein L38	ribosomal protein
2129	33485_at	RPL4	D23660	ribosomal protein L4	ribosomal protein
2130	32466_at	RPL41	Z12962	ribosomal protein L41	human homologue to yeast ribosomal protein YL41
2131	33660_at	RPL5	U14966	ribosomal protein L5	ribosomal protein L5
2132	31952_at	RPL6	X69391	ribosomal protein L6	ribosomal protein L6
2133	36333_at	RPL7	X57958	ribosomal protein L7	ribosomal protein L7
2134	31505_at	RPL8	Z28407	ribosomal protein L8	ribosomal protein L8
2135	31568_at	RPS10	U14972	ribosomal protein S10	ribosomal protein S10
2136	32330_at	RPS11	X06617	ribosomal protein S11	ribosomal protein S11
2137	33116_f_at	RPS12	AA977163	ribosomal protein S12	
2138	33619_at	RPS13	L01124	ribosomal protein S13	ribosomal protein S13
2139	34317_g_at	RPS15A	W52024	ribosomal protein S15a	ribosomal protein S15a
2140	38061_at	RPS16	A1541256	ribosomal protein S16	

Fig. 21

	A	B	C	D	E
2141	34593_g_at	RPS17	M13932	ribosomal protein S17	ribosomal protein S17
2142	34592_at	RPS17	M13932	ribosomal protein S17	ribosomal protein S17
2143	31330_at	RPS19	M81757	ribosomal protein S19	S19 ribosomal protein
2144	31527_at	RPS2	X17206	ribosomal protein S2	ribosomal protein S2
2145	32438_at	RPS20	L06498	ribosomal protein S20	ribosomal protein S20
2146	347_s_at	RPS23	D14530	ribosomal protein S23	ribosomal protein
2147	32315_at	RPS24	M31520	ribosomal protein S24	ribosomal protein S24
2148	31573_at	RPS25	M64716	ribosomal protein S25	ribosomal protein
2149	32748_at	RPS27	A1557852	ribosomal protein S27 (metallopanstimulin 1)	
2150	34570_at	RPS27A	S79522	ribosomal protein S27a	ubiquitin carboxyl extension protein
2151	39798_at	RPS28	R87876	ribosomal protein S28	
2152	34645_at	RPS3	X55715	ribosomal protein S3	ribosomal protein S3
2153	1653_at	RPS3A	M84711	ribosomal protein S3A	v-los transformation effector protein
2154	34643_at	RPS4X	M58458	ribosomal protein S4, X-linked	ribosomal protein S4X isoform
2155	32437_at	RPS5	U14970	ribosomal protein S5	ribosomal protein S5
2156	31511_at	RPS9	U14971	ribosomal protein S9	ribosomal protein S9
2157	31538_at	RPLP0	M17885	ribosomal protein, large, P0	ribosomal protein P0
2158	31956_f_at	RPLP1	M17886	ribosomal protein, large, P1	ribosomal protein P1
2159	31957_r_at	RPLP1	M17886	ribosomal protein, large, P1	ribosomal protein P1
2160	33213_g_at	RRBP1	AF006751	ribosome binding protein 1 homolog 180kD (dog)	ES/130
2161	38331_at	RIT	Y07566	Ric-like, expressed in many tissues (Drosophila)	Ric-like, expressed in many tissues
2162	35656_at	RNF6	AJ010346	ring finger protein (C3H2C3 type) 6	RING-H2
2163	39150_at	RNF11	U69559	ring finger protein 11	
2164	35811_at	RNF13	AF037204	ring finger protein 13	RING zinc finger protein
2165	33343_at	RNF14	AB022663	ring finger protein 14	ring finger protein 14
2166	33484_at	RNF2	Y10571	ring finger protein 2	ring finger protein 2
2167	37964_at	RNF3	W25793	ring finger protein 3	
2168	35777_at	RNF4	AB000468	ring finger protein 4	zinc finger protein
				ring zinc-finger protein; escapes X chromosome inactivation; Human ring zinc finger protein (ZNF127-Xp) gene and 5' flanking sequence.	
2169	37650_at	ZNF127-Xp	U41315		ZNF127-Xp
2170	37732_at	RYBP	AL049940	RING1 and YY1 binding protein	

Fig. 21



	A	B	C	D	E
2171	38073_at	RNMT	AB007858	RNA (guanine-7-) methyltransferase	RNA (guanine-7-) methyltransferase
2172	41460_at	RBM14	AF080561	RNA binding motif protein 14	SYT interacting protein SIP
2173	41741_at	RBM3	U28686	RNA binding motif protein 3	RNPL
2174	35351_at	RBM4	U89505	RNA binding motif protein 4	Hlark
2175	32804_at	RBM5	AF091263	RNA binding motif protein 5	RNA binding motif protein 5
2176	40870_g_at	RBM6	AF069517	RNA binding motif protein 6	RNA binding protein DEF-3
2177	40260_g_at	RBM9	AL009266	RNA binding motif protein 9	hypothetical protein
2178	39731_at	RBMX	Z23064	RNA binding motif protein, X chromosome	hnRNP G protein
2179	33867_s_at	RBMS1	X77494	RNA binding motif, single stranded interacting protein 1	RNA binding motif, single stranded interacting protein 1, isoform a
2180	36186_at	RNPS1	L37368	RNA binding protein S1, serine-rich domain	RNA-binding protein
2181	35202_at	RNGTT	AF025654	RNA guanylyltransferase and 5'-phosphatase	mRNA capping enzyme
2182	33237_at	KIAA0801	AB018344	RNA helicase	KIAA0801 protein
2183	36045_at	RNAH	AJ223948	RNA helicase family	RNA helicase
2184	38762_at	RNAHP	AF083255	RNA helicase-related protein	RNA helicase-related protein
2185	38049_g_at	BPMS	D84110	RNA-binding protein gene with multiple splicing	RBP-MS/type 4
2186	38047_at	BPMS	D84109	RNA-binding protein gene with multiple splicing	RBP-MS/type 3
2187	38974_at	DJ-1	AF021819	RNA-binding protein regulatory subunit	RNA-binding protein regulatory subunit
2188	39725_at	RNPC2	L10910	RNA-binding region (RNP1, RRM) containing 2	splicing factor
2189	38011_at	RMP	AB006572	RPB5-mediated protein	RPB5 mediating protein
2190	35195_at	RTCD1	Y11651	RTC domain containing 1	phosphate cyclase
2191	943_at	RUNX1	D43968	runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene)	AML1b protein
2192	40124_at	RUVBL1	Y18418	RuvB-like 1 (E. coli)	erythrocyte cytosolic protein of 54 kDa, ECP-54
2193	35758_at	RUVBL2	AB024301	RuvB-like 2 (E. coli)	RuvB-like DNA helicase TIP49b
2194	39338_at	S100A10	AI201310	S100 calcium binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11))	

Fig. 21

275/303

	A	B	C	D	E
2195	36089_at	SAC2	AB023183	Sac domain-containing inositol phosphatase 2	KIAA0966 protein
2196	41101_at	SAC3	D87464	Sac domain-containing inositol phosphatase 3	KIAA0274 gene product
2197	36511_at	SACM1L	AB020658	SAC1 suppressor of actin mutations 1-like (yeast)	KIAA0851 protein
2198	34792_at	AHCYL1	AL049954	S-adenosylhomocysteine hydrolase-like 1	hypothetical protein
2199	41302_at	AHCYL1	R59606	S-adenosylhomocysteine hydrolase-like 1	
2200	36685_at	AMD1	W63793	S-adenosylmethionine decarboxylase 1	S-adenosylmethionine decarboxylase 1 precursor
2201	263_g_at	AMD1	M21154	S-adenosylmethionine decarboxylase 1	epsilon-sarcoglycan
2202	41449_at	SGCE	AJ000534	sarcoglycan, epsilon	SAS
2203	36083_at	SAS	U01160	sarcoma amplified sequence	schwannomin interacting protein 1
2204	36536_at	SCHIP1	AF070614	schwannomin interacting protein 1	SEC13 (S. cerevisiae)-like 1
2205	33423_g_at	SEC13L1	AF052155	SEC13-like 1 (S. cerevisiae)	SEC13 (S. cerevisiae)-like 1
2206	33422_at	SEC13L1	AF052155	SEC13-like 1 (S. cerevisiae)	SEC13 (S. cerevisiae)-like 1
2207	36207_at	SEC14L1	D67029	SEC14-like 1 (S. cerevisiae)	SEC14 (S. cerevisiae)-like 1
2208	39099_at	SEC23A	X97064	Sec23 homolog A (S. cerevisiae)	Sec23 protein
2209	34199_at	SEC24A	AJ131244	SEC24 related gene family, member A (S. cerevisiae)	Sec24A protein
2210	35845_at	SEC24B	AJ131245	SEC24 related gene family, member B (S. cerevisiae)	Sec24B protein
2211	32770_at	SEC24D	AB018298	SEC24 related gene family, member D (S. cerevisiae)	KIAA0755 protein
2212	34349_at	SEC63L	AJ011779	SEC63 protein	SEC63 protein
2213	32521_at	SFRP1	AF056087	secreted frizzled-related protein 1	secreted frizzled related protein
2214	34342_s_at	SPP1	AF052124	secreted phosphoprotein 1 (osteopontin, bone sialoprotein 1, early T-lymphocyte activation 1)	osteopontin
2215	671_at	SPARC	J03040	secreted protein, acidic, cysteine-rich (osteonectin)	secreted protein, acidic, cysteine-rich (osteonectin)
2216	34265_at	SGNE1	Y00757	secretory granule, neuroendocrine protein 1 (7B2 protein)	secretory granule, neuroendocrine protein 1 (7B2 protein)
2217	37405_at	SELENBP1	U29091	selenium binding protein 1	selenium-binding protein

fig. 21

	A	B	C	D	E
2218	39078_at	SPS2	U43286	selenophosphate synthetase 2	selenophosphate synthetase 2
2219	34363_at	SEPP1	Z11793	selenoprotein P, plasma, 1	selenoprotein P
2220	377_g_at	SEMA3C	AB000220	sema domain, immunoglobulin domain (lg), short basic domain, secreted, (semaphorin) 3C	semaphorin E
2221	376_at	SEMA3C	AB000220	sema domain, immunoglobulin domain (lg), short basic domain, secreted, (semaphorin) 3C	semaphorin E
2222	35666_at	SEMA3F	U38276	sema domain, immunoglobulin domain (lg), short basic domain, secreted, (semaphorin) 3F	semaphorin III family homolog
2223	38826_at	2-Sep	D50918	sepin 6	sepin 2
2224	40898_at	SQSTM1	U46751	sequestosome 1	phosphotyrosine independent ligand for the Lck SH2 domain p62
2225	34789_at	SERPINEB6	S69272	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6	cytoplasmic antiproteinase
2226	38125_at	SERPINE1	M14083	serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1
2227	39167_r_at	SERPINEH2	D83174	serine (or cysteine) proteinase inhibitor, clade H (heat shock protein 47), member 2	collagen binding protein 2
2228	38818_at	SPTLC1	Y08685	serine palmitoyltransferase, long chain base subunit 1	serine palmitoyltransferase, subunit I
2229	40966_at	STK39	AF099989	serine threonine kinase 39 (STE20/SPS1 homolog, yeast)	Ste-20 related kinase SPAK
2230	41737_at	SRRM1	AF048977	serine/arginine repetitive matrix 1	Ser/Arg-related nuclear matrix protein
2231	36019_at	STK19	L26260	serine/threonine kinase 19	RP protein
2232	40473_at	STK24	AF024636	serine/threonine kinase 24 (STE20 homolog, yeast)	STE20-like kinase 3
2233	32142_at	STK3	U26424	serine/threonine kinase 3 (STE20 homolog, yeast)	MST2
2234	32784_at	PRP4	AB011108	serine/threonine-protein kinase PRP4 homolog	KIAA0536 protein

Fig. 21

A	B	C	D	E
2235 40109_at	SRF	J03161	serum response factor (c-fos serum response element-binding transcription factor)	serum response factor (c-fos serum response element-binding transcription factor)
2236 1409_at	SRF	J03161	serum response factor (c-fos serum response element-binding transcription factor)	serum response factor (c-fos serum response element-binding transcription factor)
2237 41544_at	SNK	AF059617	serum-inducible kinase	serum-inducible kinase
2238 34849_at	SARS	X91257	seryl-tRNA synthetase	seryl-tRNA synthetase
2239 40189_at	SET	M93651	SET translocation (myeloid leukemia-associated)	SET translocation (myeloid leukemia-associated)
2240 32160_at	SIAH1	U76247	seven in absentia homolog 1 (Drosophila)	hSIAH1
2241 33799_at	SIAH2	U76248	seven in absentia homolog 2 (Drosophila)	hSIAH2
2242 39088_at	NIFIE14	Y18007	seven transmembrane domain protein	seven transmembrane domain protein
2243 39747_at	tpb-7	U52427	seventh largest subunit; Human RNA polymerase II seventh subunit (pbp-7)	RNA polymerase II seventh subunit
2244 38518_at	SCML2	Y18004	gene, complete cds.	SCML2 protein
2245 36040_at	SH3BGR	AI337192	sex comb on midleg-like 2 (Drosophila)	SH3 domain binding glutamic acid-rich protein
2246 39714_at	SH3BGR	AF042081	SH3 domain binding glutamic acid-rich protein like	SH3 domain binding glutamic acid-rich-like protein
2247 38968_at	SH3BP5	AB005047	SH3-domain binding protein 5 (BTK-associated)	SH3 binding protein
2248 39691_at	SH3GLB1	AB007960	SH3-domain GRB2-like endophillin B1	SH3-containing protein SH3GLB1
2249 38118_at	SHC1	U73377	SHC (Src homology 2 domain containing) transforming protein 1	p66shc
2250 34256_at	SIAT9	AB018356	sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase)	GM3 synthase
2251 39139_at	SPC18	AI357653	signal peptidase complex (18kD)	
2252 41194_at	SRP14	AI525652	signal recognition particle 14kD (homologous Alu RNA binding protein)	
2253 35231_at	SRP19	X12791	signal recognition particle 19kD	signal recognition particle 19kD
2254 36060_at	SRP54	U51920	signal recognition particle 54kD	signal recognition particle

fig-21

	A	B	C	D	E
2255	33837_at	SRP72	AF069765	signal recognition particle 72kD	signal recognition particle 72
2256	36981_at	SRP9	AF070649	signal recognition particle 9kD	signal recognition particle receptor (docking protein)
2257	36679_at	SRPR	X06272	signal recognition particle receptor ('docking protein')	transcription factor ISGF-3
2258	AFFX-HUMISGF-STAT1		M97935	signal transducer and activator of transcription 1, 91kD	transcription factor ISGF-3
2259	32860_g_at	STAT1	M97935	signal transducer and activator of transcription 1, 91kD	transcription factor ISGF-3
2260	32859_at	STAT1	M97935	signal transducer and activator of transcription 1, 91kD	transcription factor ISGF-3
2261	33338_at	STAT1	M97936	signal transducer and activator of transcription 1, 91kD	
2262	39708_at	STAT3	L29277	signal transducer and activator of transcription 3 (acute-phase response factor)	DNA-binding protein
2263	160_at	STAM	U43899	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	STAM
2264	35804_at	ASH2L	AB022785	similar to Drosophila ash2 gene; Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene.	
2265	41552_g_at	RER1	AW044624	similar to S. cerevisiae RER1	
2266	41551_at	RER1	AW044624	similar to S. cerevisiae RER1	
2267	33632_g_at	DIM1	AF023612	similar to S. pombe dim1+	Dim1p homolog
2268	35083_at	G1L	AL031670	similar to SW:GOLI_DROME Q06003 GOLIATH PROTEIN'	ring finger protein 24
2269	37178_at	na	M74089	similar to TB1	
2270	40787_at	WIRE	U90911	similar to Wiskott-Aldrich syndrome protein interacting protein	
2271	34705_at	BET3	AJ224335	similar to yeast BET3 (S. cerevisiae)	hBET3 protein
2272	39131_at	UPF3A	N36842	similar to yeast Upf3, variant A	
2273	41277_at	SAP18	AW021542	sin3-associated polypeptide, 18kD	sin3 associated polypeptide p18
2274	33859_at	SAP18	U96915	sin3-associated polypeptide, 18kD	mSin3A associated polypeptide p30
2275	40992_s_at	SAP30	AF055993	sin3-associated polypeptide, 30kD	sin3 associated polypeptide p30
2276	40004_at	SIX1	X91868	sin oculis homeobox homolog 1 (Drosophila)	sin oculis homeobox (Drosophila) homolog 1

Fig. 21

A	B	C	D	E
2277 39070_at	SNL	U03057	singed-like (fascin homolog, sea urchin) (Drosophila)	actin bundling protein
2278 39086_g_at	SSBP1	AA768912	single-stranded DNA binding protein	
2279 32668_at	SSBP2	AL080076	single-stranded DNA binding protein 2	hypothetical protein
2280 35294_at	SSA2	M25077	Sjogren syndrome antigen A2 (60kD, ribonucleoprotein autoantigen SS-A/Ro)	60kD Ro/SSA autoantigen
2281 35295_g_at	SSA2	M25077	Sjogren syndrome antigen A2 (60kD, ribonucleoprotein autoantigen SS-A/Ro)	60kD Ro/SSA autoantigen
2282 38450_at	SSB	X69804	Sjogren syndrome antigen B (autoantigen La)	Sjogren syndrome antigen B (autoantigen La)
2283 37715_at	SNW1	AF045184	SKI-interacting protein	nuclear receptor coactivator NCoA-62
2284 37389_at	IMAGE145052	AI346580	small acidic protein	
2285 40875_s_at	SNRP70	X06815	small nuclear ribonucleoprotein 70kD polypeptide (RNP antigen)	hU1-70K-like protein (216 AA)
2286 38679_g_at	SNRPE	AA733050	small nuclear ribonucleoprotein polypeptide E	
2287 37337_at	SNRPG	AI803447	small nuclear ribonucleoprotein polypeptide G	
2288 34842_at	SNRPN	U41303	small nuclear ribonucleoprotein polypeptide N	small nuclear ribonucleoprotein particle N
2289 35247_at	SNAPC5	AI557062	small nuclear RNA activating complex, polypeptide 5, 19kD	
2290 32172_at	SHARP	AL096858	SMART/HDAC1 associated repressor protein	hypothetical protein
2291 32849_at	SMC1L1	D80000	SMC1 structural maintenance of chromosomes 1-like 1 (yeast)	
2292 38738_at	SMT3H1	X99584	SMT3 suppressor of mif two 3 homolog 1 (yeast)	SMT3A protein
2293 41185_f_at	SMT3H2	AI971724	SMT3 suppressor of mif two 3 homolog 2 (yeast)	
2294 38288_at	SNAI2	U69196	snail homolog 2 (Drosophila)	
2295 38659_at	SHOC2	AB020669	soc-2 suppressor of clear homolog (C. elegans)	KIAA0862 protein
2296 40928_at	WSB1	W26496	SOCS box-containing WD protein SWiP-1	

fig-21

A	B	C	D	E
2297 36609_at	SLC1A3	D26443	solute carrier family 1 (glial high affinity glutamate transporter), member 3	glutamate transporter
2298 35320_at	SLC11A2	AB004857	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	NRAMP2
2299 33143_s_at	SLC16A3	U81800	solute carrier family 16 (monocarboxylic acid transporters), member 3	monocarboxylate transporter
2300 39260_at	SLC16A4	U59185	solute carrier family 16 (monocarboxylic acid transporters), member 4	solute carrier family 16 (monocarboxylic acid transporters), member 4
2301 36979_at	SLC2A3	M20681	solute carrier family 2 (facilitated glucose transporter), member 3	solute carrier family 2 (facilitated glucose transporter), member 3
2302 32084_at	SLC22A5	AF057164	solute carrier family 22 (organic cation transporter), member 5	organic cation transporter OCTN2
2303 38122_at	SLC23A1	D87075	solute carrier family 23 (nucleobase transporters), member 1	
2304 32822_at	SLC25A4	J02966	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4
2305 37740_r_at	SLC25A5	J02683	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5
2306 40436_g_at	SLC25A6	J03592	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	
2307 40435_at	SLC25A6	J03592	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	
2308 37675_at	SLC25A3	X60036	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3	phosphate carrier protein
2309 33901_at	SLC29A1	U81375	solute carrier family 29 (nucleoside transporters), member 1	equilibrative nucleoside transporter 1
2310 40364_at	SLC31A1	U83460	solute carrier family 31 (copper transporters), member 1	high-affinity copper uptake protein

Fig-21

	A	B	C	D	E
2311	34749_at	SLC31A2	U83461	solute carrier family 31 (copper transporters), member 2	putative copper uptake protein
2312	37895_at	SLC35A1	D87969	solute carrier family 35 (CMP-sialic acid transporter), member 1	CMP-sialic acid transporter
2313	38208_at	SLC35A3	AB021981	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member 3	UDP-N-acetylglucosamine transporter
2314	34936_at	SLC4A7	AB012130	solute carrier family 4, sodium bicarbonate cotransporter, member 7	sodium bicarbonate cotransporter2
2315	34166_at	SLC6A7	S80071	solute carrier family 6 (neurotransmitter transporter, L-proline), member 7	brain-specific L-proline transporter
2316	32186_at	SLC7A5	M80244	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5
2317	39533_at	SLC7A6	D87432	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6
2318	32681_at	SLC9A1	S68616	solute carrier family 9 (sodium/hydrogen exchanger), isoform 1 (antiporter, Na+/H+, amiloride sensitive)	Na+/H+ exchanger NHE-1 isoform
2319	36542_at	SLC9A6	AF030409	solute carrier family 9 (sodium/hydrogen exchanger), isoform 6	sodium-hydrogen exchanger 6
2320	39097_at	SON	X63753	SON DNA binding protein	SON DNA-binding protein
2321	32857_at	SOS2	L13858	son of sevenless homolog 2 (Drosophila)	guanine nucleotide exchange factor
2322	41462_at	SNX2	AF065482	sorting nexin 2	sorting nexin 2
2323	39360_at	SNX3	AF034546	sorting nexin 3	sorting nexin 3
2324	40605_at	SNX4	AA524345	sorting nexin 4	
2325	37808_at	SNX7	AL049989	sorting nexin 7	hypothetical protein
2326	33352_at	H2A	X57985	Source: H.sapiens genes for histones H2B.1 and H2A.	histone H2A
2327	36112_r_at	SC-35	X75755	Source: H.sapiens PR264 gene.	splicing factor, arginine/serine-rich 2
2328	36111_s_at	SC-35	X75755	Source: H.sapiens PR264 gene.	splicing factor, arginine/serine-rich 2

fig. 21



	A	B	C	D	E
2329	1173_g_at		HG172-HT3924	Source: Homo sapiens chromosome 10 clone RP11-96B5, WORKING DRAFT SEQUENCE, 8 unordered pieces.	
2330	40617_at	44M2.1	AC004381	Source: Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.	hypothetical protein FLJ20274
				Source: Homo sapiens clk2 kinase (CLK2), propin1, cote1, glucocerebrosidase (GBA), and metaxin genes, complete cds; metaxin pseudogene and glucocerebrosidase pseudogene; and thrombospondin3 (THBS3) gene, partial cds.	chromosome 1 open reading frame 2
2331	33740_at	COTE1	AF023268	Source: Homo sapiens hJTB gene, complete cds.	jumping translocation breakpoint
2332	41834_g_at	HJTB PAR	AB016492	Source: Homo sapiens hJTB gene, complete cds.	jumping translocation breakpoint
2333	41833_at	HJTB PAR	AB016492	Source: Homo sapiens mRNA for polyubiquitin UbC, complete cds.	polyubiquitin UbC
2334	32335_r_at	UbC2	AB009010	Source: Homo sapiens mRNA for polyubiquitin UbC, complete cds.	polyubiquitin UbC
2335	32334_f_at	UbC2	AB009010	Source: Human CCAAT-box-binding factor (CBF) mRNA, complete cds.	CCAAT-box-binding transcription factor
2336	32194_at	CBF	M37197	Source: Human CCAAT-box-binding factor (CBF) mRNA, complete cds.	CCAAT-box-binding transcription factor
2337	229_at	CBF	M37197	Source: Human Chromosome 16 BAC clone CIT987SK-A-101F10, complete sequence.	hypothetical protein
2338	41791_at	101F10.3	AC002550	Source: Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence.	hypothetical protein A-211C6.1
2339	41488_at	A-211C6.1	AC002394	Source: Human Chromosome 16 BAC clone CIT987SK-A-362G6, complete sequence.	hypothetical protein A-362G6.1
2340	35742_at	A-362G6.1	U95740		

Fig-21

A	B	C	D	E
2341 41733_at	61E3.1	AC003007	Source: Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence.	Unknown gene product (partial)
2342 36894_at		AL031846	Source: Human DNA sequence from clone RP4-742C19 on chromosome 22, complete sequence.	
2343 37383_f_at	HLA class I - locus	X58536	Source: Human mRNA for HLA class I locus C heavy chain.	HLA class I heavy chain
2344 39778_at	GLYT1 GLCNAC-	M55621	Source: Human N-acetylglucosaminyltransferase I (GlcNAc-TI) mRNA, complete cds.	mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase
2345 41573_at	SP3	X68560	Sp3 transcription factor	
2346 32102_at	SACS	AB018273	spastic ataxia of Charlevoix-Saguenay (sacsin)	KIAA0730 protein
2347 35171_at	SPG4	AB029006	spastic paraplegia 4 (autosomal dominant; spastin)	KIAA1083 protein
2348 39423_f_at	SPOP	AJ000644	speckle-type POZ protein	SPOP
2349 38924_s_at	SSH3BP1	AF001628	spectrin SH3 domain binding protein 1	interactor protein AblBP4
2350 33886_at	SSH3BP1	AF006516	spectrin SH3 domain binding protein 1	e3B1
2351 39556_at	SPTBN1	M96803	spectrin, beta, non-erythrocytic 1	beta-spectrin
2352 34304_s_at	SAT	AL050290	spermidine/spermine N1-acetyltransferase	
2353 32574_at	SMPD1	X59960	sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase)	sphingomyelin phosphodiesterase
2354 36142_at	SCA1	X79204	spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1)	ataxin-1
2355 36998_s_at	SCA2	Y08262	spinocerebellar ataxia 2 (olivopontocerebellar ataxia 2, autosomal dominant, ataxin 2)	ataxin 2
2356 38040_at	SPF30	AF107463	splicing factor 30, survival of motor neuron related	splicing factor
2357 36973_at	SF3B2	U41371	splicing factor 3b, subunit 2, 145kD	spliceosome associated protein

fig. 21

284/303

A	B	C	D	E
2358 36224_g_at	SFPQ	A1827895	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	
2359 40638_at	SFPQ	X70944	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	PTB-associated splicing factor
2360 36098_at	SFRS1	M72709	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)
2361 140_s_at	SFRS10	U68063	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)	transformer-2 beta
2362 32183_at	SFRS11	M74002	splicing factor, arginine/serine-rich 11	arginine-rich nuclear protein
2363 35258_f_at	SFRS2IP	AF030234	splicing factor, arginine/serine-rich 2, interacting protein	splicing factor Sip1
2364 40457_at	SFRS3	AF038250	splicing factor, arginine/serine-rich 3	
2365 36991_at	SFRS4	L14076	splicing factor, arginine/serine-rich 4	pre-mRNA splicing factor
2366 40453_s_at	SFRS5	U30826	splicing factor, arginine/serine-rich 5	SRp40-1
2367 40262_at	SRP46	AF031166	Splicing factor, arginine/serine-rich, 46kD	SRp46 splicing factor
2368 35839_at	SOLE	D78130	squalene epoxidase	squalene epoxidase
2369 39047_at	SART3	AB020880	squamous cell carcinoma antigen recognised by T cells 3	squamous cell carcinoma antigen SART-3
2370 41784_at	DKFZp564B0769	AL080186	SR rich protein	hypothetical protein
2371 36091_at	SCAP2	AF051323	src family associated phosphoprotein 2	Src-associated adaptor protein
2372 41354_at	STC1	U25997	stanniocalcin 1	stanniocalcin precursor
2373 32043_at	STC2	AF098462	stanniocalcin 2	stanniocalcin-related protein
2374 41295_at	STARD7	AL041780	START domain containing 7	
2375 38800_at	STMN2	D45352	stathmin-like 2	
2376 41823_at	STAU	AJ132258	stauflin, RNA binding protein (Drosophila)	stauflin protein
2377 38669_at	SLK	D86959	Ste20-related serine/threonine kinase	KIAA0204 protein
2378 37147_at	SCGF	AF020044	stem cell growth factor; lymphocyte secreted C-type lectin	lymphocyte secreted C-type lectin precursor
2379 36913_at	SLBP	U75679	stem-loop (histone) binding protein	histone stem-loop binding protein
2380 38034_at	STS	M16505	steroid sulfatase (microsomal), arylsulfatase C, isozyme S	steroid sulfatase (microsomal), arylsulfatase C, isozyme S

Fig. 21

	A	B	C	D	E
2381 589_at				steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)
2382 33369_at	SRD5A1		M32313	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	
	SC4MOL		A1535653	sterol-C4-methyl oxidase-like	
2383 33421_s_at	SC5DL		AB016247	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, fungal)-like	sterol-C5-desaturase
2384 40419_at	EPB72		X85116	stomatin; H.sapiens epb72 gene exon 1.	band 7 integral membrane protein
2385 33322_i_at	SFN		X57348	stratifin	stratifin
				stress-associated endoplasmic reticulum protein 1; ribosome associated membrane protein 4	
2386 37035_at	SERP1		A1557272		stromal cell derived factor receptor 1 isoform b; stromal cell derived factor receptor 1 isoform a
2387 35747_at	SDFR1		AF035287	stromal cell derived factor receptor 1	intercrine-alpha
2388 32666_at	SDF1		U19495	stromal cell-derived factor 1	pre-B cell stimulating factor homologue
2389 33834_at	SDF1		L36033	stromal cell-derived factor 1	SDF2
2390 41627_at	SDF2		D50645	stromal cell-derived factor 2	succinate dehydrogenase flavoprotein subunit
2391 34826_at	SDHA		L21936	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	
				succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD	integral membrane protein CII-3
2392 34385_at	SDHC		U57877	succinate dehydrogenase complex, subunit D, integral membrane protein	cytochrome b small subunit of complex II
2393 40467_at	SDHD		AB006202	succinate-CoA ligase, ADP-forming, beta subunit	ATP-specific succinyl-CoA synthetase beta subunit
2394 40893_at	SUCLA2		AF058953	sulfatase FP	KIAA1077 protein
2395 35832_at	KIAA1077		AB029000	sulfotransferase family 4A, member 1	
2396 33712_at	SULT4A1		N63574	SUMO-1 activating enzyme subunit 2	
2397 34814_at	UBA2		AL041443	superkiller viralicidic activity 2-like (S. cerevisiae)	helicase-like protein
2398 37998_at	SKIV2L		U09877	superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))	superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))
2399 36620_at	SOD1		X02317	superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))	superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))
2400 40069_at	SVIL		AF051850	supervillin	supervillin
2401 36676_at	GHRF GRF		AL031659	supported by FGENESH	growth hormone releasing hormone

Fig. 21

A	B	C	D	E
2402 33297_at	CBF-B HAP2 NF- $\kappa$ B	AL031778	supported by GENEWISE, GENSCAN and FGENES	nuclear transcription factor Y, alpha, isoform 1
2403 34825_at	TTRAP	AL031775	supported by GENSCAN	TRAF and TNF receptor-associated protein
2404 1640_at	ST13	U17714	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)	putative tumor suppressor ST13
2405 37745_s_at	ST5	U15780	suppression of tumorigenicity 5	p82
2406 37805_at	SRPUL	AF060567	sushi-repeat protein	sushi-repeat protein
2407 31855_at	SRPX	U61374	sushi-repeat-containing protein, X chromosome	
2408 31869_at	KIAA0640	AB014540	SWAP-70 protein	KIAA0640 protein
2409 40213_at	SMARCA1	M88163	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1	transcription activator
2410 40961_at	SMARCA2	X72889	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	HBRM
2411 32579_at	SMARCA4	U29175	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	transcriptional activator
2412 39132_at	SMARCA5	AB010882	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	hSNF2H
2413 34753_at	SYBL1	X92396	synaptobrevin-like 1	synaptobrevin-like 1
2414 41692_at	SYNJ1	AB020717	synaptotagmin 1	KIAA0910 protein
2415 38075_at	SYPL	X68194	synaptophysin-like protein	synaptophysin-like protein
2416 36452_at	KIAA1029	AB028952	synaptopodin	KIAA1029 protein
2417 32178_r_at	SNAP23	AJ011915	synaptosomal-associated protein, 23kD	synaptosome associated protein of 23 kilodaltons, isoform A
2418 39757_at	SDC2	J04621	syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan)	
2419 32092_at	SDC3	AB007937	syndecan 3 (N-syndecan)	KIAA0468 protein
2420 38110_at	SDCBP	AF000652	syndecan binding protein (syntenin)	syntenin
2421 38685_at	STX12	AL035306	syntaxin 12	hypothetical protein
2422 38381_at	STX3A	U32315	syntaxin 3A	syntaxin 3

Fig. 2

A	B	C	D	E
2423 38774_at	STX7	U77942	syntaxin 7	syntaxin 7
2424 37510_at	STX8	AF036715	syntaxin 8	syntaxin 8
2425 33942_s_at	STXBP1	AF004563	syntaxin binding protein 1	hUNC18b
2426 37962_r_at	STXBP3	D63506	syntaxin binding protein 3	unc-18homologue
2427 33315_at		M29204	Synthetic construct chimeric DNA-binding factor mRNA, complete cds.	chimeric DNA-binding factor
2428 192_at	TAF7	U18062	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 55 kD	TFIID subunit TAFII55
2429 193_at	TAF9	U21858	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32 kD	TAFII32 precursor
2430 37620_at	TAF12; TAF2J; TAF15	U57693	TAF120; contains homology to histone H2B; TFIID subunit; contains homology to histone H2B; TFIID subunit; Human TFIID subunits TAF20 and TAF15 mRNA, complete cds.	TAF20; TAF15
2431 32166_at	TLN1	AB028950	taln 1	KIAA1027 protein
2432 39765_at	TLN2	AB002318	taln 2	tapasin
2433 41168_at	TAPBP	AF029750	TAP binding protein (tapasin)	TAR RNA loop binding protein
2434 39779_at	TARBP1	U38847	TAR (HIV) RNA binding protein 1	hypothetical protein
2435 32241_at	TARDBP	AL050265	TAR DNA binding protein	Tax interaction protein 1
2436 39416_at	TIP-1	U90913	Tax interaction protein 1	tax1-binding protein TXBP151
2437 498_at	TAX1BP1	U33821	Tax1 (human T-cell leukemia virus type I) binding protein 1	tax1-binding protein TXBP151
2438 35279_at	TAX1BP1	U33821	Tax1 (human T-cell leukemia virus type I) binding protein 1	TBX19 protein
2439 36702_at	TBX19	AJ010277	T-box 19	KIAA0829 protein
2440 32196_at	TIP120A	AB020636	TBP-interacting protein	t-complex 1
2441 34791_at	TCP1	X52882	t-complex 1	t-complex-associated-testis-expressed 1-like
2442 36921_at	TCTE1L	U02556	t-complex-associated-testis-expressed 1-like	t-complex-associated-testis-expressed 1-like
2443 946_at	TCTEL1	D50663	t-complex-associated-testis-expressed 1-like	1

Fig. 21

	A	B	C	D	E
2444	38374_at	TIEG; EGRA; KLF4F050110		TEIG; EGRA; Homo sapiens TGFB inducible early protein and early growth response protein alpha genes, complete cds.	TGFB inducible early protein; early growth response protein alpha
2445	32255_i_at	TERF1	U40705	telomeric repeat binding factor (NIMA-interacting) 1	telomeric repeat binding factor 1, isoform 2; telomeric repeat binding factor 1, isoform 1
2446	32134_at	TES	AL050162	testis derived transcript (3 LIM domains)	hypothetical protein
2447	33988_at	TEGT	X75861	testis enhanced gene transcript (BAX inhibitor 1)	testis enhanced gene transcript (BAX inhibitor 1)
2448	32080_at	TETRA	L11669	tetracycline transporter-like protein	tetracycline transporter-like protein
2449	38612_at	TSPAN-3	M69023	tetraspan 3	
2450	37321_at	TTC1	U46570	tetratricopeptide repeat domain 1	tetratricopeptide repeat protein
2451	39065_s_at	TTC3	D83077	tetratricopeptide repeat domain 3	TPRD
2452	224_at	TIEG	S81439	TGFB inducible early growth response	zinc finger transcription factor
2453	38805_at	TGIF	X89750	TGFB-induced factor (TALE family homeobox)	TGIF protein
2454	37319_at	IGFBP3	M35878	The AAs encoded by bases 5728-5736 and 5917-5926 may be ASN-linked glycosylation sites; insulin-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, complete cds.	growth factor-binding protein-3 precursor
2455	1586_at	IGFBP3	M35878	The AAs encoded by bases 5728-5736 and 5917-5926 may be ASN-linked glycosylation sites; insulin-like precursor; Homo sapiens growth factor-binding protein-3 precursor (IGFBP3) gene, complete cds.	growth factor-binding protein-3 precursor

Fig. 21

A	B	C	D	E
			The first in-frame ATG codon is located at nucleotides 17-19, followed by a second ATG codon 52 codons downstream. And the second ATG codon is potential initiation point for translation of NPPase.; Human mRNA for nucleotide pyrophosphatase, complete cds.	
2456 342_at	ENPP1; M6S1; NFD12485			NPPase
2457 36992_at	TXN	AL653621	thioredoxin	
2458 34768_at	TXND	AL080080	thioredoxin domain-containing	hypothetical protein
2459 31508_at	TXNIP	S73591	thioredoxin interacting protein	brain-expressed HHCPA78 homolog VDUP1
2460 39425_at	TXNRD1	X91247	thioredoxin reductase 1	thioredoxin reductase (NADPH)
2461 32214_at	TXNL	AF003938	thioredoxin-like, 32kD	thioredoxin-like protein
2462 38473_at	TARS	M63180	threonyl-tRNA synthetase	threonyl-tRNA synthetase
2463 659_g_at	THBS2	L12350	thrombospondin 2	thrombospondin 2
2464 658_at	THBS2	L12350	thrombospondin 2	thrombospondin 2
2465 40865_at	TDG	U51166	thymine-DNA glycosylase	G/T mismatch-specific thymine DNA glycosylase
2466 31557_at	TMSB4X	M17733	thymosin, beta 4, X chromosome	thymosin, beta 4
2467 32654_g_at	SMAP	AW020536	thyroid hormone receptor coactivating protein	
2468 39699_at	TRIP12	D28476	thyroid hormone receptor interactor 12	thyroid hormone receptor interactor 12
2469 41251_at	TRIP3	L40410	thyroid hormone receptor interactor 3	thyroid receptor interactor
2470 39341_at	TRIP6	AJ001902	thyroid hormone receptor interactor 6	TRIP6
2471 37348_s_at	TRIP7	AA845349	thyroid hormone receptor interactor 7	
2472 41625_at	TRAP240	AB011165	thyroid hormone receptor-associated protein, 240 kDa subunit	KIAA0593 protein
2473 34323_at	TRIP15	AF084260	thyroid receptor interacting protein 15	signalosome subunit 2
2474 33852_at	TIA1	M77142	TIA1 cytotoxic granule-associated RNA binding protein	TIA1 protein, isoform 1; TIA1 protein, isoform 2
2475 41763_g_at	TIAL1	D64015	TIA1 cytotoxic granule-associated RNA binding protein-like 1	T-cluster binding protein
2476 36655_at	TJP2	L27476	tight junction protein 2 (zona occludens 2)	tight junction protein 2 (zona occludens 2)
2477 37801_at	TJ6	AF112972	TJ6 protein	TJ6

Fig-21



	A	B	C	D	E
2478	35238_at	TRAF5	AB000509	TNF receptor-associated factor 5	TRAF5
2479	33243_at	GG2-1	AF099935	TNF-induced protein	MDC-3.13 isoform 2
2480	40310_at	TLR2	AF051152	tol-like receptor 2	Toll/interleukin-1 receptor-like protein 4
2481	1030_s_at	TOP1	U07806	topoisomerase (DNA) I	DNA topoisomerase I
2482	36571_at	TOP2B	X68060	topoisomerase (DNA) II beta (180kD)	DNA topoisomerase II
2483	32233_at	TOR1B	AF007872	torsin family 1, member B (torsin B)	torsinB
2484	32219_at	TLK1	D50927	tousled-like kinase 1	KIAA0137 protein
2485	35321_at	TLK2	AB004884	tousled-like kinase 2	PKU-alpha
2486	39742_at	TANK	U59863	TRAF family member-associated NFKB activator	I-TRAF
2487	40051_at	KIAA0057	D31762	TRAM-like protein	TRAM-like protein
2488	1073_at	TCEA1	M81601	transcription elongation factor A (SII), 1	transcription elongation factor SII
2489	38317_at	TCEAL1	M99701	transcription elongation factor A (SII)-like 1	transcription elongation factor A (SII)-like 1
2490	1399_at	TCEB1	L34587	transcription elongation factor B (SIII), polypeptide 1 (15kD, elongin C)	RNA polymerase II elongation factor SIII, p15 subunit
2491	41759_at	TCEB1L	Z47087	transcription elongation factor B (SIII), polypeptide 1-like	RNA polymerase II elongation factor-like protein
2492	39426_at	TCERG1	AF017789	transcription elongation regulator 1 (CA150)	putative transcription factor CA150
2493	33348_at	TCF12	M80627	transcription factor 12 (HTF4, helix-loop-helix transcription factors 4)	helix-loop-helix protein
2494	1373_at	TCF3	M31523	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	
2495	33440_at	TCF8	U19969	transcription factor 8 (represses interleukin 2 expression)	ZEB
2496	39638_at	TFAP4	S73885	transcription factor AP-4 (activating enhancer binding protein 4)	AP-4
2497	37757_at	TFDP1	L23959	transcription factor Dp-1	E2F-related transcription factor
2498	32578_at	TCFL4	AW005997	transcription factor-like 4	
2499	35614_at	TCFL5	AB012124	transcription factor-like 5 (basic helix-loop-helix)	transcription factor-like 5
2500	35749_at	TADA3L	AF069733	transcriptional adaptor 3-like	ADA3-like protein

Fig. 21

	A	B	C	D	E
2501	35297_at	GGA2 VEAR	AC002400	Transcriptional coactivator P15 like	KIAA1080 protein; Golgi-associated, gamma-adaptin ear containing, ARF-binding protein 2
2502	33876_at	TAZ	AL050107	transcriptional co-activator with PDZ-binding motif (TAZ)	hypothetical protein
				transcriptional co-repressor; Human silencing mediator of retinoid and thyroid hormone action (SMRT) mRNA, complete cds.	silencing mediator of retinoid and thyroid hormone action
2503	39358_at	SMRT	U37146		
2504	37312_at	TRIP-Br2	D50917	transcriptional regulator interacting with the PHS-bromodomain 2	KIAA0127 gene product
2505	40631_at	TOB1	D38305	transducer of ERBB2, 1	Tob
2506	32554_s_at	TBL1	Y12781	transducin (beta)-like 1	transducin (beta) like 1 protein
2507	37324_at	TFRC	X01060	transferrin receptor (p90, CD71)	transferrin receptor (p90, CD71)
2508	39344_at	HSU53209	U53209	transformer-2 alpha (hira-2 alpha)	transformer-2 alpha
2509	39032_at	TSC22	AJ222700	transforming growth factor beta-stimulated protein TSC-22	TSC-22
2510	41445_at	TGFB1	X02812	transforming growth factor, beta 1 (Camurati-Engelmann disease)	transforming growth factor, beta 1 (Camurati-Engelmann disease)
2511	1815_g_at	TGFBR2	D50683	transforming growth factor, beta receptor II (70-80kD)	TGF-beta1R alpha
2512	1814_at	TGFBR2	D50683	transforming growth factor, beta receptor II (70-80kD)	TGF-beta1R alpha
2513	1385_at	TGFBI	M77349	transforming growth factor, beta-induced, 68kD	transforming growth factor induced protein
2514	40841_at	TACC1	AF049910	transforming, acidic coiled-coil containing protein 1	TACC1
2515	38816_at	TACC2	AF095791	transforming, acidic coiled-coil containing protein 2	TACC2 protein
2516	36931_at	TAGLN	M95787	transgelin	smooth muscle protein
2517	36678_at	TAGLN2	D21261	transgelin 2	transgelin 2
2518	31829_r_at	TGOLN2	AF027515	trans-golgi network protein 2	hTGN48
2519	39124_r_at	TRPC1	X89066	transient receptor potential cation channel, subfamily C, member 1	TRPC1 protein
2520	39123_s_at	TRPC1	X89066	transient receptor potential cation channel, subfamily C, member 1	TRPC1 protein

Fig. 21

292/303

A	B	C	D	E
2521	34380_at		RETICULUM ATPASE (TER ATPASE) (15S MG(2+)-ATPASE P97 SUBUNIT) (VALOSIN CONTAINING PROTEIN) (VCP); Human homolog of spIQ01853TERA_MOUSE TRANSITIONAL ENDOPLASMIC RETICULUM ATPASE (TER ATPASE) (15S MG(2+)-ATPASE P97 SUBUNIT) (VALOSIN CONTAINING PROTEIN) (VCP) pirlS25197 transitional endoplasmic reticulum ATPase - mouse gil55217 (Z14044) murine valosin- containing protein; 99% identical to mouse, rat, and pig homologs; X-ray cross complementing gene 9; Putative DNA repair protein; Hypothetical 96.6 kDa putative membrane protein; Most similar to hypothetical proteins in fission and budding yeast, and C. elegans: (AB004539) ORF YLL031c [Schizosaccharomyces pombe] producing hypothetical protein (AL021766) [Schizosaccharomyces pombe]; probable membrane protein YLL031c - yeast (Saccharomyces cerevisiae) gnlPIDle245463 (Z73136) ORF YLL031c [Saccharomyces cerevisiae]; (AF003137) C27A12.9 [Caenorhabditis elegans]; Hypothetical 38.8 kDa putative membrane protein; Most similar to hypothetical proteins: PIDle276130 (Z81072) F30A10.5 [Caenorhabditis elegans]; spIP72655YB28 translation factor suil1 homolog translation initiation factor IF2	TERA_HUMAN; XRCC9; P1.11659_3; P1.11659_4; P1.11659_5 GC20 protein KIAA0741 protein
2522	33351_at	AC004472		
2523	40537_at	AF064607 AB018284		
2524	32173_at	UK114	translation inhibitor protein p14.5	14.5 kDa translational inhibitor protein, p14.5

Fig. 21

A	B	C	D	E
2525 41051_at	TSNAX	X95073	translin-associated factor X	Translin associated protein X
2526 32831_at	TIMM17A	AA453183	translocase of inner mitochondrial membrane 17 homolog A (yeast)	
2527 36198_at	TOMM20-PENDIN	D13641	translocase of outer mitochondrial membrane 20 (yeast) homolog	mitochondrial outer membrane protein 19
2528 37050_r_at	TOMM34	AI130910	translocase of outer mitochondrial membrane 34	
2529 32853_at	TOMM70A	AB018262	translocase of outer mitochondrial membrane 70 homolog A (yeast)	KIAA0719 protein
2530 34796_at	TRAM	X63679	translocating chain-associating membrane protein	TRAM protein
2531 38100_at	TLOC1	D87127	translocation protein 1	translocation protein-1
2532 950_at	TLOC1	D87127	translocation protein 1	translocation protein-1
2533 41531_at	TM4SF1	AI445461	transmembrane 4 superfamily member 1	
2534 39362_r_at	TM4SF6	AF043906	transmembrane 4 superfamily member 6	T245 protein
2535 32083_at	TM7SF1	AF027826	transmembrane 7 superfamily member 1 (upregulated in kidney)	putative seven pass transmembrane protein
2536 38835_at	TM9SF1	U94831	transmembrane 9 superfamily member 1	multispanning membrane protein
2537 34307_at	TM9SF2	U81006	transmembrane 9 superfamily member 2	p76
2538 37955_at	TMEM4	AB015631	transmembrane protein 4	type II membrane protein
2539 37445_at	TMEM5	AB015633	transmembrane protein 5	type II membrane protein
2540 36128_at	TMP21	L40397	transmembrane trafficking protein	
2541 38982_at	RAP1	W28865	TRF2-interacting telomeric RAP1 protein	
2542 39382_at	TRIM2	AB011089	tripartite motif-containing 2	KIAA0517 protein
2543 36825_at	TRIM22	X82200	tripartite motif-containing 22	gpStaf50
2544 38537_at	TRIM32	U18543	tripartite motif-containing 32	zinc-finger protein
2545 32635_at	TRIM33	AB029036	tripartite motif-containing 33	KIAA1113 protein
2546 33107_at	TRIM37	AB020705	tripartite motif-containing 37	KIAA0898 protein
2547 40461_at	TIX1	AB007855	triple homeobox 1	
2548 36791_g_at	TPM1	M19267	tropomyosin 1 (alpha)	tropomyosin 1 (alpha)
2549 36790_at	TPM1	M19267	tropomyosin 1 (alpha)	tropomyosin 1 (alpha)

Fig. 21

	A	B	C	D	E
2550	36792_at	TPM1	Z24727	tropomyosin 1 (alpha)	tropomyosin isoform
2551	32313_at	TPM2	M12125	tropomyosin 2 (beta)	tropomyosin 2 (beta)
2552	32777_at	WRB	Y12478	tryptophan rich basic protein	congenital heart disease 5 protein
2553	38121_at	WARS	X59892	tryptophanyl-tRNA synthetase	471 aa polypeptide (gamma2)
2554	39867_at	TUFM	S75463	Tu translation elongation factor, mitochondrial	P43
2555	31944_at	TULP3	A1028290	tubby like protein 3	
2556	32272_at	K-ALPHA-1	K00558	tubulin, alpha, ubiquitous	tubulin, alpha, ubiquitous
2557	39332_at	TUBB	AF035316	tubulin, beta polypeptide	
2558	39331_at	TUBB	X79535	tubulin, beta polypeptide	beta tubulin
2559	33346_r_at	TUBG1	M61764	tubulin, gamma 1	gamma-tubulin
2560	36176_at	TBCC	U61234	tubulin-specific chaperone c	cofactor C
2561	35159_at	TBCE	U61232	tubulin-specific chaperone e	cofactor E
2562	37007_at	TDE1	U49188	tumor differentially expressed 1	tumor differentially expressed 1
2563	34892_at	TNFRSF10B	AF016266	tumor necrosis factor receptor superfamily, member 10b	TRAIL receptor 2
2564	41190_at	TNFRSF12	U83598	tumor necrosis factor receptor superfamily, member 12 (translocating chain-association membrane protein)	death domain receptor 3 soluble form
2565	1563_s_at	TNFRSF1A	M58286	tumor necrosis factor receptor superfamily, member 1A	tumor necrosis factor receptor
2566	35150_at	TNFRSF5	X60592	tumor necrosis factor receptor superfamily, member 5	CDw40
2567	37643_at	TNFRSF6	X63717	tumor necrosis factor receptor superfamily, member 6	APO-1 cell surface antigen precursor
2568	36988_at	TNFAIP1	M80783	tumor necrosis factor, alpha-induced protein 1 (endothelial)	B12 protein
2569	38631_at	TNFAIP2	M92357	tumor necrosis factor, alpha-induced protein 2	B94 protein
2570	595_at	TNFAIP3	M59465	tumor necrosis factor, alpha-induced protein 3	A20
2571	40076_at	TPD52L2	AF004430	tumor protein D52-like 2	hD54+ins2 isoform
2572	1711_at	TP53BP1	U09477	tumor protein p53 binding protein, 1	p53-binding protein
2573	34822_at	TP53BP2	U58334	tumor protein p53 binding protein, 2	Bbp/53BP2
2574	38568_at	TP53BPL	U82939	tumor protein p53-binding protein	p53 binding protein

F5-21

A	B	C	D	E
2575 31584_at	TPT1	X16064	tumor protein, translationally-controlled 1	tumor protein, translationally-controlled 1
2576 31888_s_at	TSSC3	AF001294	tumor suppressing subtransferase candidate 3	IPL
2577 147_at	TSG101	U82130	tumor susceptibility gene 101	tumor susceptibility protein
2578 40328_at	TWIST	X99268	twist homolog (acrocephalosyndactyly 3; Saethre-Chotzen syndrome) (Drosophila)	B-HLH DNA binding protein
2579 2086_s_at	TYRO3	D17517	TYRO3 protein tyrosine kinase	Sky
2580 35246_at	TYRO3	U18934	TYRO3 protein tyrosine kinase	receptor tyrosine kinase
2581 32324_at	YWHAH	X57346	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide
2582 409_at	YWHAQ	X56468	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	14.3.3 protein
2583 32530_at	YWHAQ	X56468	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	14.3.3 protein
2584 1235_at	YWHAZ	M86400	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	phospholipase A2
2585 32718_at	TPST1	AF038009	tyrosylprotein sulfotransferase 1	tyrosylprotein sulfotransferase-1
2586 35172_at	TPST2	AF049891	tyrosylprotein sulfotransferase 2	tyrosylprotein sulfotransferase-2
2587 38977_at	YARS	U89436	tyrosyl-tRNA synthetase	tyrosyl-tRNA synthetase
2588 36517_at	U2AF1	M96982	U2(RNU2) small nuclear RNA auxiliary factor 1	U2 snRNP auxiliary factor small subunit
2589 32858_at	UBN1	A1341565	ubiquitin 1	ubiquitin 2
2590 34824_at	UBQLN2	AB015344	ubiquitin 2	ubiquitin 2
2591 38451_at	UQCR	T58471	ubiquinol-cytochrome c reductase (6.4kD) subunit	
2592 39427_at	UQCRB	T79616	ubiquinol-cytochrome c reductase binding protein	
2593 40854_at	UQCRC2	J04973	ubiquinol-cytochrome c reductase core protein II	ubiquinol-cytochrome c reductase core protein II

Fig-21

	A	B	C	D	E
2594	36104_at	UQCRH	AA526497	ubiquinol-cytochrome c reductase hinge protein	
2595	1366_i_at	UBC	M26880	ubiquitin C	ubiquitin C
2596	1367_f_at	UBC	M26880	ubiquitin C	ubiquitin C
2597	36990_at	UCHL1	X04741	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)	ubiquitin carboxyl-terminal esterase L1
2598	811_at	UFD1L	U64444	ubiquitin fusion degradation 1-like	(ubiquitin thiolesterase)
2599	40623_at	UBE3B	A1749193	ubiquitin protein ligase	ubiquitin fusion-degradation 1 like protein
				ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome)	E6-associated protein E6-AP/ubiquitin-protein ligase
2600	41205_at	UBE3A	U84404	ubiquitin specific protease 1	ubiquitin specific protease
2601	34383_at	USP1	AB014458	ubiquitin specific protease 10	
2602	37683_at	USP10	D80012	ubiquitin specific protease 11	
2603	162_at	USP11	U44839	ubiquitin specific protease 14 (tRNA-guanine transglycosylase)	UHX1 protein
2604	36982_at	USP14	U30888	ubiquitin specific protease 22	tRNA-Guanine Transglycosylase
2605	39866_at	USP22	AB028986	ubiquitin specific protease 24	KIAA1063 protein
2606	35847_at	USP24	AB028980	ubiquitin specific protease 4 (proto-oncogene)	KIAA1057 protein
2607	1357_at	USP4	U20657	ubiquitin specific protease 5 (isopeptidase T)	ubiquitin protease
2608	34405_at	USP5	U47927	ubiquitin specific protease 7 (herpes virus-associated)	isopeptidase T
2609	37672_at	USP7	Z72499	ubiquitin specific protease 8	herpesvirus associated ubiquitin-specific protease (HAUSP)
2610	39794_at	USP8	D29956	ubiquitin specific protease 9, X	ubiquitin specific protease 8
2611	32572_at	USP9X	X98296	ubiquitin-activating enzyme E1C (UBA3 homolog, yeast)	ubiquitin hydrolase
2612	40066_at	UBE1C	AF046024	ubiquitination factor E4A (UFD2 homolog, yeast)	UBA3
2613	36579_at	UBE4A	D50916	ubiquitination factor E4B (UFD2 homolog, yeast)	ubiquitination factor E4A (UFD2 homolog, yeast)
2614	41339_at	UBE4B	AF043117	ubiquitin-conjugating enzyme E2 variant 1	ubiquitin-fusion degradation protein 2
2615	36959_at	UBE2V1	U49278		UEV-1

fig-21

A	B	C	D	E
2616 890_at	UBE2A	M74524	ubiquitin-conjugating enzyme E2A (RAD6 homolog)	ubiquitin-conjugating enzyme E2A (RAD6 homolog)
2617 37826_at	UBE2D1	AF020761	ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast)	
2618 38705_at	UBE2D2	A1310002	ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast)	
2619 832_at	UBE2D2	U39317	ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast)	UbcH5B
2620 39083_at	UBE2D3	U39318	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	UbcH5C
2621 504_at	UBE2D3	U39318	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	UbcH5C
2622 34850_at	UBE2E3	AB017644	ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast)	ubiquitin-conjugating enzyme E2
2623 32236_at	UBE2G2	AF032456	ubiquitin-conjugating enzyme E2G 2 (UBC7 homolog, yeast)	ubiquitin conjugating enzyme G2
2624 38480_s_at	UBE2I	U66867	ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast)	ubiquitin conjugating enzyme 9
2625 838_s_at	UBE2I	U45328	ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast)	ubiquitin-conjugating enzyme
2626 223_at	UBE2L3	S81003	ubiquitin-conjugating enzyme E2L 3	L-UBC
2627 40505_at	UBE2L6	AA883502	ubiquitin-conjugating enzyme E2L 6	
2628 36604_at	UBE2N	D83004	ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast)	ubiquitin-conjugating enzyme E2 UbcH-ben
2629 457_s_at	UBL1	U67122	ubiquitin-like 1 (sentrin)	SUMO-1
2630 155_s_at	UBL1	U61397	ubiquitin-like 1 (sentrin)	ubiquitin-homology domain protein PIC1
2631 40839_at	UBL3	AL080177	ubiquitin-like 3	hypothetical protein
2632 37336_at	UBXD2	D87684	UBX domain-containing 2	KIAA0242 protein
2633 40960_at	B4GALT1	D29805	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1	beta-1,4-galactosyltransferase
2634 34177_at	B4GALT2	AF038660	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 2	beta-1,4-galactosyltransferase
2635 39445_at	B4GALT3	AF038661	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3	beta-1,4-galactosyltransferase
2636 40215_at	UGCG	D50840	UDP-glucose ceramide glucosyltransferase	ceramide glucosyltransferase

fig. 21



	A	B	C	D	E
2637	35214_at	UGDH	AF061016	UDP-glucose dehydrogenase	UDP-glucose dehydrogenase
2638	37373_at	UGP2	U27460	UDP-glucose pyrophosphorylase 2 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 1 (GalNAc-T1)	uridine diphosphoglucose pyrophosphorylase
2639	38041_at	GALNT1	U41514		UDP-GalNAc:polypeptide N-acetylglucosaminyltransferase
2640	36515_at	GNE	AJ238764	UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine kinase	UDP-N-acetylglucosamine-2-epimerase / N-acetylmannosamine kinase
2641	41242_at	UAP1	AB011004	UDP-N-acetylglucosamine pyrophosphorylase 1	UDP-N-acetylglucosamine pyrophosphorylase
2642	34827_at	ULK1	AF045458	unc-51-like kinase 1 (C. elegans)	serine/threonine kinase ULK1
2643	37315_f_at	BM036	AI057607	uncharacterized bone marrow protein BM036	
2644	35750_at	HT010	AL049948	uncharacterized hypothalamus protein HT010	
2645	41058_g_at	HT012	AI760162	uncharacterized hypothalamus protein HT012	
2646	41057_at	HT012	AI760162	uncharacterized hypothalamus protein HT012	
2647	38610_s_at	KRT10; KPP	X14487	unnamed protein product; Human gene for acidic (type I) cytokeratin 10.	keratin 10
2648	34402_at	UNRIP	AB024327	unr-interacting protein	WD-40 repeat protein
2649	34372_at	UREB1	AB002310	upstream regulatory element binding protein 1	upstream regulatory element binding protein 1
2650	37686_s_at	UNG	Y09008	uracil-DNA glycosylase	uracil-DNA glycosylase
2651	33815_at	UMPS	J03626	uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase)	uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase)
2652	41859_at	UST	AB020316	uronyl-2-sulfotransferase	dermatan/chondroitin sulfate 2-sulfotransferase
2653	39429_at	UVRAG	X99050	UV Radiation Resistance Associated Gene; H.sapiens mRNA; UV Radiation Resistance Associated Gene.	p63 (processed form)

fig. 21

A	B	C	D	E
			v-abl Abelson murine leukemia viral oncogene homolog 1 isoform a; v-abl Abelson murine leukemia viral oncogene homolog 1 isoform b	v-abl Abelson murine leukemia viral oncogene homolog 1 isoform a; v-abl Abelson murine leukemia viral oncogene homolog 1 isoform b
2654 39730_at	ABL1	X16416	v-abl Abelson murine leukemia viral oncogene homolog 1	
2655 35779_at	VPS45A	AJ133421	vacuolar protein sorting 45A (yeast)	vacuolar protein sorting
2656 38801_at	VAPA	A1742846	VAMP (vesicle-associated membrane protein)-associated protein A (33kD)	
				vascular cell adhesion molecule 1, isoform a precursor; vascular cell adhesion molecule 1, isoform b precursor
2657 583_s_at	VCAM1	M30257	vascular cell adhesion molecule 1	vascular endothelial growth factor
2658 1953_at	VEGF	AF024710	vascular endothelial growth factor	vascular endothelial growth factor
2659 36100_at	VEGF	AF022375	vascular endothelial growth factor	VEGF related factor isoform VRF186 precursor
2660 37268_at	VEGFB	U43368	vascular endothelial growth factor B	vascular endothelial growth factor related protein
2661 159_at	VEGFC	U43142	vascular endothelial growth factor C	
			VDAC protein; similar to mouse VDAC 3; Homo sapiens voltage dependent anion channel protein mRNA, complete cds.	voltage dependent anion channel protein
2662 36102_at	VDAC3; HD-VDAC	AF038962	vesicle amine transport protein 1	vesicle amine transport protein 1
2663 40147_at	VATI	U18009	vesicle transport-related protein	KIAA0917 protein
2664 33930_at	RA410	AB020724	vesicle-associated membrane protein 2 (synaptobrevin 2)	
2665 32254_at	VAMP2	AL050223	vesicle-associated membrane protein 3 (cellubrevin)	
2666 35783_at	VAMP3	H93123	villin 2 (ezrin)	villin 2
2667 40103_at	VIL2	X51521	vimentin	vimentin
2668 34091_s_at	VIM	Z19554	vinculin	vinculin isoform VCL; VCL isoform meta-VCL
2669 36601_at	VCL	M33308		
2670 39091_at	JWA	AF070523	vitamin A responsive; cytoskeleton related	JWA protein
2671 1388_g_at	VDR	J03258	vitamin D (1,25-dihydroxyvitamin D3) receptor	vitamin D (1,25-dihydroxyvitamin D3) receptor
2672 1940_at	KRAS2	M54968	v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogene homolog	K-ras oncogene protein

fig-21

	A	B	C	D	E
2673	41504_s_at	MAF	AF055376	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	short form transcription factor C-MAF
2674	32835_at	MAFF	AA725102	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	
2675	40198_at	VDAC1	L06132	voltage-dependent anion channel 1	voltage-dependent anion channel
2676	37696_at	VDAC2	L06328	voltage-dependent anion channel 2	voltage-dependent anion channel
2677	171_at	VBP1	U56833	von Hippel-Lindau binding protein 1	VHL binding protein-1
2678	38743_f_at	RAF1	X06409	v-raf-1 murine leukemia viral oncogene homolog 1	
2679	32776_at	RALB	M35416	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein)	v-ral simian leukemia viral oncogene homolog B
2680	36645_at	RELA	L19067	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian)	NF-kappa-B transcription factor subunit
2681	1295_at	RELA	L19067	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian)	NF-kappa-B transcription factor subunit
2682	1674_at	YES1	M15990	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog 1	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1
2683	1402_at	LYN	M16038	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog
2684	1058_at	WASF3	S69790	WAS protein family, member 3	hypothetical protein
2685	38736_at	WDR1	AL050108	WD repeat domain 1	KIAA0541 protein
2686	41430_at	WDR7	AB011113	WD repeat domain 7	
2687	36009_at	CL683	AF091092	weakly similar to glutathione peroxidase 2	weakly similar to glutathione peroxidase 2
2688	36909_at	WEE1	X62048	WEE1+ homolog (S. pombe)	wee1 tyrosine kinase
2689	41212_r_at	WBSCR1	D26068	Williams-Beuren syndrome chromosome region 1	eukaryotic translation initiation factor 4H, isoform 1; eukaryotic translation initiation factor 4H, isoform 2
2690	41635_at	WTAP	D14661	Wilms' tumour 1-associating protein	Wilms' tumour 1-associating protein
2691	31862_at	WNT5A	L20861	wingless-type MMTV integration site family, member 5A	wingless-type MMTV integration site family, member 5A precursor

fig-21

	A	B	C	D	E
2692	34225_at	WHSC2	AF101434	Wolf-Hirschhorn syndrome candidate 2	Wolf-Hirschhorn syndrome candidate 2 protein
2693	33438_at	WBP2	AL049981	WW domain binding protein 2	
2694	35213_at	WBP4	AF071185	WW domain binding protein 4 (formin binding protein 21)	formin binding protein 21
2695	39995_s_at	WBOX	U13395	WW domain containing oxidoreductase	oxidoreductase
2696	36822_at	WAC	U51334	WW domain-containing adapter with a coiled-coil region	putative RNA binding protein RBP56
2697	1307_at	XPA	D14533	xeroderma pigmentosum, complementation group A	XPAC protein
2698	1873_at	XPC	D21089	xeroderma pigmentosum, complementation group C	XP-C repair complementing protein (p125)
2699	41756_at	NTPBP	AJ010842	XPA binding protein 1; putative ATP(GTP)-binding protein	ATP(GTP)-binding protein
2700	38733_at	XRCC5	M30938	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen, 80kD)	ATP-dependant DNA helicase II
2701	585_at	XRCC5	M30938	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen, 80kD)	ATP-dependant DNA helicase II
2702	2093_s_at	XRCC5	J04977	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen, 80kD)	ATP-dependant DNA helicase II
2703	35827_at	KIAA0905	AB020712	yeast Sec31p homolog	KIAA0905 protein
2704	40988_at	YME1L1	AJ132637	YME1-like 1 (S. cerevisiae)	ATP-dependent metalloprotease YME1L
2705	891_at	YY1	M77698	YY1 transcription factor	GLI-Krupple related protein
2706	34887_at			zb29g04.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:305046 3', mRNA sequence.	
2707	36308_at	ZIC1	N92548	Zic family member 1 (odd-paired homolog, Drosophila)	Zic protein
2708	35681_r_at	ZFX1B	AB011141	zinc finger homeobox 1b	KIAA0569 protein

fig. 21

	A	B	C	D	E
2709	34786_at	TSGA	AB018285	zinc finger protein	KIAA0742 protein
2710	39977_at	ZNF-U69274	U69274	zinc finger protein	zinc finger protein
2711	40140_at	ZFP103	D76444	zinc finger protein 103 homolog (mouse)	zinc finger protein 103 homolog
2712	36295_at	ZNF134	U09412	zinc finger protein 134 (clone pHZ-15)	zinc finger protein ZNF134
2713	32192_g_at	ZNF144	D13969	zinc finger protein 144 (Mel-18)	Mel-18 protein
2714	36928_at	ZNF146	X70394	zinc finger protein 146	zinc finger protein
2715	41532_at	ZNF151	Y09723	zinc finger protein 151 (pHZ-67)	Miz-1 protein
2716	32628_at	ZNF161	D28118	zinc finger protein 161	DB1
2717	41436_at	ZNF198	AJ224901	zinc finger protein 198	ZNF198 protein
2718	40724_at	ZNF200	Y14443	zinc finger protein 200	zinc finger protein
2719	35368_at	ZNF207	AF046001	zinc finger protein 207	zinc finger protein 207
2720	41542_at	ZNF216	AF062346	zinc finger protein 216	zinc finger protein 216 splice variant 1
2721	840_at	ZNF220	U47742	zinc finger protein 220	monocytic leukaemia zinc finger protein
2722	39762_at	ZNF262	AB007885	zinc finger protein 262	zinc finger protein 262
2723	34299_at	ZNF278	AL096880	zinc finger protein 278	hypothetical protein
2724	39005_s_at	ZNF294	AB018257	zinc finger protein 294	KIAA0714 protein
2725	37860_at	ZNF337	AL049942	zinc finger protein 337	hypothetical protein
2726	40448_at	ZFP36	M92843	zinc finger protein 36, C3H type, homolog (mouse)	zinc finger transcriptional regulator
2727	38740_at	ZFP36L1	X79067	zinc finger protein 36, C3H type-like 1	butyrate response factor 1
2728	36046_at	ZNF363	AL050144	zinc finger protein 363	hypothetical protein
2729	32129_at	ZNF364	AL079314	zinc finger protein 364	hypothetical protein, similar to (U06944)
2730	41033_at	ZNF84	M27878	zinc finger protein 84 (HPF2)	PRAJA1 [Mus musculus]
2731	40610_at	ZFR	A1743507	zinc finger RNA binding protein	DNA binding protein
2732	39751_at	ZDHHC3	AF052182	zinc finger, DHHC domain containing 3	
2733	33912_at	ZMPSTE24	Y13834	zinc metalloproteinase (STE24 homolog, yeast)	larnesylated-proteins converting enzyme 1
2734	36521_at	DZIP1	AB023213	zinc-finger protein DZIP1	KIAA0996 protein
2735	35995_at	ZWINT	AF067656	ZW10 interactor	ZW10 interactor Zwiint
2736	706_at		HG4582-HT4987		
2737	960_g_at		HG2463-HT2559		
2738	956_at		HG1980-HT2023		
2739	955_at		HG1862-HT1897		
2740	324_f_at		HG1515-HT1515		

Fig. 21

	A	B	C	D	E
2741	327_f_at		HG1800-HT1823		
2742	333_s_at		HG2639-HT2735		
2743	1840_g_at		HG1112-HT1112		
2744	1664_at		HG3543-HT3739		
2745	1624_at		HG2036-HT2090		
2746	1278_at		HG162-HT3165		
2747	1179_at		HG2855-HT2995		
2748	1180_g_at		HG2855-HT2995		
2749	32243_g_at		AL038340		
2750	311_s_at		HG3044-HT3742		
2751	297_g_at		HG4322-HT4592		
2752	296_at		HG4322-HT4592		
2753	1839_at		HG1112-HT1112		
2754	723_s_at		HG1322-HT5143		
2755	33300_at	dJ283E3.1	AL031282		guanine nucleotide binding protein (G protein), beta polypeptide 1
2756	41249_at	dJ283E3.1	AL031282		guanine nucleotide binding protein (G protein), beta polypeptide 1

Fig. 21